

SEQUENCE LISTING

<110> Dumas Milne Edwards, Jean Baptiste
Bougueleret, Lydie
Jobert, Severin

<120> FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS

<130> 78.US3.REG

<150> US 60/169,629

<151> 1999-12-08

<150> US 60/187,470

<151> 2000-03-06

<160> 482

<170> Patent.pm

<210> 1

<211> 2201

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 169..1692

<220>

<221> sig_peptide

<222> 169..249

<223> Von Heijne matrix

score 7.15265901862021

seq VLLLLLLRGMFS/SP

<400> 1

```

agatgtgaat agctccacta taccagcctc gtcttccttc cgggggacaa cgtgggtcag      60
ggcacagaga gatatttaat gtcaccctct tggggctttc atgggactcc ctctgccaca      120
ttttttggag gttgggaaag ttgctagagg cttcagaact ccagccta atg gat ccc      177
                                   Met Asp Pro
                                   -25
aaa ctc ggg aga atg gct gcg tcc ctg ctg gct gtg ctg ctg ctg ctg      225
Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val Leu Leu Leu Leu
                                   -20                                   -15                                   -10
ctg ctg gag cgc ggc atg ttc tcc tca ccc tcc ccg ccc ccg gcg ctg      273
Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro Pro Pro Ala Leu
                                   -5                                   1                                   5
tta gag aaa gtc ttc cag tac att gac ctc cat cag gat gaa ttt gtg      321
Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His Gln Asp Glu Phe Val
                                   10                                   15                                   20
cag acg ctg aag gag tgg gtg gcc atc gag agc gac tct gtc cag cct      369
Gln Thr Leu Lys Glu Trp Val Ala Ile Glu Ser Asp Ser Val Gln Pro
25                                   30                                   35                                   40

```

gtg cct cgc ttc aga caa gag ctc ttc aga atg atg gcc gtg gct gcg	417
Val Pro Arg Phe Arg Gln Glu Leu Phe Arg Met Met Ala Val Ala Ala	
45 50 55	
gac acg ctg cag cgc ctg ggg gcc cgt gtg gcc tcg gtg gac atg ggt	465
Asp Thr Leu Gln Arg Leu Gly Ala Arg Val Ala Ser Val Asp Met Gly	
60 65 70	
cct cag cag ctg ccc gat ggt cag agt ctt cca ata cct ccc gtc atc	513
Pro Gln Gln Leu Pro Asp Gly Gln Ser Leu Pro Ile Pro Pro Val Ile	
75 80 85	
ctg gcc gaa ctg ggg agc gat ccc acg aaa ggc acc gtg tgc ttc tac	561
Leu Ala Glu Leu Gly Ser Asp Pro Thr Lys Gly Thr Val Cys Phe Tyr	
90 95 100	
ggc cac ttg gac gtg cag cct gct gac cgg ggc gat ggg tgg ctc acg	609
Gly His Leu Asp Val Gln Pro Ala Asp Arg Gly Asp Gly Trp Leu Thr	
105 110 115 120	
gac ccc tat gtg ctg acg gag gta gac ggg aaa ctt tat gga cga gga	657
Asp Pro Tyr Val Leu Thr Glu Val Asp Gly Lys Leu Tyr Gly Arg Gly	
125 130 135	
gcg acc gac aac aaa ggc cct gtc ttg gct tgg atc aat gct gtg agc	705
Ala Thr Asp Asn Lys Gly Pro Val Leu Ala Trp Ile Asn Ala Val Ser	
140 145 150	
gcc ttc aga gcc ctg gag caa gat ctt cct gtg aat atc aaa ttc atc	753
Ala Phe Arg Ala Leu Glu Gln Asp Leu Pro Val Asn Ile Lys Phe Ile	
155 160 165	
att gag ggg atg gaa gag gct ggc tct gtt gcc ctg gag gaa ctt gtg	801
Ile Glu Gly Met Glu Glu Ala Gly Ser Val Ala Leu Glu Glu Leu Val	
170 175 180	
gaa aaa gaa aag gac cga ttc ttc tct ggt gtg gac tac att gta att	849
Glu Lys Glu Lys Asp Arg Phe Phe Ser Gly Val Asp Tyr Ile Val Ile	
185 190 195 200	
tca gat aac ctg tgg atc agc caa agg aag cca gca atc act tat gga	897
Ser Asp Asn Leu Trp Ile Ser Gln Arg Lys Pro Ala Ile Thr Tyr Gly	
205 210 215	
acc cgg ggg aac agc tac ttc atg gtg gag gtg aaa tgc aga gac cag	945
Thr Arg Gly Asn Ser Tyr Phe Met Val Glu Val Lys Cys Arg Asp Gln	
220 225 230	
gat ttt cac tca gga acc ttt ggt ggc atc ctt cat gaa cca atg gct	993
Asp Phe His Ser Gly Thr Phe Gly Gly Ile Leu His Glu Pro Met Ala	
235 240 245	
gat ctg gtt gct ctt ctc ggt agc ctg gta gac tcg tct ggt cat atc	1041
Asp Leu Val Ala Leu Leu Gly Ser Leu Val Asp Ser Ser Gly His Ile	
250 255 260	
ctg gtc cct gga atc tat gat gaa gtg gtt cct ctt aca gaa gag gaa	1089
Leu Val Pro Gly Ile Tyr Asp Glu Val Val Pro Leu Thr Glu Glu Glu	
265 270 275 280	
ata aat aca tac aaa gcc atc cat cta gac cta gaa gaa tac cgg aat	1137
Ile Asn Thr Tyr Lys Ala Ile His Leu Asp Leu Glu Glu Tyr Arg Asn	
285 290 295	
agc agc cgg gtt gag aaa ttt ctg ttc gat act aag gag gag att cta	1185
Ser Ser Arg Val Glu Lys Phe Leu Phe Asp Thr Lys Glu Glu Ile Leu	
300 305 310	
atg cac ctc tgg agg tac cca tct ctt tct att cat ggg atc gag ggc	1233
Met His Leu Trp Arg Tyr Pro Ser Leu Ser Ile His Gly Ile Glu Gly	
315 320 325	

gcg ttt gat gag cct gga act aaa aca gtc ata cct ggc cga gtt ata	1281
Ala Phe Asp Glu Pro Gly Thr Lys Thr Val Ile Pro Gly Arg Val Ile	
330 335 340	
gga aaa ttt tca atc cgt cta gtc cct cac atg aat gtg tct gcg gtg	1329
Gly Lys Phe Ser Ile Arg Leu Val Pro His Met Asn Val Ser Ala Val	
345 350 355 360	
gaa aaa cag gtg aca cga cat ctt gaa gat gtg ttc tcc aaa aga aat	1377
Glu Lys Gln Val Thr Arg His Leu Glu Asp Val Phe Ser Lys Arg Asn	
365 370 375	
agt tcc aac aag atg gtt gtt tcc atg act cta gga cta cac ccg tgg	1425
Ser Ser Asn Lys Met Val Val Ser Met Thr Leu Gly Leu His Pro Trp	
380 385 390	
att gca aat att gat gac acc cag tat ctc gca gca aaa aga gcg atc	1473
Ile Ala Asn Ile Asp Asp Thr Gln Tyr Leu Ala Ala Lys Arg Ala Ile	
395 400 405	
aga aca gtg ttt gga aca gaa cca gat atg atc cgg gat gga tcc acc	1521
Arg Thr Val Phe Gly Thr Glu Pro Asp Met Ile Arg Asp Gly Ser Thr	
410 415 420	
att cca att gcc aaa atg ttc cag gag atc gtc cac aag agc gtg gtg	1569
Ile Pro Ile Ala Lys Met Phe Gln Glu Ile Val His Lys Ser Val Val	
425 430 435 440	
cta att ccg ctg gga gct gtt gat gat gga gaa cat tcg cag aat gag	1617
Leu Ile Pro Leu Gly Ala Val Asp Asp Gly Glu His Ser Gln Asn Glu	
445 450 455	
aaa atc aac agg tgg aac tac ata gag gga acc aaa tta ttt gct gcc	1665
Lys Ile Asn Arg Trp Asn Tyr Ile Glu Gly Thr Lys Leu Phe Ala Ala	
460 465 470	
ttt ttc tta gag atg gcc cag ctc cat taatcacaag aaccttctag	1712
Phe Phe Leu Glu Met Ala Gln Leu His	
475 480	
tctgatctga tccactgaca gattcacctc cccacatcc ctagacaggg atggaatgta	1772
aatatccaga gaatttgggt ctagtatagt acattttccc ttccatttaa aatgtcttgg	1832
gatatctgga tcagtaataa aatatttcaa aggcacagat gttggaaatg gtttaaggct	1892
ccccactgca caccttcctc aagtcatagc tgcttgacgc aacttgattt cccaagtcc	1952
tgtgcaatag cccaggatt ggattccttc caacctttta gcatatctcc aaccttgcaa	2012
tttgattggc ataatcactc cagtttgctt tctaggtcct caagtgctcg tgacacataa	2072
tcattccatc caatgatcgc ctttgcttta ccactcttcc cttttatctt attaataaaa	2132
atgttggtct ccaccactga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaagaaaaaa	2192
aaaaaaaaa	2201

<210> 2

<211> 1631

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 148..1140

<220>

<221> sig_peptide

<222> 148..240

<223> Von Heijne matrix

score 10.0910253445132

seq LVLLLVTRSPVNA/CL

<400> 2

```

gtctgctgcc gccattgtgc ggcgctggtc ccctcagagg gttcctgctg ctgccggtgc      60
cttgaccct cccctcgtct tctcgttcta ctgccccagg agcccggcgg gtccgggact      120
cccgtccgtg ccggtgcggg cgccggc atg tgg ctg tgg gag gac cag ggc ggc      174
                               Met Trp Leu Trp Glu Asp Gln Gly Gly
                               -30                               -25
ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg      222
Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Val Thr
                               -20                               -15                               -10
cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta      270
Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu
                               -5                               1                               5                               10
ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag      318
Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln
                               15                               20                               25
gtg ctc aag ccc ccg gac cgc att tct gcc atc gcc cac cgt ggc ggc      366
Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly
                               30                               35                               40
agc cac gac gcg ccc gag aac acg ctg gcg gcc att ccg cag gca gct      414
Ser His Asp Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala
                               45                               50                               55
aag aat gga gca aca ggc gtg gag ttg gac att gag ttt act tct gac      462
Lys Asn Gly Ala Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp
                               60                               65                               70
ggg att cct gtc tta atg cac gat aac aca gta gat agg acg act gat      510
Gly Ile Pro Val Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp
75                               80                               85                               90
ggg act ggg cga ttg tgt gat ttg aca ttt gaa caa att agg aag ctg      558
Gly Thr Gly Arg Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu
                               95                               100                               105
aat cct gca gca aac cac aga ctc agg aat gat ttc cct gat gaa aag      606
Asn Pro Ala Ala Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys
                               110                               115                               120
atc cct acc cta atg gaa gct gtt gca gag tgc cta aac cat aac ctc      654
Ile Pro Thr Leu Met Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu
                               125                               130                               135
aca atc ttc ttt gat gtc aaa ggc cat gca cac aag gct act gag gct      702
Thr Ile Phe Phe Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala
140                               145                               150
cta aag aaa atg tat atg gaa ttt cct caa ctg tat aat aat agt gtg      750
Leu Lys Lys Met Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val
155                               160                               165                               170
gtc tgt tct ttc ttg cca gaa gtt atc tac aag atg aga caa aca gat      798
Val Cys Ser Phe Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp
                               175                               180                               185
cgg gat gta ata aca gca tta act cac aga cct tgg agc cta agc cat      846
Arg Asp Val Ile Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His
                               190                               195                               200
aca gga gat ggg aaa cca cgc tat gat act ttc tgg aaa cat ttt ata      894
Thr Gly Asp Gly Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile
205                               210                               215
ttt gtt atg atg gac att ttg ctc gat tgg agc atg cat aat atc ttg      942

```


Phe	Val	Met	Met	Asp	Ile	Leu	Leu	Asp	Trp	Ser	Met	His	Asn	Ile	Leu		
220						225					230						
tgg	tac	ctg	tgt	gga	att	tca	gct	ttc	ctc	atg	caa	aag	gat	ttt	gta	990	
Trp	Tyr	Leu	Cys	Gly	Ile	Ser	Ala	Phe	Leu	Met	Gln	Lys	Asp	Phe	Val		
235					240					245					250		
tcc	ccg	gcc	tac	ttg	aag	aag	tgg	tca	gct	aaa	gga	atc	cag	gtt	gtt	1038	
Ser	Pro	Ala	Tyr	Leu	Lys	Lys	Trp	Ser	Ala	Lys	Gly	Ile	Gln	Val	Val		
				255					260					265			
ggt	tgg	act	gtt	aat	acc	ttt	gat	gaa	aag	agt	tac	tac	gaa	tcc	cat	1086	
Gly	Trp	Thr	Val	Asn	Thr	Phe	Asp	Glu	Lys	Ser	Tyr	Tyr	Glu	Ser	His		
				270				275					280				
ctt	ggt	tcc	agc	tat	atc	act	gac	agc	atg	gta	gaa	gac	tgc	gaa	cct	1134	
Leu	Gly	Ser	Ser	Tyr	Ile	Thr	Asp	Ser	Met	Val	Glu	Asp	Cys	Glu	Pro		
		285				290					295						
cac	ttc	tagactttca	cggtgggacg	aaacgggttc	agaaactgcc	aggggcctca										1190	
His	Phe																
300																	
tacagggata	tcaaaatacc	ctttgtgcta	gcccaggccc	tggggaatca	ggtgactcac											1250	
acaaatgcaa	tagttggtca	ctgcattttt	acctgaacca	aagctaaacc	cggtgttgcc											1310	
accatgcacc	atggcatgcc	agagttcaac	actgttgctc	ttgaaaatct	ggggtctgaa											1370	
aaaacgcaca	agagcccctg	ccctgcccta	gctgaggcac	acagggagac	ccagtggagga											1430	
taagcacaga	ttgaattgta	caatttgcag	atgcagatgt	aaatgcatgg	gacatgcatg											1490	
ataactcaga	gttgacattt	taaaacttgc	cacacttatt	tcaaataatt	gtactcagct											1550	
atgttaacat	gtactgtaga	catcaaactt	gtggccatac	taataaaaatt	attaaaagga											1610	
gcacaaaaaa	aaaaaaaaaa	a														1631	

<210> 3

<211> 1245

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 85..906

<220>

<221> sig_peptide

<222> 85..135

<223> Von Heijne matrix

score 3.86022363031904

seq GFVAALVAGGVAG/VS

<400> 3

aaaacatggc	ggcgcccagc	gcgcgaggac	gtgatccgct	tctgctccgg	cttggattgt	60	
agccttgacg	aggtctgagc	gacc	atg	gac	cgg	ccg	ggg
			ttc	gtg	gca	gcg	111

Met Asp Arg Pro Gly Phe Val Ala Ala

-15

-10

ctg	gtg	gct	ggt	ggg	gta	gca	ggt	gtt	tct	gtt	gac	ttg	ata	tta	ttt	159	
Leu	Val	Ala	Gly	Gly	Val	Ala	Gly	Val	Ser	Val	Asp	Leu	Ile	Leu	Phe		

-5

1

5

cct	ctg	gat	acc	att	aaa	acc	agg	ctg	cag	agt	ccc	caa	gga	ttt	agt	207	
Pro	Leu	Asp	Thr	Ile	Lys	Thr	Arg	Leu	Gln	Ser	Pro	Gln	Gly	Phe	Ser		

10

15

20

aag	gct	ggt	ggt	ttt	cat	gga	ata	tat	gct	ggc	gtt	cct	tct	gct	gct	255	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

Lys	Ala	Gly	Gly	Phe	His	Gly	Ile	Tyr	Ala	Gly	Val	Pro	Ser	Ala	Ala		
25					30					35					40		
att	gga	tcc	ttt	cct	aat	gct	gct	gca	ttt	ttt	atc	acc	tat	gaa	tat	303	
Ile	Gly	Ser	Phe	Pro	Asn	Ala	Ala	Ala	Phe	Phe	Ile	Thr	Tyr	Glu	Tyr		
				45					50					55			
gtg	aag	tgg	ttt	ttg	cat	gct	gat	tca	tct	tca	tat	ttg	aca	cct	atg	351	
Val	Lys	Trp	Phe	Leu	His	Ala	Asp	Ser	Ser	Ser	Tyr	Leu	Thr	Pro	Met		
			60					65					70				
aaa	cat	atg	ttg	gct	gcc	tct	gct	gga	gaa	gtg	gtt	gcc	tgc	ctg	att	399	
Lys	His	Met	Leu	Ala	Ala	Ser	Ala	Gly	Glu	Val	Val	Ala	Cys	Leu	Ile		
			75				80					85					
cga	gtt	cca	tct	gaa	gtg	gtt	aag	cag	agg	gca	cag	gta	tct	gct	tct	447	
Arg	Val	Pro	Ser	Glu	Val	Val	Lys	Gln	Arg	Ala	Gln	Val	Ser	Ala	Ser		
	90					95				100							
aca	aga	aca	ttt	cag	att	ttc	tct	aac	atc	tta	tat	gaa	gag	ggg	atc	495	
Thr	Arg	Thr	Phe	Gln	Ile	Phe	Ser	Asn	Ile	Leu	Tyr	Glu	Glu	Gly	Ile		
	105			110				115						120			
caa	ggg	ttg	tat	cga	ggc	tat	aaa	agc	aca	ggt	tta	aga	gag	att	cct	543	
Gln	Gly	Leu	Tyr	Arg	Gly	Tyr	Lys	Ser	Thr	Val	Leu	Arg	Glu	Ile	Pro		
			125					130					135				
ttt	tct	ttg	gtc	cag	ttt	ccc	tta	tgg	gag	tcc	tta	aaa	gcc	ctc	tgg	591	
Phe	Ser	Leu	Val	Gln	Phe	Pro	Leu	Trp	Glu	Ser	Leu	Lys	Ala	Leu	Trp		
		140					145				150						
tcc	tgg	agg	cag	gat	cat	gtg	gtg	gat	tct	tgg	cag	tca	gca	gtc	tgt	639	
Ser	Trp	Arg	Gln	Asp	His	Val	Val	Asp	Ser	Trp	Gln	Ser	Ala	Val	Cys		
		155				160					165						
gga	gct	ttt	gca	ggg	gga	ttt	gcc	gct	gca	gtc	acc	acc	cct	cta	gac	687	
Gly	Ala	Phe	Ala	Gly	Gly	Phe	Ala	Ala	Ala	Val	Thr	Thr	Pro	Leu	Asp		
	170				175					180							
gtg	gca	aag	aca	aga	att	atg	ctg	gca	aag	gct	ggc	tcc	agc	act	gct	735	
Val	Ala	Lys	Thr	Arg	Ile	Met	Leu	Ala	Lys	Ala	Gly	Ser	Ser	Thr	Ala		
	185			190				195						200			
gat	ggg	aat	gtg	ctc	tct	gtc	ctg	cat	ggg	gtc	tgg	cgg	tca	cag	ggg	783	
Asp	Gly	Asn	Val	Leu	Ser	Val	Leu	His	Gly	Val	Trp	Arg	Ser	Gln	Gly		
			205					210				215					
ctg	gca	gga	tta	ttt	gca	ggg	gtc	ttc	cct	cga	atg	gca	gcc	atc	agt	831	
Leu	Ala	Gly	Leu	Phe	Ala	Gly	Val	Phe	Pro	Arg	Met	Ala	Ala	Ile	Ser		
		220				225					230						
ctg	gga	ggg	ttc	atc	ttt	ctg	ggg	gct	tat	gac	cga	acg	cac	agc	ttg	879	
Leu	Gly	Gly	Phe	Ile	Phe	Leu	Gly	Ala	Tyr	Asp	Arg	Thr	His	Ser	Leu		
		235				240					245						
ctg	ttg	gaa	gtt	ggc	aga	aag	agt	cct	tgaagcagag	acaagcctca						926	
Leu	Leu	Glu	Val	Gly	Arg	Lys	Ser	Pro									
	250					255											
cctccacttc	tgtaagaga	ggggcctgca	gtgcaaacc	tcttcgctg	agcagctgtc											986	
tgaactatag	gccccagtgc	tgaagaccag	ttgtgctaag	ataccggcat	ggagattgtg											1046	
ccatccgtgg	tataggctgg	ctggtatgaa	gtcattggcc	tgtatgccag	agagctaaga											1106	
gaagaaaacg	gggtctgtgg	cggtactctg	aacaatttcc	tcagaacctc	ttaataaata											1166	
agtttggtta	tgctgagaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa											1226	
agaaaaaaaa	aaaaaaaaaa															1245	

<210> 4
 <211> 1623
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 31..1248

<220>

<221> sig_peptide

<222> 31..135

<223> Von Heijne matrix

score 6.3770152988307

seq TLLLFAAPFGLLG/EK

<400> 4

aac	ctt	ctt	cc	gtc	gg	ct	gaa	ttg	cgg	cc	atg	cgc	ggc	tct	gtg	gag	tgc	acc	54
											Met	Arg	Gly	Ser	Val	Glu	Cys	Thr	
											-35								-30
tgg	ggt	tgg	ggg	cac	tgt	gcc	ccc	agc	ccc	ctg	ctc	ctt	tgg	act	cta				102
Trp	Gly	Trp	Gly	His	Cys	Ala	Pro	Ser	Pro	Leu	Leu	Leu	Trp	Thr	Leu				
			-25				-20												
ctt	ctg	ttt	gca	gcc	cca	ttt	ggc	ctg	ctg	ggg	gag	aag	acc	cgc	cag				150
Leu	Leu	Phe	Ala	Ala	Pro	Phe	Gly	Leu	Leu	Gly	Glu	Lys	Thr	Arg	Gln				
		-10				-5				1					5				
gtg	tct	ctg	gag	gtc	atc	cct	aac	tgg	ctg	ggc	ccc	ctg	cag	aac	ctg				198
Val	Ser	Leu	Glu	Val	Ile	Pro	Asn	Trp	Leu	Gly	Pro	Leu	Gln	Asn	Leu				
			10					15					20						
ctt	cat	ata	cgg	gca	gtg	ggc	acc	aat	tcc	aca	ctg	cac	tat	gtg	tgg				246
Leu	His	Ile	Arg	Ala	Val	Gly	Thr	Asn	Ser	Thr	Leu	His	Tyr	Val	Trp				
			25				30						35						
agc	agc	ctg	ggg	cct	ctg	gca	gtg	gta	atg	gtg	gcc	acc	aac	acc	ccc				294
Ser	Ser	Leu	Gly	Pro	Leu	Ala	Val	Val	Met	Val	Ala	Thr	Asn	Thr	Pro				
		40				45					50								
cac	agc	acc	ctg	agc	gtc	aac	tgg	agc	ctc	ctg	cta	tcc	cct	gag	ccc				342
His	Ser	Thr	Leu	Ser	Val	Asn	Trp	Ser	Leu	Leu	Leu	Ser	Pro	Glu	Pro				
		55				60				65									
gat	ggg	ggc	ctg	atg	gtg	ctc	cct	aag	gac	agc	att	cag	ttt	tct	tct				390
Asp	Gly	Gly	Leu	Met	Val	Leu	Pro	Lys	Asp	Ser	Ile	Gln	Phe	Ser	Ser				
		70			75				80					85					
gcc	ctt	ggt	ttt	acc	agg	ctg	ctt	gag	ttt	gac	agc	acc	aac	gtg	tcc				438
Ala	Leu	Val	Phe	Thr	Arg	Leu	Leu	Glu	Phe	Asp	Ser	Thr	Asn	Val	Ser				
			90					95					100						
gat	acg	gca	gca	aag	cct	ttg	gga	aga	cca	tat	cct	cca	tac	tcc	ttg				486
Asp	Thr	Ala	Ala	Lys	Pro	Leu	Gly	Arg	Pro	Tyr	Pro	Pro	Tyr	Ser	Leu				
			105				110						115						
gcc	gat	ttc	tct	tgg	aac	aac	atc	act	gat	tca	ttg	gat	cct	gcc	acc				534
Ala	Asp	Phe	Ser	Trp	Asn	Asn	Ile	Thr	Asp	Ser	Leu	Asp	Pro	Ala	Thr				
		120				125						130							
ctg	agt	gcc	aca	ttt	caa	ggc	cac	ccc	atg	aac	gac	cct	acc	agg	act				582
Leu	Ser	Ala	Thr	Phe	Gln	Gly	His	Pro	Met	Asn	Asp	Pro	Thr	Arg	Thr				
		135				140					145								
ttt	gcc	aat	ggc	agc	ctg	gcc	ttc	agg	gtc	cag	gcc	ttt	tcc	agg	tcc				630
Phe	Ala	Asn	Gly	Ser	Leu	Ala	Phe	Arg	Val	Gln	Ala	Phe	Ser	Arg	Ser				
		150			155					160					165				
agc	cga	cca	gcc	caa	ccc	cct	cgc	ctc	ctg	cac	aca	gca	gac	acc	tgt				678

Ser	Arg	Pro	Ala	Gln	Pro	Pro	Arg	Leu	Leu	His	Thr	Ala	Asp	Thr	Cys	
				170					175					180		
cag	cta	gag	gtg	gcc	ctg	att	gga	gcc	tct	ccc	cgg	gga	aac	cgt	tcc	726
Gln	Leu	Glu	Val	Ala	Leu	Ile	Gly	Ala	Ser	Pro	Arg	Gly	Asn	Arg	Ser	
				185				190					195			
ctg	ttt	ggg	ctg	gag	gta	gcc	aca	ttg	ggc	cag	ggc	cct	gac	tgc	ccc	774
Leu	Phe	Gly	Leu	Glu	Val	Ala	Thr	Leu	Gly	Gln	Gly	Pro	Asp	Cys	Pro	
		200					205					210				
tca	atg	cag	gag	cag	cac	tcc	atc	gac	gat	gaa	tat	gca	ccg	gcc	gtc	822
Ser	Met	Gln	Glu	Gln	His	Ser	Ile	Asp	Asp	Glu	Tyr	Ala	Pro	Ala	Val	
	215					220					225					
ttc	cag	ttg	gac	cag	cta	ctg	tgg	ggc	tcc	ctc	cca	tca	ggc	ttt	gca	870
Phe	Gln	Leu	Asp	Gln	Leu	Leu	Trp	Gly	Ser	Leu	Pro	Ser	Gly	Phe	Ala	
230					235					240					245	
cag	tgg	cga	cca	gtg	gct	tac	tcc	cag	aag	ccg	ggg	ggc	cga	gaa	tca	918
Gln	Trp	Arg	Pro	Val	Ala	Tyr	Ser	Gln	Lys	Pro	Gly	Gly	Arg	Glu	Ser	
				250				255					260			
gcc	ctg	ccc	tgc	caa	gct	tcc	cct	ctt	cat	cct	gcc	tta	gca	tac	tct	966
Ala	Leu	Pro	Cys	Gln	Ala	Ser	Pro	Leu	His	Pro	Ala	Leu	Ala	Tyr	Ser	
			265				270					275				
ctt	ccc	cag	tca	ccc	att	gtc	cga	gcc	ttc	ttt	ggg	tcc	cag	aat	aac	1014
Leu	Pro	Gln	Ser	Pro	Ile	Val	Arg	Ala	Phe	Phe	Gly	Ser	Gln	Asn	Asn	
		280				285					290					
ttc	tgt	gcc	ttc	aat	ctg	acg	ttc	ggg	gct	tcc	aca	ggc	cct	ggc	tat	1062
Phe	Cys	Ala	Phe	Asn	Leu	Thr	Phe	Gly	Ala	Ser	Thr	Gly	Pro	Gly	Tyr	
	295				300						305					
tgg	gac	caa	cac	tac	ctc	agc	tgg	tcg	atg	ctc	ctg	ggg	gtg	ggc	ttc	1110
Trp	Asp	Gln	His	Tyr	Leu	Ser	Trp	Ser	Met	Leu	Leu	Gly	Val	Gly	Phe	
310					315					320					325	
cct	cca	gtg	gac	ggc	ttg	tcc	cca	cta	gtc	ctg	ggc	atc	atg	gca	gtg	1158
Pro	Pro	Val	Asp	Gly	Leu	Ser	Pro	Leu	Val	Leu	Gly	Ile	Met	Ala	Val	
				330				335					340			
gcc	ctg	ggg	gcc	cca	ggg	ctc	atg	ctg	cta	ggg	ggc	ggc	ttg	gtt	ctg	1206
Ala	Leu	Gly	Ala	Pro	Gly	Leu	Met	Leu	Leu	Gly	Gly	Gly	Leu	Val	Leu	
			345			350						355				
ctg	ctg	cac	cac	aag	aag	tac	tca	gag	tac	cag	tcc	ata	aat			1248
Leu	Leu	His	His	Lys	Lys	Tyr	Ser	Glu	Tyr	Gln	Ser	Ile	Asn			
		360				365					370					
taaggcccg	c	tctctggagg	gaaggacatt	actgaacctg	tcttgctgtg	cctcgaaact										1308
ctggagggtg	gagcatcaag	ttccagcccc	cttcactccc	ccatcttgct	tttctgtgga											1368
acctcagagg	ccagcctcga	cttcctggag	acccccaggt	ggggcttcct	tcatactttg											1428
ttgggggact	ttggaggcgg	gcaggggaca	gggctattga	taagggtcccc	ttggtgttgc											1488
cttcttgcat	ctccacacat	ttcccttga	tgggacttgc	aggcctaaat	gagaggcatt											1548
ctgactggtt	ggctgccctg	gaaggcaaga	aaatagattt	atTTTTTTTT	cacagggcaa											1608
aaaaaaaaa	aaaaa															1623

<210> 5
 <211> 1454
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 72..143

```

<220>
<221> sig_peptide
<222> 72..119
<223> Von Heijne matrix
      score 5.68931280801877
      seq LGMLLGLLMAACT/PS

<400> 5
gtgtctgcc ctcggctgcc ggaggccgaa ggtccctgac tatggctccc cagagcctgc      60
cttcatctag g atg gct cct ctg ggc atg ctg ctt ggg ctg ctg atg gcc      110
          Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala
          -15 -10 -5
gcc tgc aca cct tct gcc tca gtc atc aga acc tgaaggagtt tgcctgacc      163
Ala Cys Thr Pro Ser Ala Ser Val Ile Arg Thr
          1 5
aaccagaga agagcagcac caaagaaacg gagagaaaag aaaccaaagc cgaggaggag      223
ctggatgccg aagtcctgga ggtgttccac ccgacgcatg agtggcaggc ccttcagcca      283
gggcaggctg tccctgcagg atcccacgta cggctgaatc ttcagactgg ggaaagagag      343
gcaaaactcc aatatgagga caagttccga aataatttga aaggcaaaaag gctggatatc      403
aacaccaaca cctacacatc tcaggatctc aagagtgcac tggcaaaatt caaggagggg      463
gcagagatgg agagttcaaa ggaagacaag gcaaggcagg ctgaggtaaa gcggctcttc      523
cgccccattg aggaactgaa gaaagacttt gatgagctga atgttgtcat tgagactgac      583
atgcagatca tggtagcggt gatcaacaag ttcaatagtt ccagctccag tttggaagag      643
aagattgctg cgctctttga tcttgaatat tatgtccatc agatggacaa tgcgcaggac      703
ctgctttcct ttggtggtct tcaagtgggt atcaatgggc tgaacagcac agagcccctc      763
gtgaaggagt atgctgcggt tgtgctgggc gctgcctttt ccagcaacct caaggtccag      823
gtggaggcca tcgaaggggg agccctgcag aagctgctgg tcatcctggc cacggagcag      883
ccgctcactg caaagggagg tgctcaccgt gcgctgggtc acactgctct acgacctggt      943
cacggagaag atgttcgccg aggaggaggc tgagctgacc caggagatgt ccccagagaa     1003
gctgcagcag tatcgccagg tacacctcct gccakgcctg tgggaacagg gctggtgcga     1063
gatcacggcc cacctcctgg cgctgcccgga gcatgatgcc ygtgagaagg tgctgcwgac     1123
actgggcgtc ctctgacca cctgccggga ccgctaccgt caggaccccc agctcggcag     1183
gacactggcc agcctgcagg ctgagtacca ggtgctggcc agcctggagc tgcaggatgg     1243
tgaggacgag ggctacttcc aggagctgct gggctctgtc aacagcttgc tgaaggagct     1303
gagatgaggc cccacaccag gactggactg ggatgccgct agtgaggctg aggggtgcca     1363
gcgtgggtgg gcttctcagg caggaggaca tcttggcagt gctggcttgg ccattaaatg     1423
gaaacctgaa ggccaaaaaa aaaaaaaaaa a                                     1454

<210> 6
<211> 1639
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 111..1154

<220>
<221> sig_peptide
<222> 111..197
<223> Von Heijne matrix
      score 4.68065944212013
      seq LLGPLMAACFTFC/LS

```

<400> 6

agacggtcgc	cgccgcgttt	gcgccagggg	agctggtcgc	cgccgcggcc	gcctggaatt	60
gtgggagttg	tgtctgccac	tcggctgccg	gaggccgaag	gtccctgact	atg gct	116
					Met Ala	
ccc cag agc ctg cct tca tct agg atg gct cct ctg ggc atg ctg ctt						164
Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met Leu Leu						
	-25		-20		-15	
ggg ccg ctg atg gcc gcc tgc ttc acc ttc tgc ctc agt cat cag aac						212
Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His Gln Asn						
	-10		-5		1	5
ctg aag gag ttt gcc ctg acc aac cca gag aag agc agc acc aaa gaa						260
Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr Lys Glu						
	10		15		20	
aca gag aga aaa gaa acc aaa gcc gag gag gag ctg gat gcc gaa gtc						308
Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala Glu Val						
	25		30		35	
ctg gag gtg ttc cac ccg acg cat gag tgg cag gcc ctt cag cca ggg						356
Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln Pro Gly						
	40		45		50	
cag gct gtc cct gca gga tcc cac gta cgg ctg aat ctt cag act ggg						404
Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln Thr Gly						
	55		60		65	
gaa aga gag gca aaa ctc caa tat gag gac aag ttc cga aat aat ttg						452
Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn Asn Leu						
	70		75		80	85
aaa ggc aaa agg ctg gat atc aac acc aac acc tac aca tct cag gat						500
Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp						
	90		95		100	
ctc aag agt gca ctg gca aaa ttc aag gag ggg gca gag atg gag agt						548
Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser						
	105		110		115	
tca aag gaa gac aag gca agg cag gct gag gta aag cgg ctc ttc cgc						596
Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu Phe Arg						
	120		125		130	
ccc att gag gaa ctg aag aaa gac ttt gat gag ctg aat gtt gtc att						644
Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val Val Ile						
	135		140		145	
gag act gac atg cag atc atg gta cgg ctg atc aac aag ttc aat agt						692
Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe Asn Ser						
	150		155		160	165
tcc agc tcc agt ttg gaa gag aag att gct gcg ctc ttt gat ctt gaa						740
Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp Leu Glu						
	170		175		180	
tat tat gtc cat cag atg gac aat gcg cag gac ctg ctt tcc ttt ggt						788
Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser Phe Gly						
	185		190		195	
ggt ctt caa gtg gtg atc aat ggg ctg aac agc aca gag ccc ctc gtg						836
Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro Leu Val						
	200		205		210	
aag gag tat gct gcg ttt gtg ctg ggc gct gcc ttt tcc agc aac ccc						884
Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser Ser Asn Pro						
	215		220		225	
aag gtc cag gtg gag gcc atc gaa ggg gga gcc ctg cag aag ctg ctg						932

Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln Lys Leu Leu
 230 235 240 245
 gtc atc ctg gcc acg gag cag ccg ctc act gca aag aag aag gtc ctg 980
 Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys Lys Val Leu
 250 255 260
 ttt gca ctg tgc tcc ctg ctg cgc cac ttc ccc tat gcc cag cgg cag 1028
 Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala Gln Arg Gln
 265 270 275
 ttc ctg aag ctc ggg ggg ctg cag gtc ctg agg acc ctg gtg cag gag 1076
 Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu Val Gln Glu
 280 285 290
 aag ggc acg gag gtg ctc gcc gtg cgc gtg gtc aca ctg ctc tac gac 1124
 Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu Leu Tyr Asp
 295 300 305
 ctg gtc acg gag aag atg ttc gcc gag gag taggctgagc tgaccagga 1174
 Leu Val Thr Glu Lys Met Phe Ala Glu Glu
 310 315
 gatgtcccca gagaagctgc agcagtatcg ccagggtacac ctccctgccag gcctgtggga 1234
 acagggctgg tgcgagatca cggcccacct cctggcgctg cccgagcatg atgcccgta 1294
 gaagggtctg cagacactgg gcgtccctcct gaccacctgc cgggaccgct accgtcagga 1354
 cccccagctc ggcaggacac tggccagcct gcaggctgag taccaggtgc tggccagcct 1414
 ggagctgcag gatggtgagg acgagggcta cttccaggag ctgctgggct ctgtcaacag 1474
 cttgctgaag gagctgagat gaggcccccac accaggactg gactgggatg ccgctagtga 1534
 ggctgagggg tgccagcgtg ggtgggcttc tcaggcagga ggacatcttg gcagtgctgg 1594
 cttggccatt aaatggaaac ctgaaggcaa aaaaaaaaaa aaaaa 1639

 <210> 7
 <211> 1768
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 66..1256

 <220>
 <221> sig_peptide
 <222> 66..173
 <223> Von Heijne matrix
 score 4.89555877630516
 seq LLLLRNLDAALRA/LQ

 <400> 7
 agaggaggtg gcggtggtgg ccctcgctg tggccccgt gctgcttgca ctggaactcg 60
 tcgcc atg gag gag ctc cag gag cct ctg aga gga cag ctc cgg ctc tgc 110
 Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys
 -35 -30 -25
 ttc acg caa gct gcc cgg act agc ctc tta ctg ctc agg ctc aac gac 158
 Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp
 -20 -15 -10
 gct gcc ctg cgg gcg ctg caa gag tgt cag cgg caa cag gta cgg ccg 206
 Ala Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro
 -5 1 5 10
 gtg att gct ttc caa ggc cac cga ggg tat ctg aga ctc cca ggc cct 254

Val	Ile	Ala	Phe	Gln	Gly	His	Arg	Gly	Tyr	Leu	Arg	Leu	Pro	Gly	Pro	
		15						20					25			
ggg	tgg	tcc	tgc	ctc	ttc	tcc	ttc	ata	gtg	tcc	cag	tgt	tgt	cag	gag	302
Gly	Trp	Ser	Cys	Leu	Phe	Ser	Phe	Ile	Val	Ser	Gln	Cys	Cys	Gln	Glu	
		30					35					40				
ggc	gct	ggg	ggg	agc	ttg	gac	ctt	gtg	tgc	caa	cgc	ttc	ctc	agg	tct	350
Gly	Ala	Gly	Gly	Ser	Leu	Asp	Leu	Val	Cys	Gln	Arg	Phe	Leu	Arg	Ser	
	45					50				55						
ggg	cct	aac	agc	ctc	cac	tgc	ctg	ggc	tca	ctc	agg	gag	cgc	ctc	att	398
Gly	Pro	Asn	Ser	Leu	His	Cys	Leu	Gly	Ser	Leu	Arg	Glu	Arg	Leu	Ile	
	60				65					70					75	
att	tgg	gca	gcc	atg	gat	tct	atc	cca	gcc	cca	tca	tca	ggt	cag	gga	446
Ile	Trp	Ala	Ala	Met	Asp	Ser	Ile	Pro	Ala	Pro	Ser	Ser	Val	Gln	Gly	
			80						85					90		
cac	aac	ctg	act	gaa	gat	gcc	aga	cat	cct	gag	agt	tgg	cag	aac	aca	494
His	Asn	Leu	Thr	Glu	Asp	Ala	Arg	His	Pro	Glu	Ser	Trp	Gln	Asn	Thr	
		95						100					105			
gga	ggc	tat	tct	gaa	gga	gat	gca	gta	tca	cag	cca	cag	atg	gca	cta	542
Gly	Gly	Tyr	Ser	Glu	Gly	Asp	Ala	Val	Ser	Gln	Pro	Gln	Met	Ala	Leu	
		110					115					120				
gag	gag	gtg	tca	gtg	tca	gat	cca	ctg	gca	agc	aac	caa	gga	cag	tca	590
Glu	Glu	Val	Ser	Val	Ser	Asp	Pro	Leu	Ala	Ser	Asn	Gln	Gly	Gln	Ser	
		125				130					135					
ctc	cca	gga	tcc	tca	agg	gag	cac	atg	gca	cag	tgg	gaa	gtg	aga	agc	638
Leu	Pro	Gly	Ser	Ser	Arg	Glu	His	Met	Ala	Gln	Trp	Glu	Val	Arg	Ser	
	140				145					150					155	
cag	acc	cat	ggt	cca	aac	aga	gaa	cct	ggt	cag	gca	ctg	cct	tcc	tct	686
Gln	Thr	His	Val	Pro	Asn	Arg	Glu	Pro	Val	Gln	Ala	Leu	Pro	Ser	Ser	
			160						165					170		
gcc	agc	cgg	aaa	cgt	ctg	gac	aag	aaa	cgt	tca	gtg	cct	gta	gcc	act	734
Ala	Ser	Arg	Lys	Arg	Leu	Asp	Lys	Lys	Arg	Ser	Val	Pro	Val	Ala	Thr	
		175						180					185			
gta	gaa	ctg	gaa	gaa	aag	agg	ttc	aga	act	ctg	cct	tta	gtg	cca	agc	782
Val	Glu	Leu	Glu	Glu	Lys	Arg	Phe	Arg	Thr	Leu	Pro	Leu	Val	Pro	Ser	
		190					195					200				
ccc	cta	caa	ggc	ctg	acc	aat	cag	gat	tta	caa	gag	gga	gaa	gat	tgg	830
Pro	Leu	Gln	Gly	Leu	Thr	Asn	Gln	Asp	Leu	Gln	Glu	Gly	Glu	Asp	Trp	
	205					210					215					
gag	caa	gaa	gat	gag	gac	atg	gac	ccc	aga	tta	gaa	cac	agt	tcc	tca	878
Glu	Gln	Glu	Asp	Glu	Asp	Met	Asp	Pro	Arg	Leu	Glu	His	Ser	Ser	Ser	
	220				225					230					235	
ggt	caa	gaa	gat	tct	gaa	tcc	cca	agt	cct	gaa	gat	ata	cca	gac	tac	926
Val	Gln	Glu	Asp	Ser	Glu	Ser	Pro	Ser	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	
			240						245					250		
ctc	ctg	caa	tac	agg	gcc	atc	cac	agt	gca	gaa	cag	caa	cat	gcc	tat	974
Leu	Leu	Gln	Tyr	Arg	Ala	Ile	His	Ser	Ala	Glu	Gln	Gln	His	Ala	Tyr	
		255						260					265			
gag	cag	gac	ttt	gag	aca	gat	tat	gct	gaa	tac	cgc	atc	ctg	cat	gcc	1022
Glu	Gln	Asp	Phe	Glu	Thr	Asp	Tyr	Ala	Glu	Tyr	Arg	Ile	Leu	His	Ala	
		270					275					280				
cgt	ggt	ggg	act	gca	agc	caa	agg	ttc	ata	gag	ctg	gga	gca	gag	att	1070
Arg	Val	Gly	Thr	Ala	Ser	Gln	Arg	Phe	Ile	Glu	Leu	Gly	Ala	Glu	Ile	
		285				290						295				
aaa	aga	ggt	cgg	cga	gga	act	cca	gaa	tac	aag	gtc	ctg	gaa	gac	aag	1118

[illegible]

Leu	Ser	Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr		
			45					50					55				
acc	tca	ctc	tgc	tcc	ttc	cct	gtt	gcc	aat	gtc	tcg	ctg	act	aag	ggg	471	
Thr	Ser	Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly		
		60					65					70					
gga	cgt	gat	cgg	gtg	ctg	atg	tat	gga	cag	ccg	tat	cgt	gtt	acc	tta	519	
Gly	Arg	Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu		
	75					80					85						
gag	ctt	gag	ctg	cca	gag	tcc	cct	gtg	aat	caa	gat	ttg	ggc	atg	ttc	567	
Glu	Leu	Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe		
	90				95					100					105		
ttg	gtc	acc	att	tcc	tgc	tac	acc	aga	ggg	ggc	cga	atc	atc	tcc	act	615	
Leu	Val	Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr		
			110						115					120			
tct	tcg	cgt	tcg	gtg	atg	ctg	cat	tac	cgc	tca	gac	ctg	ctc	cag	atg	663	
Ser	Ser	Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met		
			125					130						135			
ctg	gac	aca	ctg	gtc	ttc	tct	agc	ctc	ctg	cta	ttt	ggc	ttt	gca	gag	711	
Leu	Asp	Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu		
		140						145				150					
cag	aag	cag	ctg	ctg	gag	gtg	gaa	ctc	tac	gca	gac	tat	aga	gag	aac	759	
Gln	Lys	Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn		
	155				160						165						
tcg	gtg	agt	gag	tac	gtg	ccg	acc	act	gga	gcg	atc	att	gag	atc	cac	807	
Ser	Val	Ser	Glu	Tyr	Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His		
	170				175					180					185		
agc	aag	cgc	atc	cag	ctg	tat	gga	gcc	tac	ctc	cgc	atc	cac	gcg	cac	855	
Ser	Lys	Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His		
			190						195					200			
ttc	act	ggg	ctc	aga	tac	ctg	cta	tac	aac	ttc	ccg	atg	acc	tgc	gcc	903	
Phe	Thr	Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala		
		205						210					215				
ttc	ata	ggg	gtt	gcc	agc	aac	ttc	acc	ttc	ctc	agc	gtc	atc	gtg	ctc	951	
Phe	Ile	Gly	Val	Ala	Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu		
		220					225					230					
ttc	agc	tac	atg	cag	tgg	gtg	tgg	ggg	ggc	atc	tgg	ccc	cga	cac	cgc	999	
Phe	Ser	Tyr	Met	Gln	Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg		
	235				240						245						
ttc	tct	ttg	cag	gtt	aac	atc	cga	aaa	aga	gac	aat	tcc	cgg	aag	gaa	1047	
Phe	Ser	Leu	Gln	Val	Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu		
	250				255					260					265		
gtc	caa	cga	agg	atc	tct	gct	cat	cag	cca	ggg	gca	ggg	cct	gaa	ggc	1095	
Val	Gln	Arg	Arg	Ile	Ser	Ala	His	Gln	Pro	Gly	Ala	Gly	Pro	Glu	Gly		
			270						275					280			
cag	gag	gag	tca	act	ccg	caa	tca	gat	gtt	aca	gag	gat	ggg	gag	agc	1143	
Gln	Glu	Glu	Ser	Thr	Pro	Gln	Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser		
			285					290					295				
cct	gaa	gat	ccc	tca	ggg	aca	gag	ggg	cag	ctg	tcc	gag	gag	gag	aaa	1191	
Pro	Glu	Asp	Pro	Ser	Gly	Thr	Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys		
		300					305					310					
cca	gat	cag	cag	ccc	ctg	agc	gga	gaa	gag	gag	cta	gag	cct	gag	gcc	1239	
Pro	Asp	Gln	Gln	Pro	Leu	Ser	Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala		
		315				320					325						
agt	gat	ggg	tca	ggc	tcc	tgg	gaa	gat	gca	gct	ttg	ctg	acg	gag	gcc	1287	

Ser Asp Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu Thr Glu Ala
 330 335 340 345
 aac ctg cct gct cct gct cct gct tct gct tct gcc cct gtc cta gag 1335
 Asn Leu Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro Val Leu Glu
 350 355 360
 act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga cag cgc ccc 1383
 Thr Leu Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg Gln Arg Pro
 365 370 375
 acc tgc tct agt tcc tgaagaaaag gggcagactc ctcacattcc agcactttcc 1438
 Thr Cys Ser Ser Ser
 380
 cacctgactc ctctcccctc gtttttcctt caataaacta ttttgtgtca gctccaaaaa 1498
 aaaaaaaaaa aa 1510

<210> 9
 <211> 882
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..410

<220>
 <221> sig_peptide
 <222> 78..155
 <223> Von Heijne matrix
 score 10.0731536331164
 seq LWLALVSCILTQA/SA

<400> 9
 atggctggcc agaggaggaa cgctttgtgt tctcatcgga gctgcatggg aagtctgcat 60
 acagcaaagt gacctgc atg cct cac ctt atg gaa agg atg gtg ggc tct 110
 Met Pro His Leu Met Glu Arg Met Val Gly Ser
 -25 -20
 ggc ctc ctg tgg ctg gcc ttg gtc tcc tgc att ctg acc cag gca tct 158
 Gly Leu Leu Trp Leu Ala Leu Val Ser Cys Ile Leu Thr Gln Ala Ser
 -15 -10 -5 1
 gca gtg cag cga ggt tat gga aac ccc att gaa gcc agt tcg tat ggg 206
 Ala Val Gln Arg Gly Tyr Gly Asn Pro Ile Glu Ala Ser Ser Tyr Gly
 5 10 15
 ctg gac ctg gac tgc gga gct cct ggc acc cca gag gct cat gtc tgt 254
 Leu Asp Leu Asp Cys Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys
 20 25 30
 ttt gac ccc tgt cag aat tac acc ctc cta gat ttg ggg ccc atc act 302
 Phe Asp Pro Cys Gln Asn Tyr Thr Leu Leu Asp Leu Gly Pro Ile Thr
 35 40 45
 cgg aga ggt gca cag tct ccc ggt gtc atg aat gga acc cct agc act 350
 Arg Arg Gly Ala Gln Ser Pro Gly Val Met Asn Gly Thr Pro Ser Thr
 50 55 60 65
 gca ggg ttc ctg gtg gcc tgg cct atg gtc ctc ctg act gtc ctc ctg 398
 Ala Gly Phe Leu Val Ala Trp Pro Met Val Leu Leu Thr Val Leu Leu
 70 75 80
 gct tgg ctg ttc tgagagctcc gctgagcatc tggccttgaa gtttgtgttc 450

Ala Trp Leu Phe

```

      85
ttccctctgg caatggctcc cttcagcact tctgctttcc actccaattc acacaggctt 510
gggattaaca gaatcaaggc caggctaggt taggaaaagg gaagagcttt caccttcttt 570
aaaactctcg gctgggcgca gtgggtcatg cctgtaatcc cagcattttg ggaggctgag 630
gcagggtgat cacctgaggt cagcagttca aaatcagcct ggccaaaatg ctgaaactcc 690
gtctctacta aaaatacaaa aattagccag gcatgggtgac aggcgcctgt aatcccagct 750
actcgggagg ccaaggcagg agaattgctc gaactcaggg ggtggaggtt gcagtgaagt 810
gagattgtgc cattgcactc cagcctgggc aacagagcaa gactctgtct caggcaaaaa 870
aaaaaaaaaa aa 882

```

<210> 10
 <211> 1849
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..299

<220>
 <221> sig_peptide
 <222> 84..134
 <223> Von Heijne matrix
 score 3.86022363031904
 seq GFVAALVAGGVAG/VS

```

<400> 10
aaacatggcg gcgcccagcg cgcgaggacg tgatccgctt ctgctccggc ttggattgta 60
gccttgacga ggtctgagcg acc atg gac cgg ccg ggg ttc gtg gca gcg ctg 113
                        Met Asp Arg Pro Gly Phe Val Ala Ala Leu
                        -15                               -10

gtg gct ggt ggg gta gca ggt gtt tct gtt gac ttg ata tta ttt cct 161
Val Ala Gly Gly Val Ala Gly Val Ser Val Asp Leu Ile Leu Phe Pro
      -5                               1                               5

ctg gat acc att aaa acc agg ctg cag agt ccc caa gga ttt aat aag 209
Leu Asp Thr Ile Lys Thr Arg Leu Gln Ser Pro Gln Gly Phe Asn Lys
10                               15                               20                               25

gct ggt ggt ttt cat gga ata tat gct ggc gtt cct tct gct gct att 257
Ala Gly Gly Phe His Gly Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile
      30                               35                               40

gga tcc ttt cct aat ggt tgc ctg cct gat tcg agt tcc atc 299
Gly Ser Phe Pro Asn Gly Cys Leu Pro Asp Ser Ser Ser Ile
      45                               50                               55

tgaagtgggt aagcagaggg cacaggtatc tgcttctaca agaacatttc agattttctc 359
taacatctta tatgaagagg gtatccaagg gttgtatcga ggctataaaa gcacagtttt 419
aagagagatt cttttttctt tgggtccagtt tcccttatgg gaggccttaa aagccctctg 479
gtcctggagg caggatcatg tgggtggattc ttggcagtcg gcagtctgtg gagcttttgc 539
aggtggattt gccgctgcag tcaccacccc tctagacgtg gcgaagacaa gaattatgct 599
ggcaaaggct ggctccagca ctgctgatgg gaatgtgctc tctgtcctgc atggggctctg 659
gcggtcacag gggctggcag gattatttgc aggtgtcttc cctcgaatgg cagccatcag 719
tctgggaggt ttcattcttc tgggggctta tgaccgaacg cacagcttgc tgttggaagt 779
tggcagaaaag agtccttgaa gcagagacaa gcctcacctc cacttctgtc aagagagggg 839
cctgcagtggt aaacctctt cgcgtgagca gctgtctgaa ctataggccc cagtgtctgaa 899

```

gaccagttgt	gctaagatac	cggcatggag	attgtgccat	ccgtggtata	ggctggctgg	959
tatgaagtca	ttggcctgta	tgccagagag	ctaagagaag	aaaacggggt	ctgtggcagt	1019
actctgaaca	atttcctcag	aacctcttaa	taaataagtt	tggtaatgct	gaggccaggc	1079
cttttagagc	tttcatttga	tctgtatctg	atctttcatt	tcctgccacc	tgatggtgga	1139
ttcagcagaa	ggcaagatgg	ttataattct	aaaagaatag	cttgtttggt	tgtttgtttg	1199
ggaaaaggag	acttggggaa	gagttgtgta	tgtgggtggt	tctcccccta	gttaattcct	1259
gttgtgtaag	ggtaggcttt	gttgaaaaag	aaagaaagat	tgaactacag	gtgcatagca	1319
agcactcttt	ctgggtaact	aggctgctgg	ttttaattac	cctcagattt	caccataaaa	1379
aacgcacaat	tgtattattt	tacagagatg	tgtccagcgc	cccctgtggt	gtgtgagaga	1439
aagcagctgc	aactcaagtg	actaggtggg	cccagctggc	ttcgtgcagg	agggcacggt	1499
gggtgagcca	ttctcgccat	tctcatgtca	gactgaaagg	agggcctggg	ccagctttga	1559
aaaggcagga	tgaaatggaa	aggtcaccac	acttagggat	tttagacctt	gactaacaag	1619
ctccaggtgt	agaaaaattc	aaaacaaaat	gtcaggaatc	tagcagtgtt	gtctgccctg	1679
gagcaaacia	acagtatgtg	attttgcttc	gcctattttt	tttttctttt	ttgggggaag	1739
ataattaaag	gcagaatgac	tgcgtttgta	aaagaaggac	caccaactat	actgacattt	1799
ataaatgaac	ctttattaaa	gacacttcaa	tgcaaaaaaa	aaaaaaaaaa		1849

<210> 11
 <211> 565
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 55..468

<220>
 <221> sig_peptide
 <222> 55..99
 <223> Von Heijne matrix
 score 8.96936032049195
 seq FTLLFLAAVAGA/LV

<400> 11																
attccccaga ctttctgcag attctgtggt tatactcact cctcatccca aaga atg															57	
															Met	
															-15	
aaa	ttt	acc	act	ctc	ctc	ttc	ttg	gca	gct	gta	gca	ggg	gcc	ctg	gtc	105
Lys	Phe	Thr	Thr	Leu	Leu	Phe	Leu	Ala	Ala	Val	Ala	Gly	Ala	Leu	Val	
															-10	
															-5	
															1	
tat	gct	gaa	gat	gcc	tcc	tct	gac	tcg	acg	ggg	gct	gat	cct	gcc	cag	153
Tyr	Ala	Glu	Asp	Ala	Ser	Ser	Asp	Ser	Thr	Gly	Ala	Asp	Pro	Ala	Gln	
															5	
															10	
															15	
gaa	gct	ggg	acc	tct	aag	cct	aat	gaa	gag	atc	tca	ggg	cca	gca	gaa	201
Glu	Ala	Gly	Thr	Ser	Lys	Pro	Asn	Glu	Glu	Ile	Ser	Gly	Pro	Ala	Glu	
															20	
															25	
															30	
cca	gct	tca	ccc	cca	gag	aca	acc	aca	aca	gcc	cag	gag	act	tcg	gcg	249
Pro	Ala	Ser	Pro	Pro	Glu	Thr	Thr	Thr	Thr	Ala	Gln	Glu	Thr	Ser	Ala	
															35	
															40	
															45	
															50	
gca	gca	gtt	cag	ggg	aca	gcc	aag	gtc	acc	tca	agc	agg	cag	gaa	cta	297
Ala	Ala	Val	Gln	Gly	Thr	Ala	Lys	Val	Thr	Ser	Ser	Arg	Gln	Glu	Leu	
															55	
															60	
															65	
aac	ccc	ctg	aaa	tcc	ata	gtg	gag	aaa	agt	atc	tta	cta	aca	gaa	caa	345
Asn	Pro	Leu	Lys	Ser	Ile	Val	Glu	Lys	Ser	Ile	Leu	Leu	Thr	Glu	Gln	

	70		75		80	
gcc ctt gca aaa gca gga aaa gga atg cac gga ggc gtg cca ggt gga						393
Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly Gly						
	85		90		95	
aaa caa ttc atc gaa aat gga agt gaa ttt gca caa aaa tta ctg aag						441
Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu Lys						
	100		105		110	
aaa ttc agt cta tta aaa cca tgg gca tgagaagctg aataatggga						488
Lys Phe Ser Leu Leu Lys Pro Trp Ala						
	115		120			
tcattggact taaagcctta aatacccttg tagcccagag ctattaaac gaaagcatcc						548
aaaaaaaaa aaaaaaa						565

<210> 12
 <211> 1663
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 152..475

<220>
 <221> sig_peptide
 <222> 152..244
 <223> Von Heijne matrix
 score 10.0910253445132
 seq LVLLLVTRSPVNA/CL

<400> 12	
atgtgtctgc tgccgccatt gtgcggcgct ggtccctca gagggttcct gctgctgccg	60
gtgccttggga cctcccccct cgcttctcgt tctactgcc caggagcccg gcgggtccgg	120
gactcccgtc cgtgccggtg cgggcgcgcg c atg tgg ctg tgg gag gac cag	172
	Met Trp Leu Trp Glu Asp Gln
	-30 -25
ggc ggc ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg	220
Gly Gly Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu	
	-20 -15 -10
gtg acg cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc	268
Val Thr Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe	
	-5 1 5
gtt cta ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc	316
Val Leu Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala	
	10 15 20
ctg cag gtg ctc aag ccc cgg gac cgc att tct gcc atc gcc cac cgt	364
Leu Gln Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg	
	25 30 35 40
ggc ggc agc aam sag gcg ccc gag aac acg ctg gcg gcc att cgg cag	412
Gly Gly Ser Xaa Xaa Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln	
	45 50 55
cta aga atg gag caa cag gcg tgg agt tgg aca ttg agt tta ctt ctg	460
Leu Arg Met Glu Gln Gln Ala Trp Ser Trp Thr Leu Ser Leu Leu Leu	
	60 65 70
acg gga ttc ctg tct taatgcacga taacacagta gataggacga ctgatgggac	515

Thr Gly Phe Leu Ser

75
 tgggcgattg tgtgatttga catttgaaca aattaggaag ctgaatcctg cagcaaacca 575
 cagactcagg aatgatttcc ctgatgaaaa gatccctacc ctaagggaag ctgttgcaga 635
 gtgcctaaac cataacctca caatcttctt tgatgtcaaa ggccatgcac acaaggctac 695
 tgaggctcta aagaaaatgt atatggaatt tcctcaactg tataataata gtgtggtctg 755
 ttctttcttg ccagaagtta tctacaaggt aacattcggg atttttcttg tacatattag 815
 atgagacaaa cagatcgga tgtaataaca gcattaactc acagaccttg gagcctaagc 875
 catacaggag atgggaaacc acgctatgat actttctgga aacattttat atttgttatg 935
 atggacattt tgctcgattg gagcatgcat aatatcttgt ggtacctgtg tgggaatttca 995
 gctttcctca tgcaaaagga ttttgtatcc ccggcctact tgaagaagtg gtcagctaaa 1055
 ggaatccagg ttgttggttg gactgttaat acctttgatg aaaagagtta ctacgaatcc 1115
 catcttggtt ccagctatat cactgacagc atggtagaag actgcgaacc tcacttctag 1175
 actttcacgg tgggacgaaa cgggttcaga aactgccagg ggccctcatac agggatatca 1235
 aaataccctt tgtgctagcc caggccctgg ggaatcagg gactcacaca aatgcaatag 1295
 ttggtcactg catttttacc tgaaccaaag ctaaaccggg tgttgccacc atgcaccatg 1355
 gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa cgcacaagag 1415
 ccctgccct gccctagctg aggcacacag ggagaccag tgaggataag cacagattga 1475
 attgtacaat ttgcagatgc agatgtaa gcatgggaca tgcagataa ctcagagttg 1535
 acattttaaa acttgccaca cttatttcaa atatttgtac tcagctatgt taacatgtac 1595
 tgtagacatc aaacttgttg ccatactaata aaaattatta aaaggagcac taaaaaaaaa 1655
 aaaaaaaaaa 1663

<210> 13
 <211> 744
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 112..552

<220>
 <221> sig_peptide
 <222> 112..183
 <223> Von Heijne matrix
 score 11.7298925418815
 seq FVLGLGLTPPTLA/QD

<400> 13
 tcacaactgg aaccatctc caggaacaaa cagctggaac ccattctccg ttgaaggga 60
 actgccagat ttttgaaga ttcttcctcc tgggagcctg tgttgaaga g atg gtg 117
 Met Val
 atg ggc ctg ggc gtt ttg ttg ttg gtc ttc gtg ctg ggt ctg ggt ctg 165
 Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu Gly Leu
 -20 -15 -10
 acc cca ccg acc ctg gct cag gat aac tcc agg tac aca cac ttc ctg 213
 Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His Phe Leu
 -5 1 5 10
 acc cag cac tat gat gcc aaa cca cag ggc cgg gat gac aga tac tgt 261
 Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg Tyr Cys
 15 20 25
 gaa agc atc atg agg aga cgg ggc ctg acc tca ccc tgc aaa gac atc 309
 Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp Ile

	30		35		40	
aac aca ttt att cat ggc aac aag cgc acg atc aag gcc atc tgt gaa						357
Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile Cys Glu						
	45		50		55	
aac aag aat gga aac cct cac aga gaa aac cta aga ata agc aag tct						405
Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser Lys Ser						
	60		65		70	
tct ttc cag gtc acc act tgc aag cta cat gga ggt tcc ccc tgg cct						453
Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro Trp Pro						
	75		80		85	90
cca tgc cag tac cga gcc aca gcg ggg ttc aga aac gtt gtt gtt gct						501
Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val Val Ala						
	95		100		105	
tgt gaa aat ggc tta cct gtc cac ttg gat cag tca att ttc cgt cgt						549
Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe Arg Arg						
	110		115		120	
ccg taaccagcgg gccctgggc aagtgtggc tctgtgtcc ttgccttcca						602
Pro						
tttcccctct gcaccagaa cagtgggtggc aacattcatt gccaagggcc caaagaaaga						662
gctacctgga ccttttggtt tctgtttgac aacatgttta ataaataaaa atgtcttgat						722
atcagcaaaa aaaaaaaaaa aa						744

<210> 14
 <211> 1759
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 101..1243

<220>
 <221> sig_peptide
 <222> 101..199
 <223> Von Heijne matrix
 score 3.57142340200611
 seq FLCLGMALCPRQA/TR

<400> 14	
gtagagtgtc gaaggtcctg ccaacggctc tcttggcgtc tcaacgttcg gatcagcagc	60
ttttttccat tctctctctc cacttcttca gtgagcagcc atg agt tgg act gtg	115
	Met Ser Trp Thr Val
	-30
cct gtt gtg cgg gcc agc cag aga gtg agc tcg gtg gga gcg aat ttc	163
Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser Val Gly Ala Asn Phe	
	-25 -20 -15
cta tgc ctg ggg atg gcc ctg tgt ccg cgt caa gca acg cgc atc ccg	211
Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln Ala Thr Arg Ile Pro	
	-10 -5 1
ctc aac ggc acc tgg ctc ttc acc ccc gtg agc aag atg gcg act gtg	259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val	
	5 10 15 20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac	307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His	

agc	aag	gtc	tcc	atc	ata	gga	act	gga	tcg	gtg	ggc	atg	gcc	tgc	gct	355
Ser	Lys	Val	Ser	Ile	Ile	Gly	Thr	Gly	Ser	Val	Gly	Met	Ala	Cys	Ala	
			40					45					50			
atc	agc	atc	tta	tta	aaa	ggc	ttg	agt	gat	gaa	ctt	gcc	ctt	gtg	gat	403
Ile	Ser	Ile	Leu	Leu	Lys	Gly	Leu	Ser	Asp	Glu	Leu	Ala	Leu	Val	Asp	
		55				60						65				
ctt	gat	gaa	gac	aaa	ctg	aag	ggg	gag	acg	atg	gat	ctt	caa	cat	ggc	451
Leu	Asp	Glu	Asp	Lys	Leu	Lys	Gly	Glu	Thr	Met	Asp	Leu	Gln	His	Gly	
	70				75						80					
agc	cct	ttc	acg	aaa	atg	cca	aat	att	gtt	tgt	agc	aaa	gat	tac	ttt	499
Ser	Pro	Phe	Thr	Lys	Met	Pro	Asn	Ile	Val	Cys	Ser	Lys	Asp	Tyr	Phe	
85					90				95						100	
gtc	aca	gca	aac	tcc	aac	cta	gtg	att	atc	aca	gca	ggg	gca	cgc	caa	547
Val	Thr	Ala	Asn	Ser	Asn	Leu	Val	Ile	Ile	Thr	Ala	Gly	Ala	Arg	Gln	
			105					110						115		
gaa	aag	gga	gaa	acg	cgc	ctt	aat	tta	gtc	cag	cga	aat	gtg	gcc	atc	595
Glu	Lys	Gly	Glu	Thr	Arg	Leu	Asn	Leu	Val	Gln	Arg	Asn	Val	Ala	Ile	
			120					125					130			
ttc	aag	tta	atg	att	tcc	agt	att	gtc	cag	tac	agc	ccc	cac	tgc	aaa	643
Phe	Lys	Leu	Met	Ile	Ser	Ser	Ile	Val	Gln	Tyr	Ser	Pro	His	Cys	Lys	
		135				140						145				
ctg	att	att	gtt	tcc	aat	cca	gtg	gat	atc	tta	act	tat	gta	gct	tgg	691
Leu	Ile	Ile	Val	Ser	Asn	Pro	Val	Asp	Ile	Leu	Thr	Tyr	Val	Ala	Trp	
	150				155					160						
aag	ttg	agt	gca	ttt	ccc	aaa	aac	cgt	att	att	gga	agc	ggc	tgt	aat	739
Lys	Leu	Ser	Ala	Phe	Pro	Lys	Asn	Arg	Ile	Ile	Gly	Ser	Gly	Cys	Asn	
165					170				175						180	
ctg	gat	act	gct	cgt	ttt	cgt	ttc	ttg	att	gga	caa	aag	ctt	ggg	atc	787
Leu	Asp	Thr	Ala	Arg	Phe	Arg	Phe	Leu	Ile	Gly	Gln	Lys	Leu	Gly	Ile	
			185					190						195		
cat	tct	gaa	agc	tgc	cat	gga	tgg	atc	ctc	gga	gag	cat	gga	gac	tca	835
His	Ser	Glu	Ser	Cys	His	Gly	Trp	Ile	Leu	Gly	Glu	His	Gly	Asp	Ser	
		200						205					210			
agt	gtt	cct	gtg	tgg	agt	gga	gtg	aac	ata	gct	ggg	gtc	cct	ttg	aag	883
Ser	Val	Pro	Val	Trp	Ser	Gly	Val	Asn	Ile	Ala	Gly	Val	Pro	Leu	Lys	
		215				220						225				
gat	ctg	aac	tct	gat	ata	gga	act	gat	aaa	gat	cct	gag	caa	tgg	aaa	931
Asp	Leu	Asn	Ser	Asp	Ile	Gly	Thr	Asp	Lys	Asp	Pro	Glu	Gln	Trp	Lys	
	230					235					240					
aat	gtc	cac	aaa	gaa	gtg	act	gca	act	gcc	tat	gag	att	att	aaa	atg	979
Asn	Val	His	Lys	Glu	Val	Thr	Ala	Thr	Ala	Tyr	Glu	Ile	Ile	Lys	Met	
245					250				255						260	
aaa	ggg	tat	act	tct	tgg	gcc	att	ggc	cta	tct	gtg	gcc	gat	tta	aca	1027
Lys	Gly	Tyr	Thr	Ser	Trp	Ala	Ile	Gly	Leu	Ser	Val	Ala	Asp	Leu	Thr	
			265					270						275		
gaa	agt	att	ttg	aag	aat	ctt	agg	aga	ata	cat	cca	gtt	tcc	acc	ata	1075
Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Arg	Ile	His	Pro	Val	Ser	Thr	Ile	
		280						285					290			
att	aag	ggc	ctc	tat	gga	ata	gat	gaa	gaa	gta	ttc	ctc	agt	att	cct	1123
Ile	Lys	Gly	Leu	Tyr	Gly	Ile	Asp	Glu	Glu	Val	Phe	Leu	Ser	Ile	Pro	
		295				300						305				
tgt	atc	ctg	gga	gag	aac	ggg	att	acc	aac	ctt	ata	aag	ata	aag	ctg	1171
Cys	Ile	Leu	Gly	Glu	Asn	Gly	Ile	Thr	Asn	Leu	Ile	Lys	Ile	Lys	Leu	

310	315	320	
acc cct gaa gaa gag gcc cat ctg aaa aaa agt gca aaa aca ctc tgg			1219
Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser Ala Lys Thr Leu Trp			
325	330	335	340
gaa att cag aat aag ctt aag ctt taaagttgcc taaaactacc attccgaaat			1273
Glu Ile Gln Asn Lys Leu Lys Leu			
345			
tattgaagag atcatagata caggattata taacgaaatt ttgaataaac ttgaattcct			1333
aaaagatgga aacaggaaaag taggtagagt gattttccta tttatttagt cctccagctc			1393
ttttattgag catccacgtg ctggacgata cttattttaca attcctaagt atttttggtgta			1453
cctctgatgt agcagcactt gccatgttat atatatgtag ttggcatttg gttcccaaaa			1513
agtaggatgt aggtatttat tgtgttctag aaattccgac tcttttcatt agatatatgc			1573
tatttctttc attccttgctg gtttatacct atgttcattt atatgctgta aaaaagtagt			1633
agcttcttct acaatgtaaa aataaatgta catacaaaaa aatgcagtag tatatacaat			1693
cttttgtttt gcttcctttg atagttaata aattccgttt gttgaatcaa taaaaaaaaa			1753
aaaaaa			1759

<210> 15
 <211> 1755
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 101..517

<220>
 <221> sig_peptide
 <222> 101..199
 <223> Von Heijne matrix
 score 3.57613483592743
 seq FLCLGMALCLRQA/TR

<400> 15	
gtagagtgct gaaggtcctg ccaacggctc tcttggcgctc tcaacgttcg gatcagcagc	60
ttttttccat tctctctctc cacttcttca gtgagcagcc atg agt tgg act gtg	115
Met Ser Trp Thr Val	
-30	
cct gtt gtg cgg gcc agc cag aga atg agc tcg gtg gga gcg aat ttc	163
Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser Val Gly Ala Asn Phe	
-25 -20 -15	
cta tgc ctg ggg atg gcc ctg tgt ctg cgt caa gca acg cgc atc ccg	211
Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln Ala Thr Arg Ile Pro	
-10 -5 1	
ctc aac ggc acc tgg ctc ttc aca ccc gtg agc aag atg gcg act gtg	259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val	
5 10 15 20	
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac	307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His	
25 30 35	
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct	355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala	
40 45 50	
atc agc atc ttg tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat	403

```

Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
55 60 65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc 451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
70 75 80
agc cct ttc acg aaa atg cca ata ttg ttt gta gca aag att act ttg 499
Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val Ala Lys Ile Thr Leu
85 90 95 100
tca cag caa act cca acc tagtgattat cacagcaggt gcacgccaaag 547
Ser Gln Gln Thr Pro Thr
105
aaaagggaga aacgcgcctt aatttagtcc agcgaaatgt ggccatcttc aagtaatgat 607
ttccagtatt gtccagtaca gccccactg caaactgatt attgtttcca atccagtgga 667
tatcttaact tatgtagctt ggaagttgag tgcatttccc aaaaaccgta ttattggaag 727
cggctgtaat ctggatactg ctctgttttcg tttcttgatt ggacaaaagc ttggtatcca 787
ttctgaaagc tgccatggat ggatcctcgg agagcatgga gactcaagtg ttctgtgtg 847
gagtggagtg aacatagctg gtgtcccttt gaaggatctg aactctgata taggaactga 907
taaagatcct gagcaggaaa aatgtccaca aagaagtgc tgcaactgcc tatgagatta 967
ttaaaatgaa aggttatact tcttgggcca ttggcctatc tgtggccgat ttaacagaaa 1027
gtattttgaa gaatcttagg agaatacatc cagtttccac cataactaag ggcctctatg 1087
gaatagatga agaagtattc ctcagtattc cttgtatcct gggagagaac ggtattacca 1147
accttataaa gataaagctg acccctgaag aagaggccca tctgaaaaaa agtgcaaaaa 1207
cactctggga aattcagaat aagcttaagc tttaaagttg cctaaaacta ccattccgaa 1267
attattgaag agatcataga tacaggatta tataacgaaa ttttgaataa acttgaattc 1327
ctaaaagatg gaaacaggaa agtaggtaga gtgattttcc tatttattta gtcctccagc 1387
tcttttattg agcatccacg tgctggacga tacttattta caattcctaa gtatttttgg 1447
tacctctgat gtagcagcac ttgccatggt atatatatgt agttggcatt tggttcccaa 1507
aaagtaggat gtaggtatctt attgtgttct agaaattccg actcttttca ttagatatat 1567
gctattttctt tcattcttgc tggttttatac ctatgttcat ttatatgctg taaaaaagta 1627
gtagcttctt ctacaatgta aaaataaatg tacatacaaa aaaatgcagt agtatataca 1687
atcttttgtt ttgcttcctt tgatagttaa taaattccgt ttgttgaatc aataaaaaaa 1747
aaaaaaa 1755

<210> 16
<211> 936
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..853

<220>
<221> sig_peptide
<222> 59..100
<223> Von Heijne matrix
score 5.2402423806254
seq NFILFIFIPGVFS/LK

<400> 16
agaaaggagg ctctgggtag acgcactaga ttactggata aatcacttca atttccca 58
atg aat ttt ata ttg ttt att ttt ata cct gga gtt ttt tcc tta aaa 106
Met Asn Phe Ile Leu Phe Ile Phe Ile Pro Gly Val Phe Ser Leu Lys
-10 -5 1

```

agt agc act ttg aag cct act att gaa gca ttg cct aat gtg cta cct	154
Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro	
5 10 15	
tta aat gaa gat gtt aat aag cag gaa gaa aag aat gaa gat cat act	202
Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr	
20 25 30	
ccc aat tat gct cct gct aat gag aaa aat ggc aat tat tat aaa gat	250
Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp	
35 40 45 50	
ata aaa caa tat gtg ttc aca aca caa aat cca aat ggc act gag tct	298
Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser	
55 60 65	
gaa ata tct gtg aga gcc aca act gac ctg aat ttt gct cta aaa aac	346
Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn	
70 75 80	
gga tca acc cca aac gtg cct gca ttt tgg aca atg tta gct aaa gct	394
Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala	
85 90 95	
ata aat gga aca gca gtg gtc atg gat gat aaa gat caa tta ttt cac	442
Ile Asn Gly Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His	
100 105 110	
cca att cca gag tct gat gtg aat gct aca cag gga gaa aat cag cca	490
Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro	
115 120 125 130	
gat cta gag gat ctg aag atc aaa ata atg ctg gga atc tcg ttg atg	538
Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met	
135 140 145	
acc ctc ctc ctc ttt gtg gtc ctc ttg gca ttc tgt agt gct aca ctg	586
Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu	
150 155 160	
tac aaa ctg agg cat ctg agt tat aaa agt tgt gag agt cag tac tct	634
Tyr Lys Leu Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser	
165 170 175	
gtc aac cca gag ctg gcc acg atg tct tac ttt cat cca tca gaa ggt	682
Val Asn Pro Glu Leu Ala Thr Met Ser Tyr Phe His Pro Ser Glu Gly	
180 185 190	
gtt tca gat aca tcc ttt tcc aag agt gca gag agc agc aca ttt ttg	730
Val Ser Asp Thr Ser Phe Ser Lys Ser Ala Glu Ser Ser Thr Phe Leu	
195 200 205 210	
ggt acc act tct tca gat atg aga aga tca ggc aca aga aca tca gaa	778
Gly Thr Thr Ser Ser Asp Met Arg Arg Ser Gly Thr Arg Thr Ser Glu	
215 220 225	
tct aag ata atg acg gat atc att tcc ata ggc tca gat aat gag atg	826
Ser Lys Ile Met Thr Asp Ile Ile Ser Ile Gly Ser Asp Asn Glu Met	
230 235 240	
cat gaa aac gat gag tcg gtt acc cgg tgaagaaatc aaggaacccg	873
His Glu Asn Asp Glu Ser Val Thr Arg	
245 250	
gtgaagaaat cttattgatg aataaataac tttaattatt ttgtcatcaa aaaaaaaaaa	933
aaa	936

<210> 17
 <211> 747
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 73..672

<220>

<221> sig_peptide

<222> 73..132

<223> Von Heijne matrix

score 5.21332530399231

seq SPVFLVFPPEITA/SE

<400> 17

```
acaagaaaag aacatggtct agactgaagt accaactaaa tcatctcctt tcaaattatc      60
accgacacca tc atg gat tca agc acc gca cac agt ccg gtg ttt ctg gta      111
      Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val
      -20          -15          -10
ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca      159
Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser
      -5          1          5
gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga      207
Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg
10          15          20          25
aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc      255
Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr
      30          35          40
ttt tct ttt gga gtt atc ttc ctt ttc act ttg tta aaa cca tat cca      303
Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro
      45          50          55
agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt      351
Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val
      60          65          70
ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc      399
Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr
      75          80          85
aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc      447
Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
90          95          100          105
ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta      495
Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu
      110          115          120
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag      543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys
      125          130          135
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc      591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
      140          145          150
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc      639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
      155          160          165
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata      692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys
170          175          180
```

```

aagatgtgtt aaaatattaa aaaaaaaaaa aaaaaaaaag aaaaaaaaaa aaaaa 747

<210> 18
<211> 1884
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 94..1275

<220>
<221> sig_peptide
<222> 94..210
<223> Von Heijne matrix
      score 4.55778392992629
      seq LVLVKRLLAVSVS/CI

<400> 18
acagcgcgtg cagcctcgtg cagctcttct ggtctccggc gcccgcccct cagacgtaat 60
gttgaattaa agaaaatact ttatcagaag aag atg gcc act gcc cag ttg cag 114
                        Met Ala Thr Ala Gln Leu Gln
                        -35
agg act ccc atg agt gca ctg gta ttt ccc aat aag ata tca act gaa 162
Arg Thr Pro Met Ser Ala Leu Val Phe Pro Asn Lys Ile Ser Thr Glu
      -30                -25                -20
cac cag tct ttg gtg tta gtg aag agg ctt cta gca gtt tca gta tcc 210
His Gln Ser Leu Val Leu Val Lys Arg Leu Leu Ala Val Ser Val Ser
      -15                -10                -5
tgt atc acg tat ttg agg gga ata ttc cca gaa tgc gct tat gga aca 258
Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu Cys Ala Tyr Gly Thr
1      5      10      15
aga tat cta gat gat ctt tgt gtc aaa ata ctg aga gaa gat aaa aat 306
Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu Arg Glu Asp Lys Asn
      20      25      30
tgc cca gga tct aca cag tta gtg aaa tgg att cta gga tgt tat gat 354
Cys Pro Gly Ser Thr Gln Leu Val Lys Trp Ile Leu Gly Cys Tyr Asp
      35      40      45
gct tta cag aaa aaa tat cta agg atg gtt gtt cta gct gta tac aca 402
Ala Leu Gln Lys Lys Tyr Leu Arg Met Val Val Leu Ala Val Tyr Thr
      50      55      60
aac cca gaa gat cct cag aca att tca gaa tgt tac caa ttc aaa ttc 450
Asn Pro Glu Asp Pro Gln Thr Ile Ser Glu Cys Tyr Gln Phe Lys Phe
65      70      75      80
aaa tac acc aat aat gga cca ctc atg gac ttc ata agt aaa aac caa 498
Lys Tyr Thr Asn Asn Gly Pro Leu Met Asp Phe Ile Ser Lys Asn Gln
      85      90      95
agc aac gaa tct agc atg ttg tct act gac acc aag aaa gca agc att 546
Ser Asn Glu Ser Ser Met Leu Ser Thr Asp Thr Lys Lys Ala Ser Ile
      100      105      110
ctc ctc att cgc aag att tat atc cta atg caa aat ctg ggg cct tta 594
Leu Leu Ile Arg Lys Ile Tyr Ile Leu Met Gln Asn Leu Gly Pro Leu
      115      120      125
cct aat gat gtt tgt ttg acc atg aaa ctt ttt tac tat gat gaa gtt 642

```

Pro	Asn	Asp	Val	Cys	Leu	Thr	Met	Lys	Leu	Phe	Tyr	Tyr	Asp	Glu	Val	
130						135					140					
aca	ccc	cca	gat	tac	cag	cct	ccc	ggg	ttt	aag	gat	ggg	gat	tgt	gaa	690
Thr	Pro	Pro	Asp	Tyr	Gln	Pro	Pro	Gly	Phe	Lys	Asp	Gly	Asp	Cys	Glu	
145					150					155					160	
gga	gtt	ata	ttt	gaa	ggg	gaa	cct	atg	tat	tta	aat	gtg	gga	gaa	gtc	738
Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro	Met	Tyr	Leu	Asn	Val	Gly	Glu	Val	
				165					170						175	
tca	aca	cct	ttt	cac	atc	ttc	aaa	gta	aaa	gtg	acc	act	gag	aga	gaa	786
Ser	Thr	Pro	Phe	His	Ile	Phe	Lys	Val	Lys	Val	Thr	Thr	Glu	Arg	Glu	
				180				185					190			
cga	atg	gaa	aat	att	gac	tca	act	ata	cta	tca	cca	aaa	caa	ata	aaa	834
Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr	Ile	Leu	Ser	Pro	Lys	Gln	Ile	Lys	
		195					200					205				
aca	cca	ttt	caa	aaa	atc	ctg	agg	gac	aaa	gat	gta	gaa	gat	gaa	cag	882
Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg	Asp	Lys	Asp	Val	Glu	Asp	Glu	Gln	
		210					215				220					
gag	cat	tat	aca	agt	gat	gat	ttg	gac	att	gaa	act	aaa	atg	gaa	gaa	930
Glu	His	Tyr	Thr	Ser	Asp	Asp	Leu	Asp	Ile	Glu	Thr	Lys	Met	Glu	Glu	
					230					235					240	
cag	gaa	aaa	aac	cct	gca	tct	tct	gaa	ctt	gaa	gaa	cca	agt	tta	gtt	978
Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser	Glu	Leu	Glu	Glu	Pro	Ser	Leu	Val	
				245				250							255	
tgt	gag	gaa	gat	gaa	att	atg	agg	tct	aaa	gaa	agt	cca	gat	ctt	tct	1026
Cys	Glu	Glu	Asp	Glu	Ile	Met	Arg	Ser	Lys	Glu	Ser	Pro	Asp	Leu	Ser	
			260					265					270			
att	tct	cat	tct	cag	gtt	gag	cag	tta	gtc	aat	aaa	aca	tct	gaa	ctt	1074
Ile	Ser	His	Ser	Gln	Val	Glu	Gln	Leu	Val	Asn	Lys	Thr	Ser	Glu	Leu	
		275					280					285				
gat	atg	tct	gaa	agc	aaa	aca	aga	agt	gga	aaa	gtc	ttt	cag	aat	aaa	1122
Asp	Met	Ser	Glu	Ser	Lys	Thr	Arg	Ser	Gly	Lys	Val	Phe	Gln	Asn	Lys	
		290					295				300					
atg	gca	aat	gga	aat	caa	cca	gta	aaa	tct	tcc	aaa	gaa	aat	cgg	aag	1170
Met	Ala	Asn	Gly	Asn	Gln	Pro	Val	Lys	Ser	Ser	Lys	Glu	Asn	Arg	Lys	
					310					315					320	
aga	agt	caa	cat	gaa	tct	ggg	aga	ata	gtc	ctc	cat	cac	ttt	gat	tct	1218
Arg	Ser	Gln	His	Glu	Ser	Gly	Arg	Ile	Val	Leu	His	His	Phe	Asp	Ser	
				325					330						335	
tct	agt	caa	gag	tca	gtg	cca	aaa	agg	aga	aag	ttt	agt	gaa	cca	aag	1266
Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys	Arg	Lys	Phe	Ser	Glu	Pro	Lys		
			340					345				350				
gaa	cat	ata	taaaaattat	ttttgttctg	caggcttgca	gagttcttct										1315
Glu	His	Ile														
		355														
caccatttaa	actgaaggac	cctatatattat	atttccttaa	ctctgaagat	gtatatgtag											1375
tttaaagcag	tttatacaact	aaaactaagt	ttttggctga	ctgtcatatt	gtggctcctta											1435
atcttgagat	aaatccaata	gaacttttga	ataaaagcaa	aagtacaaat	gtcataattg											1495
attcggtaat	aagtaaaatt	tcaaaattga	ttttgttcat	tacctactta	atatttcctt											1555
taaatatata	ctaactgtta	aggccctcta	atgccatttt	tctaaacagt	aatggtttact											1615
ttgggtattaa	aatttgggtat	tgattcactt	tttacttatg	ttaaaattat	accattttaac											1675
tggtctctttt	gtcattgtgc	tggtattaaa	acaatgttct	tcaatatttt	gacataatgt											1735
attaacattt	taatataata	tgtacaattt	agaattgggt	gctttacctt	tactatgctt											1795
tttttacagg	acaaaaagac	tgatttttaa	agtatggcat	tttttgcagc	ataaataaaa											1855
tattgttcag	tacgaaaaaa	aaaaaaaaa														1884

<210> 19
 <211> 691
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..515

<220>
 <221> sig_peptide
 <222> 42..92
 <223> Von Heijne matrix
 score 10.7019149919754
 seq VLMLLAVLIWTGA/EN

<400> 19
 gagttgtcct gtgctggagg tctgctcaga cgaaggctctc c atg gcg tta gaa gtc 56
 Met Ala Leu Glu Val
 -15
 ttg atg ctc ctc gct gtc ttg att tgg acc ggt gct gag aac ctc cat 104
 Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly Ala Glu Asn Leu His
 -10 -5 1
 gtg aaa ata agt tgc tct ctg gac tgg ttg atg gtc tca gtt atc cca 152
 Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met Val Ser Val Ile Pro
 5 10 15 20
 gtt gca gaa agc aga aat ctg tat ata ttt gcg gat gaa tta cat ctg 200
 Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala Asp Glu Leu His Leu
 25 30 35
 gga atg ggc tgc cct gca aat cgg ata cat aca tat gta tat gag ttt 248
 Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr Tyr Val Tyr Glu Phe
 40 45 50
 ata tat ctt gtt cgt gat tgt ggc atc agg aca agg gta gtt tct gag 296
 Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr Arg Val Val Ser Glu
 55 60 65
 gaa act ctc ctt ttt caa acc gag ctg tac ttt acc cca agg aat ata 344
 Glu Thr Leu Leu Phe Gln Thr Glu Leu Tyr Phe Thr Pro Arg Asn Ile
 70 75 80
 gat cat gac cct cag gaa atc cat ttg gag tgt tcc acc tct agg aaa 392
 Asp His Asp Pro Gln Glu Ile His Leu Glu Cys Ser Thr Ser Arg Lys
 85 90 95 100
 tca gtg tgg ctt aca cca gtt tct act gag aat gaa ata aaa ttg gat 440
 Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn Glu Ile Lys Leu Asp
 105 110 115
 cct agt cct ttt att gct gac ttt cag aca aca gca gaa gag tta gga 488
 Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr Ala Glu Glu Leu Gly
 120 125 130
 tta tta tct tct agt cca aac ttg ctc tgagctaaag gagaaatgga 535
 Leu Leu Ser Ser Ser Pro Asn Leu Leu
 135 140
 aacttgaagc tgggtgttatg tatttttgcag gaaaacagtt tcatttttttc atagcaaaaa 595
 tatagttggt gtatatctct ccttaagtct ctggttttcta aaaaccctac ttcagtaaag 655
 gtccctgatta gttgattagc gaaaaaaaaa aaaaaa 691

<210> 20
 <211> 1138
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 271..969

<220>
 <221> sig_peptide
 <222> 271..366
 <223> Von Heijne matrix
 score 5.6680378526706
 seq WMGLACFRSLAAS/SP

<220>
 <221> misc_feature
 <222> 989
 <223> n=a, g, c or t

<400> 20
 aaaaaccttt caagtgtccc ctcctttcct taaagtcttt tataggggtc cccttcttgg 60
 ccctctccat cctgtgagtc aggactgaaa gggcacagac aggtcactgc cagcattgtt 120
 ggggcaagcc tgcaagcacg catcactggg gatctgacat gacaatggcc gcctgtcccc 180
 tctgagggct acaggactta cccagtgagg aagcagctaa gcaggtctga ccagccgacc 240
 tggacctggc caagggctcct gtcattccctc atg gcc acc ccg cca ttc cgg ctg 294
 Met Ala Thr Pro Pro Phe Arg Leu
 -30 -25
 ata agg aag atg ttt tcc ttc aag gtg agc aga tgg atg ggg ctt gcc 342
 Ile Arg Lys Met Phe Ser Phe Lys Val Ser Arg Trp Met Gly Leu Ala
 -20 -15 -10
 tgc ttc cgg tcc ctg gcg gca tcc tct ccc agt att cgc cag aag aaa 390
 Cys Phe Arg Ser Leu Ala Ala Ser Ser Pro Ser Ile Arg Gln Lys Lys
 -5 1 5
 cta atg cac aag ctg cag gag gaa aag gct ttt cgc gaa gag atg aaa 438
 Leu Met His Lys Leu Gln Glu Glu Lys Ala Phe Arg Glu Glu Met Lys
 10 15 20
 att ttt cgt gaa aaa ata gag gac ttc agg gaa gag atg tgg act ttc 486
 Ile Phe Arg Glu Lys Ile Glu Asp Phe Arg Glu Glu Met Trp Thr Phe
 25 30 35 40
 cga ggc aag atc cat gct ttc cgg ggc cag atc ctg ggt ttt tgg gaa 534
 Arg Gly Lys Ile His Ala Phe Arg Gly Gln Ile Leu Gly Phe Trp Glu
 45 50 55
 gag gag aga cct ttc tgg gaa gag gag aaa acc ttc tgg aaa gag gaa 582
 Glu Glu Arg Pro Phe Trp Glu Glu Glu Lys Thr Phe Trp Lys Glu Glu
 60 65 70
 aaa tcc ttc tgg gaa atg gaa aag tct ttc agg gag gaa gag aaa act 630
 Lys Ser Phe Trp Glu Met Glu Lys Ser Phe Arg Glu Glu Glu Lys Thr
 75 80 85
 ttc tgg aaa aag tac cgc act ttc tgg aag gag gat aag gcc ttc tgg 678
 Phe Trp Lys Lys Tyr Arg Thr Phe Trp Lys Glu Asp Lys Ala Phe Trp
 90 95 100

```

aaa gag gac aat gcc tta tgg gaa aga gac cgg aac ctt ctt cag gag      726
Lys Glu Asp Asn Ala Leu Trp Glu Arg Asp Arg Asn Leu Leu Gln Glu
105          110          115          120
gac aag gcc ctg tgg gag gaa gaa aag gcc ctg tgg gta gag gaa aga      774
Asp Lys Ala Leu Trp Glu Glu Glu Lys Ala Leu Trp Val Glu Glu Arg
          125          130          135
gcc ctc ctt gag ggg gag aaa gcc ctg tgg gaa gat aaa acg tcc ctc      822
Ala Leu Leu Glu Gly Glu Lys Ala Leu Trp Glu Asp Lys Thr Ser Leu
          140          145          150
tgg gag gaa gag aat gcc ctc tgg gag gaa gag agg gcc ttc tgg atg      870
Trp Glu Glu Glu Asn Ala Leu Trp Glu Glu Glu Arg Ala Phe Trp Met
          155          160          165
gag aac aat ggc cac att gcc gga gag cag atg ctc gaa gat ggg ccc      918
Glu Asn Asn Gly His Ile Ala Gly Glu Gln Met Leu Glu Asp Gly Pro
          170          175          180
cac aac gcc aac aga ggg cag cgc ttg ctg gcc ttc tcc cga ggc agg      966
His Asn Ala Asn Arg Gly Gln Arg Leu Leu Ala Phe Ser Arg Gly Arg
185          190          195          200
gcg tagccagcat gcaggtgcan gggccctgtg gtccagactc ccctggggtg      1019
Ala
ggattcaagt ccagggtgag cccatgtgct ggagaaaata cacactcatt ggtctccttg      1079
ctttgaaaga tccaataaag tcctgaggca aggtttggaa aaccaaaaaa aaaaaaaaaa      1138

```

<210> 21
 <211> 468
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 76..276

<220>
 <221> sig_peptide
 <222> 76..135
 <223> Von Heijne matrix
 score 5.21332530399231
 seq SPVFLVFPPEITA/SE

```

<400> 21
agcacaagaa aagaacatgg tctagactga agtaccact aaatcatctc ctttcaaatt      60
atcaccgaca ccatc atg gat tca agc acc gca cac agt ccg gtg ttt ctg      111
          Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu
          -20          -15          -10
gta ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt      159
Val Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu
          -5          1          5
tca gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct      207
Ser Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala
          10          15          20
aga aaa atg aaa atc tta ggg gat atc cat tct ggg gct ctg ttt tgt      255
Arg Lys Met Lys Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys
25          30          35          40
tca tta att ctg gag cct tcc taattgcagt gaaaagaaaa accacagaaa      306

```

Ser Leu Ile Leu Glu Pro Ser

45

ctctgggaat tttgattaca ttgatgactt tcagcattat tgaattattc atttctctgc	366
ctttctcaat tttgggggtgc cactcagagg attgtgattg tgaacaatgt tggtgactag	426
cactgtgaga ataaagatgt gttaaaataa aaaaaaaaaa aa	468

<210> 22
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..287

<220>
<221> sig_peptide
<222> 6..80
<223> Von Heijne matrix
score 4.17710408129886
seq ISLSHLFLDLSRS/LW

<400> 22	
atttg atg tgc ttc tta gtc tcg ttt aac ttg ccg att cat ata tcc ctg	50
Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu	
-25 -20 -15	
tct cat ttg ttc tta gat ttg tca cga agc ctc tgg ttt ttg gct tgt	98
Ser His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys	
-10 -5 1 5	
cct ggt ttg aac ttg gtg tat ctg gct ctt gac tca ttt tct gac ctc	146
Pro Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu	
10 15 20	
aga cca tcc tta aat ctg ctt ttc tac ttt gta cca ggc ttt ggc gtc	194
Arg Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val	
25 30 35	
tcc aag tac ctg acc tca gct caa cct gtc ttg ggt ttt ctt ctc ctc	242
Ser Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu	
40 45 50	
cct gac att gac aac cca gcc ctc cta ggc aca gag aga tgg agc	287
Pro Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser	
55 60 65	
tgagtgtggt tttcctgaaa taaagcttgc attatgagag ggaataaaca gaagaaaaaa	347
atagtaagta aaatcttgct tgccctctcag taaaataaag ctctattttt cgtttttttt	407
ttttccaact tcctgtacaa aaaagggaaa acttttagctt ttgggggaaa tttggagcta	467
gcctgttggt actggtgagc ttagtgtatc tataactata tattattcca caatatctta	527
aatactttat aaagatatatt tcataaatta cagcaatcct ggcttttagat gattgatggc	587
cattttttaa caattaaagc taatttctag ctttttatga gtttggtatt aagcacagta	647
gtttcttaga aagtctccag ggaatgcatt ttgcaaaata aaaatcagct aatgacccaa	707
aaaaaaaaaa aaa	720

<210> 23
<211> 727
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 171..692

<220>
 <221> sig_peptide
 <222> 171..227
 <223> Von Heijne matrix
 score 4.17573075349936
 seq LLLGQRCSLKVSG/QE

<400> 23
 attgtgacat caccgtgcac tagccaatgg ctgcctgcct aagctgggtc cctggtctcc 60
 tgggactact agccctttgt tgataggag aagccaacat ctcccgagg accccctaata 120
 cttcagggca gctccagag catggatccc tctgattcc actcagccc atg ttc 176
 Met Phe
 ctc aca gtc aag ctg ctc ctg ggc cag aga tgc agt ctg aag gtg tca 224
 Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys Val Ser
 -15 -10 -5
 ggg caa gag agt gta gcc acg ctg aag aga ctg gtg tcc agg cgg ctg 272
 Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg Arg Leu
 1 5 10 15
 aag gtg cct gag gag cag cag cac ctg ctt ttc cgt ggc cag ctc ctg 320
 Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln Leu Leu
 20 25 30
 gag gat gac aag cac ctc tct gac tac tgc att ggg ccc aat gcc tct 368
 Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn Ala Ser
 35 40 45
 atc aat gtc atc atg cag ccc ttg gag aag atg gcg cta aag gag gcc 416
 Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys Glu Ala
 50 55 60
 cac cag ccg cag acc cag ccc ctg tgg cac cag ctg gga ctg gtc cta 464
 His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu Val Leu
 65 70 75
 gct aaa cac ttt gaa cca cag gat gcc aag gcc gtg ctg cag ctg cta 512
 Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln Leu Leu
 80 85 90 95
 agg cag gag cac gag gag cgc ctg cag aag ata agc ctg gag cac ctg 560
 Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu His Leu
 100 105 110
 gag cag ctg gcc cag tac ctc ctg gca gag gag cct cac gtg gag cca 608
 Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val Glu Pro
 115 120 125
 gct gga gag agg gag ctt gag gcg aag gca cgg cct cag agc tcc tgt 656
 Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser Ser Cys
 130 135 140
 gac atg gag gag aag gag gag gca gca gct gat cag taaacggggc 702
 Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
 145 150 155
 atcctacccg aaaaaaaaaa aaaaaa 727

<210> 24
 <211> 470

```

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 137..454

<220>
<221> sig_peptide
<222> 137..187
<223> Von Heijne matrix
      score 10.7019149919754
      seq VLMLLAVLIWTGA/EN

<400> 24
atcctgtgaa ctacccaaaa ggaggaaaac gaacgcagct gagcatggga tgccatataa      60
aaatcactta aaccagtcgc cactccttgt ttcctgagtt gtcctgtgct ggaggtctgc      120
tcagacgaag gtctcc atg gcg tta gaa gtc ttg atg ctc ctc gct gtc ttg      172
          Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu
                -15                                -10

att tgg acc ggt gct gag aac ctc cat gtg aaa ata agt tgc tct ctg      220
Ile Trp Thr Gly Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu
-5              1              5              10
gac tgg ttg atg gtc tca gtt atc cca gtt gca gaa agc aga aat ctg      268
Asp Trp Leu Met Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu
          15              20              25
tat ata ttt gcg gat gaa tta cat ctg gga atg ggc tgc cct gca aat      316
Tyr Ile Phe Ala Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn
          30              35              40
cgg ata cat aca tat gta tat gag ttt ata tat ctt gtt cgt gat tgt      364
Arg Ile His Thr Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys
          45              50              55
ggc atc agg aca agg gta aga aca gtg att gtc tgt aaa aaa tac tgc      412
Gly Ile Arg Thr Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys
60              65              70              75
atg ttt tgt cag act ttt atg cct agt att aaa att gtc ttt      454
Met Phe Cys Gln Thr Phe Met Pro Ser Ile Lys Ile Val Phe
          80              85

taaaaaaaaa aaaaaa      470

<210> 25
<211> 987
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 238..609

<220>
<221> sig_peptide
<222> 238..291
<223> Von Heijne matrix
      score 10.0374888212272

```

seq LLLLVMALPPGTT/GV

```

<400> 25
attccattca cagactcttg ttgggcagca gccacccgct cacctccatc cccaggactt      60
agagggacgc agggcgcttg gaacagagga cactccaggc gctgaccctg ggaggccagg      120
accagggcca aagtcccctg ggcaagagga gtcctcagag gtccttcatt cagcggttcc      180
gggaggtctg ggaagcccac ggcctggctg gggcagggtc aacgccgcca ggccgcc      237
atg gtc ctg tgc tgg ctg ctg ctt ctg gtg atg gct ctg ccc cca ggc      285
Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
          -15          -10          -5

acg acg ggc gtc aag gac tgc gtc ttc tgt gag ctc acc gac tcc atg      333
Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
          1          5          10

cag tgt cct ggt acc tac atg cac tgt ggc gat gac gag gac tgc ttc      381
Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
          15          20          25          30

aca ggc cac ggg gtc gcc ccg ggc act ggt ccg gtc atc aac aaa ggc      429
Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
          35          40          45

tgc ctg cga gcc acc agc tgc ggc ctt gag gaa ccc gtc agc tac agg      477
Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
          50          55          60

ggc gtc acc tac agc ctc acc acc aac tgc tgc acc ggc cgc ctg tgt      525
Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
          65          70          75

aac aga gcc ccg agc agc cag aca gtg ggg gcc acc acc agc ctg gca      573
Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
          80          85          90

ctg ggg ctg ggt atg ctg ctt cct cca cgt ttg ctg tgaccaacag      619
Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
          95          100          105

ggaggacagg gcctgggact gttctcccag atccgccact ccccatgtcc ccatgtcctt      679
ccccactaa atggccagag aggccctgga caacctcttg cgccctggc ttcacccctt      739
ctaaggctgt ccaccaggag cccggtgcta ggggaagcat cccaggcct gactgagcgg      799
caggggagca cggcccgtgg gtttgattgt attactctgt tccactgggt ctaagacgca      859
gagctttctca catctcaatc aggatgcttc tctccattgg tagcacttta gagtccatga      919
aatatggtaa aaaatatata tatatcataa taaatgacag ctgatgttca tggaaaaaaa      979
aaaaaaaaa

```

<210> 26
 <211> 908
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..862

<220>
 <221> sig_peptide
 <222> 80..127
 <223> Von Heijne matrix
 score 3.66725851505537
 seq FSLLSISGPPISS/SA

```

<400> 26
gaatgtttat cctctggaca aaccagccag cctctccaga gcaggcgtgt gatctctgta      60
ccccgcagtg ggtcagaat atg gag aac ttc tca ctc ctc agc atc tct gga      112
          Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly
          -15          -10
cct cca atc tct tcc tcc gcc ctg agt gct ttt ccc gac att atg ttc      160
Pro Pro Ile Ser Ser Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe
-5          1          5          10
tct cgt gcc acc agc ctg cca gac att gca aag aca gca gta ccc act      208
Ser Arg Ala Thr Ser Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr
          15          20          25
gag gca tcc agc cca gct cag gcc ctg cca ccc cag tac caa agc atc      256
Glu Ala Ser Ser Pro Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile
          30          35          40
att gtc agg caa ggg ata cag aac aca gtg ctc tca cca gac tgc agc      304
Ile Val Arg Gln Gly Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser
          45          50          55
ttg ggg gac acc cag cac gga gag aag ctg agg cgg aac tgc act atc      352
Leu Gly Asp Thr Gln His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile
60          65          70          75
tac cgg ccc tgg ttc tcc ccc tac agc tac ttc gtg tgt gca gac aaa      400
Tyr Arg Pro Trp Phe Ser Pro Tyr Ser Tyr Phe Val Cys Ala Asp Lys
          80          85          90
gag agc cag ctg gag gcc tat gac ttc cca gag gtg cag cag gat gag      448
Glu Ser Gln Leu Glu Ala Tyr Asp Phe Pro Glu Val Gln Gln Asp Glu
          95          100          105
ggc aag tgg gac aac tgc ctt tct gag gac atg gct gag aac atc tgt      496
Gly Lys Trp Asp Asn Cys Leu Ser Glu Asp Met Ala Glu Asn Ile Cys
          110          115          120
tcg tcc tct tcc tcc cca gag aac act tgc cct cga gaa gcc acc aag      544
Ser Ser Ser Ser Ser Pro Glu Asn Thr Cys Pro Arg Glu Ala Thr Lys
          125          130          135
aaa tcc agg cat ggc ctg gac tcc atc aca tcc cag gac atc cta atg      592
Lys Ser Arg His Gly Leu Asp Ser Ile Thr Ser Gln Asp Ile Leu Met
140          145          150          155
gct tcc aga tgg cac cca gca cag cag aat ggc tac aag tgc gtg gcc      640
Ala Ser Arg Trp His Pro Ala Gln Gln Asn Gly Tyr Lys Cys Val Ala
          160          165          170
tgc tgc cgc atg tac ccc acc ctg gac ttc ctc aag agc cac atc aag      688
Cys Cys Arg Met Tyr Pro Thr Leu Asp Phe Leu Lys Ser His Ile Lys
          175          180          185
agg ggc ttc agg gag ggc ttc agc tgc aag gtg tac tac cgc aag ctc      736
Arg Gly Phe Arg Glu Gly Phe Ser Cys Lys Val Tyr Tyr Arg Lys Leu
          190          195          200
aaa gcc ctc tgg agc aag gag cag aag gcc cgg ctg gga gac agg ctc      784
Lys Ala Leu Trp Ser Lys Glu Gln Lys Ala Arg Leu Gly Asp Arg Leu
          205          210          215
tcc tcc ggc agc tgc cag gcc ttc aat agt cct gct gaa cac ctt agg      832
Ser Ser Gly Ser Cys Gln Ala Phe Asn Ser Pro Ala Glu His Leu Arg
220          225          230          235
caa att ggc ggt gaa gcc tac tta tgt ctc tagagagatg ccaataaagt      882
Gln Ile Gly Gly Glu Ala Tyr Leu Cys Leu
          240          245

```

tagtcacagc caaaaaaaaa aaaaaa

908

<210> 27
<211> 762
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..310

<220>
<221> sig_peptide
<222> 83..157
<223> Von Heijne matrix
score 4.72955689475746
seq LCALLSNFCPSTT/VK

<400> 27
ttttttctac taaaaacgcc atgggggatgc gggctctggga acagcggaaa accctaccct 60
gccctgaaaa gtccctggct ca atg tgc atg tcc ctt tct atg aaa gtt cct 112
Met Cys Met Ser Leu Ser Met Lys Val Pro
-25 -20
tgc tgc cta tgc gcc ttg ctc tct aac ttc tgt ccc tcc aca act gtg 160
Cys Cys Leu Cys Ala Leu Ser Asn Phe Cys Pro Ser Thr Thr Val
-15 -10 -5 1
aaa gga gac gtc gtg act tcc ttc ttt cgt gct gac tat gac tta gcc 208
Lys Gly Asp Val Thr Ser Phe Phe Arg Ala Asp Tyr Asp Leu Ala
5 10 15
agt agg tct gca gat cag tcc tcc cag aaa gtg aag ttg cgc atg ttc 256
Ser Arg Ser Ala Asp Gln Ser Ser Gln Lys Val Lys Leu Arg Met Phe
20 25 30
act ggg cgt ctt ccc atc ggc ccc ttc gcc agt gtg ggg aac gcg gcg 304
Thr Gly Arg Leu Pro Ile Gly Pro Phe Ala Ser Val Gly Asn Ala Ala
35 40 45
gag ctg tgagccggcg actcgggtcc ctgaggtctg gattctttct ccgctactga 360
Glu Leu
50
gacacggcgg acacacacaa acacagaacc acacagccag tcccaggagc ccagtaatgg 420
agagccccaa aaagaagaac cagcagctga aagtcgggat cctacacctg ggcagcagac 480
agaagaagat caggatacag ctgagatccc agtgcgcgac atggaagggtg atctgcaaga 540
gctgcatcag tcaaacaccg gggataaatc tggatttggg ttccggcgtc aaggtgaaga 600
taatacctaa agaggaacac tgtaaaatgc cagaagcagg tgaagagcaa ccacaagttt 660
aatgaagac aagctgaaac aacgcaagct ggttttatat tagatatttg acttaacta 720
tctcaataaa gttttgcagc tttcaccaaa aaaaaaaaaa aa 762

<210> 28
<211> 1102
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 310..906


```

<220>
<221> sig_peptide
<222> 310..357
<223> Von Heijne matrix
      score 11.0931109030915
      seq FPLLLLSLGLVLA/EA

<400> 28
atacagtgac ctagagcagg catgggtggg tcacaggctt tggagagcac tctctgtcct      60
gatcttttca gttgagagac ttcagctggt cattgctcat ttggacttag ttcaagggtca    120
tgtcaaagaa gaaggtgcac ttacgctagt tgttagctct gtcttttgta accatcaagt      180
tccatgcgat tgatcagatt taggaggggg cgttggggga taatcaattt tgggtgtcac      240
caggtaaaca gagccctcag catctgaata gaaactgaac aggaacagaa gagattcact      300
acatctgag atg gag acc ttt cct ctg ctg ctg ctc agc ctg ggc ctg gtt      351
      Met Glu Thr Phe Pro Leu Leu Leu Leu Ser Leu Gly Leu Val
            -15                -10                -5

ctt gca gaa gca tca gaa agc aca atg aag ata att aaa gaa gaa ttt      399
Leu Ala Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe
            1                5                10

aca gac gaa gag atg caa tat gac atg gca aaa agt ggc caa gaa aaa      447
Thr Asp Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys
15                20                25                30

cag acc att gag ata tta atg aac ccg atc ctg tta gtt aaa aat acc      495
Gln Thr Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr
            35                40                45

agc ctc agc atg tcc aag gat gat atg tct tcc aca tta ctg aca ttc      543
Ser Leu Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe
            50                55                60

aga agt tta cat tat aat gac ccc aag gga aac agt tcg ggt aat gac      591
Arg Ser Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp
65                70                75

aaa gag tgt tgc aat gac atg aca gtc tgg aga aaa gtt tca gaa gca      639
Lys Glu Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala
80                85                90

aac gga tcg tgc aag tgg agc aat aac ttc atc cgc agc tcc aca gaa      687
Asn Gly Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu
95                100                105                110

gtg atg cgc agg gtc cac agg gcc ccc agc tgc aag ttt gta cag aat      735
Val Met Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn
            115                120                125

cct ggc ata agc tgc tgt gag agc cta gaa ctg gaa aat aca gtg tgc      783
Pro Gly Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys
            130                135                140

cag ttc act aca ggc aaa caa ttc ccc agg tgc caa tac cat agt gtt      831
Gln Phe Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val
145                150                155

acc tca tta gag aag ata ttg aca gtg ctg aca ggt cat tct ctg atg      879
Thr Ser Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met
160                165                170

agc tgg tta gtt tgt ggc tct aag ttg taaatcccac agagctttag      926
Ser Trp Leu Val Cys Gly Ser Lys Leu
175                180

gactagggtc ttactaaaga aggacctctt cttgttcatt cttgtttaaa cctttcctta      986

```

atatctactc tttagcacta tagtgaactc ctgattatattt attctaactg gaggagtgaa 1046
 aaatccaaaa ttgtggataa ttcaattaaa agttatgact gaaaaaaaaa aaaaaa 1102

<210> 29
 <211> 436
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..287

<220>
 <221> sig_peptide
 <222> 24..131
 <223> Von Heijne matrix
 score 3.79790641648006
 seq ILMRDFSPSGIFG/AF

<400> 29
 acagcggaca ccaggactcc aaa atg gcg tca gtt gta cca gtg aag gac aag 53
 Met Ala Ser Val Val Pro Val Lys Asp Lys
 -35 -30
 aaa ctt ctg gag gtc aaa ctg ggg gag ctg cca agc tgg atc ttg atg 101
 Lys Leu Leu Glu Val Lys Leu Gly Glu Leu Pro Ser Trp Ile Leu Met
 -25 -20 -15
 cgg gac ttc agt cct agt ggc att ttc gga gcg ttt caa aga ggt tac 149
 Arg Asp Phe Ser Pro Ser Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr
 -10 -5 1 5
 tac cgg tac tac aac aag tac atc aat gtg aag aag ggg agc atc tcg 197
 Tyr Arg Tyr Tyr Asn Lys Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser
 10 15 20
 ggg att acc atg gtg ctg gca tgc tac gtg ctc ttt agc tac tcc ttt 245
 Gly Ile Thr Met Val Leu Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe
 25 30 35
 tcc tac aag cat ctc aag cac gag cgg ctc cgc aaa tac cac 287
 Ser Tyr Lys His Leu Lys His Glu Arg Leu Arg Lys Tyr His
 40 45 50
 tgaagaggac acactctgca cccccccacc ccacgacctt ggcccagagcc cctccgtgag 347
 gaacacaatc tcaatcggtg ctgaatcctt tcatatccta ataggaatta acctccaaat 407
 aaaacatgac tggtaaaaaa aaaaaaaaaa 436

<210> 30
 <211> 1938
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 132..1574

<220>
 <221> sig_peptide
 <222> 132..206

<223> Von Heijne matrix
 score 11.1130239236827
 seq LALLLTSTPEALG/AN

```

<400> 30
ctcccccttcc cgctcccagg aacccatcca gcctcaggaa ctgccccccag ccacgcagacc 60
ttggctactt aagggacctg ggcccaatcc acagctggga cagtcctggc ccaactgcact 120
gggaatctag g atg ggg gcc ttg gcc aga gcc ctg ccg tcc ata ctg ctg 170
      Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu
      -25          -20          -15
gca ttg ctg ctt acg tcc acc cca gag gct ctg ggt gcc aac ccc ggc 218
Ala Leu Leu Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly
      -10          -5          1
ttg gtc gcc agg atc acc gac aag gga ctg cag tat gcg gcc cag gag 266
Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu
      5          10          15          20
ggg cta ttg gct ctg cag agt gag ctg ctc agg atc acg ctg cct gac 314
Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp
      25          30          35
ttc acc ggg gac ttg agg atc ccc cac gtc ggc cgt ggg cgc tat gag 362
Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu
      40          45          50
ttc cac agc ctg aac atc cac agc tgt gag ctg ctt cac tct gcg ctg 410
Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu
      55          60          65
agg cct gtc cct ggc cag ggc ctg agt ctc agc atc tcc gac tcc tcc 458
Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser
      70          75          80
atc cgg gtc cag ggc agg tgg aag gtg cgc aag tca ttc ttc aaa cta 506
Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu
      85          90          95          100
cag ggc tcc ttt gat gtc agt gtc aag ggc atc agc att tcg gtc aac 554
Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn
      105          110          115
ctc ctg ttg ggc agc gat tcc tcc ggg agg ccc aca gtt act gcc tcc 602
Leu Leu Leu Gly Ser Asp Ser Ser Gly Arg Pro Thr Val Thr Ala Ser
      120          125          130
agc tgc agc agt gac atc gct gac gtg gag gtg gac atg tcg gga gac 650
Ser Cys Ser Ser Asp Ile Ala Asp Val Glu Val Asp Met Ser Gly Asp
      135          140          145
ttg ggg tgg ctg ttg aac ctc ttc cac aac cag att gag tcc aag ttc 698
Leu Gly Trp Leu Leu Asn Leu Phe His Asn Gln Ile Glu Ser Lys Phe
      150          155          160
cag aaa gta ctg gag agc agg att tgc gaa atg atc cag aaa tcg gtg 746
Gln Lys Val Leu Glu Ser Arg Ile Cys Glu Met Ile Gln Lys Ser Val
      165          170          175          180
tcc tcc gat cta cag cct tat ctc caa act ctg aca gtt aca aca gag 794
Ser Ser Asp Leu Gln Pro Tyr Leu Gln Thr Leu Thr Val Thr Thr Glu
      185          190          195
att gac agt ttc gcc gac att gat tat agc tta gtg gaa gcc cct cgg 842
Ile Asp Ser Phe Ala Asp Ile Asp Tyr Ser Leu Val Glu Ala Pro Arg
      200          205          210
gca aca gcc cag atg ctg gag gtg atg ttt aag ggt gaa atc ttt cat 890
Ala Thr Ala Gln Met Leu Glu Val Met Phe Lys Gly Glu Ile Phe His

```

215	220	225	
cgt aac cac cgt tct cca gtt acc ctc ctt gct gca gtc atg agc ctt			938
Arg Asn His Arg Ser Pro Val Thr Leu Leu Ala Ala Val Met Ser Leu			
230	235	240	
cct gag gaa cac aac aaa atg gtc tac ttt gcc atc tcg gat tat gtc			986
Pro Glu Glu His Asn Lys Met Val Tyr Phe Ala Ile Ser Asp Tyr Val			
245	250	255	260
ttc aac acg gcc agc ctg gtt tat cat gag gaa gga tat ctg aac ttc			1034
Phe Asn Thr Ala Ser Leu Val Tyr His Glu Glu Gly Tyr Leu Asn Phe			
265	270	275	
tcc atc aca gat gac atg ata ccg cct gac tct aat atc cga ctg acc			1082
Ser Ile Thr Asp Asp Met Ile Pro Pro Asp Ser Asn Ile Arg Leu Thr			
280	285	290	
acc aag tcc ttc cga ccc ttc gtc cca cgg tta gcc agg ctc tac ccc			1130
Thr Lys Ser Phe Arg Pro Phe Val Pro Arg Leu Ala Arg Leu Tyr Pro			
295	300	305	
aac atg aac ctg gaa ctc cag gga tca gtg ccc tct gct ccg ctc ctg			1178
Asn Met Asn Leu Glu Leu Gln Gly Ser Val Pro Ser Ala Pro Leu Leu			
310	315	320	
aac ttc agc cct ggg aat ctg tct gtg gac ccc tat atg gag ata gat			1226
Asn Phe Ser Pro Gly Asn Leu Ser Val Asp Pro Tyr Met Glu Ile Asp			
325	330	335	340
gcc ttt gtg ctc ctg ccc agc tcc agc aag gag cct gtc ttc cgg ctc			1274
Ala Phe Val Leu Leu Pro Ser Ser Ser Lys Glu Pro Val Phe Arg Leu			
345	350	355	
agt gtg gcc act aat gtg tcc gcc acc ttg acc ttc aat acc agc aag			1322
Ser Val Ala Thr Asn Val Ser Ala Thr Leu Thr Phe Asn Thr Ser Lys			
360	365	370	
atc act ggg ttc ctg aag cca gga aag gta aaa gtg gaa ctg aaa gaa			1370
Ile Thr Gly Phe Leu Lys Pro Gly Lys Val Lys Val Glu Leu Lys Glu			
375	380	385	
tcc aaa gtt gga cta ttc aat gca gag ctg ttg gaa gcg ctc ctc aac			1418
Ser Lys Val Gly Leu Phe Asn Ala Glu Leu Leu Glu Ala Leu Leu Asn			
390	395	400	
tat tac atc ctt aac acc ttc tac ccc aag ttc aat gat aag ttg gcc			1466
Tyr Tyr Ile Leu Asn Thr Phe Tyr Pro Lys Phe Asn Asp Lys Leu Ala			
405	410	415	420
gaa ggc ttc ccc ctt cct ctg ctg aag cgt gtt cag ctc tac gac ctt			1514
Glu Gly Phe Pro Leu Pro Leu Leu Lys Arg Val Gln Leu Tyr Asp Leu			
425	430	435	
ggg ctg cag atc cat aag gac ttc ctg ttc ttg ggt gcc aat gtc caa			1562
Gly Leu Gln Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln			
440	445	450	
tac atg aga gtt tgaggacaag aaagatgaag cttggaggtc acagctggat			1614
Tyr Met Arg Val			
455			
ctgcttggttg catttccagc tgtgcagcac gtctcagaga ttcttgaaga atgaagacat			1674
ttctgctctc agctccgggg gtgaggtgtg cctggcctct gcctccaccc tctcctctt			1734
caccaggtgc atgcatgcc tctctgagtc tggactttgc ttcccctcca ggagggacca			1794
ccctccctga ctggcctggg atatctttac aagcaggcac tgtatttttt tattcgccat			1854
ctgatcccca tgcctagcag agtgctggca cttagtaggt cctcaataaa tattttattaa			1914
atgatgacaa aaaaaaaaaa aaaa			1938

<210> 31

<211> 1116
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 117..545

<220>
 <221> sig_peptide
 <222> 117..245
 <223> Von Heijne matrix
 score 5.65876793443964
 seq VVSFALIATLVYA/LF

<400> 31
 ataaggggac gtctagtggg ttgcccggga ggggtggcgg gagcggtcct ggaaataatc 60
 tgtcctctgt cgccgggaac tggcgaggta gttccttcgc ggtggagaga cctgga atg 119
 Met
 gcc aaa tat caa ggt gaa gtt caa agt ttg aaa ctg gat gat gat tca 167
 Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp Ser
 -40 -35 -30
 gtt ata gaa gga gta agc gac caa gta ctt gtg gca gtt gtg gtc agt 215
 Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val Ser
 -25 -20 -15
 ttc gct ttg att gct acc ctg gta tat gca ctt ttc aga aat gta cat 263
 Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val His
 -10 -5 1 5
 caa aac att cac cca gaa aac cag gag cta gta agg gta ctt cga gaa 311
 Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg Glu
 10 15 20
 cag ctt caa aca gaa cag gat gca cct gct gcc act cga cag cag ttc 359
 Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Ala Thr Arg Gln Gln Phe
 25 30 35
 tac act gac atg tac tgt ccc atc tgc ctg cac caa gcc tcc ttc ccg 407
 Tyr Thr Asp Met Tyr Cys Pro Ile Cys Leu His Gln Ala Ser Phe Pro
 40 45 50
 gtg gag acc aac tgt gga cat ctt ttt tgt ggt gcc tgc att att gct 455
 Val Glu Thr Asn Cys Gly His Leu Phe Cys Gly Ala Cys Ile Ile Ala
 55 60 65 70
 tac tgg cga tat ggt tca tgg ctt ggg gca atc agt tgt cca atc tgt 503
 Tyr Trp Arg Tyr Gly Ser Trp Leu Gly Ala Ile Ser Cys Pro Ile Cys
 75 80 85
 aga caa acg aga cat ggc cac att gca ttg tcc aga aca gct 545
 Arg Gln Thr Arg His Gly His Ile Ala Leu Ser Arg Thr Ala
 90 95 100
 tagaccatga cagtttagcat cgaagccacc tgaggaggga ggcagtaacc ttactcctaa 605
 cagtatttgg tgaagatgat cagtctcagg atgttctgag attgcatcag gatattaatg 665
 attataaccg gagattctca gggcaaccca gatctgtaag taatgctaaa gcatgttcaa 725
 agttagagga agacacattt cttctctttt gtaaagtgag gtttaccac aagtattctt 785
 tgactatgag aaatcttggc caggcacagt agctaacgcc tataatccta gcactttggg 845
 aggccaaggc aggtggatca cttgagccca ggagtttgag accagccttg gaaacatgat 905
 gaaaccccat ctctagaaaa aacaccaaaa aattggacaa gagtgttggc acatgcctgt 965
 agtccttgc tcttgggagg ctgaaatggg aggatcacct gagcccagga ggttgaggct 1025

atagtgagcc atgatcgcac tattgcactc ccacctgggt ggcagtgaga cccttcctca 1085
 aaaaacaaga aaagaaaaaa aaaaaaaaaa a 1116

<210> 32
 <211> 1114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 117..362

<400> 32
 ataaggggac gtctagtggg ttgcccggga ggggtggcgg gagcggtcct ggaaataatc 60
 tgtcctctgt cgccgggaac tggcgaggta gttccttcgc ggtggagaga cctgga atg 119
 Met
 1
 gcc aaa tat caa ggt gaa gtt caa agt ttg aaa ctg gat gat gat tca 167
 Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp Ser
 5 10 15
 gtt ata gaa gga gta agc gac caa gta ctt gtg gca gtt gtg gtc agt 215
 Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val Ser
 20 25 30
 ttc gct ttg att gct acc ctg gta tat gca ctt ttc aga aat gta cat 263
 Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val His
 35 40 45
 caa aac att cac cca gaa aac cag gag cta gta agg gta ctt cga gaa 311
 Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg Glu
 50 55 60 65
 cag ctt caa aca gaa cag gat gca cct gct gac tcg aca gca gtt cta 359
 Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Asp Ser Thr Ala Val Leu
 70 75 80
 cac tgacatgtac tgtcccatct gctgcacca agcctccttc ccggtggaga 412
 His
 ccaactgtgg acatcttttt tgtgggtgcct gcattattgc ttactggcga tatggttcat 472
 ggcttggggc aatcagttgt ccaatctgta gacaaacgag acatggccac attgcattgt 532
 ccagaacagc ttagaccatg acagttagca tcgaagccac ctgaggaggg aggcagtaac 592
 cttactccta acagtatttg gtgaagatga tcagtctcag gatgttctga gattgcatca 652
 ggatattaat gattataacc ggagattctc agggcaaccc agatctgtaa gtaatgctaa 712
 agcatgttca aagttagagg aagacacatt tcttctcttt tgtaaagtga ggtttaccac 772
 caagtattct ttgactatga gaaatcttgg ccaggcacag tagctaacgc ctataatcct 832
 agcacttttg gaggccaaagg caggtggatc acttgagccc aggagtttga gaccagcctt 892
 ggaaacatga tgaacccca tctctagaaa aaacacccaaa aaattggaca agagtgttgg 952
 cacatgcctg tagtccctgc ttcttgggag gctgaaatgg gaggatcacc tgagcccagg 1012
 aggttgaggc tatagtgagc catgatcgca ctattgcact ccacacctggg tggcagtgag 1072
 acccttcctc aaaaaacaag aaaagaaaaa aaaaaaaaaa aa 1114

<210> 33
 <211> 2072
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

ttc ata cct gat atc tat att tac aca gat cac att aaa gga gtc aac	845
Phe Ile Pro Asp Ile Tyr Ile Tyr Thr Asp His Ile Lys Gly Val Asn	
195 200 205	
tct ggg aag tct ccg ggc ttt ggg ttg tca ctg gtt gct gag acc acc	893
Ser Gly Lys Ser Pro Gly Phe Gly Leu Ser Leu Val Ala Glu Thr Thr	
210 215 220	
agt ggc acc ttc ctc agt gct gaa ctg gcc tcc aac ccc cag ggc cag	941
Ser Gly Thr Phe Leu Ser Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln	
225 230 235	
gga gca gca gta ctt cca gag gac ctt ggc agg aac tgt gcc cgg ctg	989
Gly Ala Ala Val Leu Pro Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu	
240 245 250 255	
ctg ctg gag gaa atc tac agg ggt gga tgc gta gac tcg acc aac caa	1037
Leu Leu Glu Glu Ile Tyr Arg Gly Gly Cys Val Asp Ser Thr Asn Gln	
260 265 270	
agc ctg gcg cta cta ctc atg acc ctt gga cag cag gat gtt tcc aaa	1085
Ser Leu Ala Leu Leu Leu Met Thr Leu Gly Gln Gln Asp Val Ser Lys	
275 280 285	
gtc ctg cta ggc cct ctc tct ccc tac acg ata gaa ttt ttg cgg cat	1133
Val Leu Leu Gly Pro Leu Ser Pro Tyr Thr Ile Glu Phe Leu Arg His	
290 295 300	
ttg aag agc ttt ttc cag att atg ttt aaa att gaa acc aag cca tgt	1181
Leu Lys Ser Phe Phe Gln Ile Met Phe Lys Ile Glu Thr Lys Pro Cys	
305 310 315	
ggt gaa gaa ctc aag ggt ggg gat aaa gtg ctg atg acc tgt gtt ggc	1229
Gly Glu Glu Leu Lys Gly Gly Asp Lys Val Leu Met Thr Cys Val Gly	
320 325 330 335	
att ggt ttc tcc aac ctt agc agg acc ctc aag tgataacccat cacaagataa	1282
Ile Gly Phe Ser Asn Leu Ser Arg Thr Leu Lys	
340 345	
ggccccagtg cctacagaca aagcagaagc tgccacggac accaatggga ccaagtccaa	1342
atggattaat ccaggacaga atagccactt gcttaatttt ctgtgaagaa atatcaatat	1402
acaaataaaa gacatccctg tagcatatgg tttccagctg tttctccagt ggcattgcc	1462
ttgcccagga ggggcccagt caccatgaga gctcccttgc cttacctgga ggaagaatgt	1522
gccttcaggc cacagtcgtg ctgctagaac agtctcgtag ctgcagttca gctgtgcttc	1582
ctcagcctac tatcataggc ttcctcagcc ctctgtcata tggctgtttt gcaaacctgt	1642
ggagtctgtt actgttcttt ctgcaaggac tcacctcctt gagccttggg ttttgttgta	1702
gggattaaat gagataatat gaggggcagc tcttcatgag tctgagctg ctaagcaaat	1762
gtcagaaatt ggtgtattag actattttatc tttgatcttc tgaatggatt gctgtcatgg	1822
acacggacac ggatcttcat ctggttcatt gtatttata gtgagggatg gatggctgcg	1882
gggctccaag taagtatttg ggatgttttt atattccagg tgtgctgtac gttcttattt	1942
tattttcaca atagctctgt gatgtaagt ctatctccat gagaaaattc ataaagggtg	2002
ttttgttcat ttgaaatgta taatgtaaag acattaaatc tcctcattta agggaaaaaa	2062
aaaaaaaaa	2072

<210> 34
 <211> 409
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..316


```

<220>
<221> sig_peptide
<222> 35..109
<223> Von Heijne matrix
      score 5.38058532480537
      seq AVTSLLSPTPATA/LA

<400> 34
tttttttcga gaccggaagt gagtgatcga aagc atg gcg tcg gtg gtg ttg gcg      55
                               Met Ala Ser Val Val Leu Ala
                               -25                               -20
ctg agg acc cgg aca gcc gtt aca tcc ttg cta agc ccc act ccg gct      103
Leu Arg Thr Arg Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala
                               -15                               -10                               -5
aca gct ctt gct gtc aga tac gca tcc aag aag tcg ggt ggt agc tcc      151
Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser
                               1                               5                               10
aaa aac ctc ggt gga aag tca tca ggc aga cgc caa ggc att aag aaa      199
Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys
15                               20                               25                               30
atg gaa ggt cac tat gtt cat gct ggg aac atc att gca aca cag cgc      247
Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg
                               35                               40                               45
cat ttc cgc tgg cac cca ggt gcc cat gtg agt tgc tcc gtt gct gcc      295
His Phe Arg Trp His Pro Gly Ala His Val Ser Cys Ser Val Ala Ala
                               50                               55                               60
ccc ctt ttt cct ttt cta ggt tgacctctcc ttgccctaa gcatggtaat      346
Pro Leu Phe Pro Phe Leu Gly
                               65
aacagttgca tgtattgagt gcttaccaaa tggcaagcat tgtgccaaaa aaaaaaaaaa      406
aaa                                                                409

<210> 35
<211> 836
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 177..767

<220>
<221> sig_peptide
<222> 177..236
<223> Von Heijne matrix
      score 6.51720597568932
      seq LAVILTLLGLAIL/AI

<400> 35
aatctgctcc acgcaatttc tcagtgatcc tctgcatctc tgcctacaag ggccctccctg      60
acacccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct      120
ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaataca tggaaa atg      179
                               Met
                               -20

```

aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt	227
Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu	
-15 -10 -5	
gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt	275
Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser	
1 5 10	
gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg	323
Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu	
15 20 25	
gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt	371
Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser	
30 35 40 45	
gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg	419
Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu	
50 55 60	
tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa	467
Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys	
65 70 75	
tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg	515
Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met	
80 85 90	
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc	563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu	
95 100 105	
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct	611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro	
110 115 120 125	
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc	659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu	
130 135 140	
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc	707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser	
145 150 155	
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt	755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu	
160 165 170	
ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaatatg	807
Phe Ser Pro Ala	
175	
atagtgtata aatgaaaaaa aaaaaaaaaa	836

<210> 36
 <211> 1323
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 208..1239

<220>
 <221> sig_peptide
 <222> 208..294
 <223> Von Heijne matrix

score 5.73027134157378
seq GLVLICVCSKTHS/LK

<400> 36

```

agtctcgtat cgcgcccggg aggcgcggga gcccagcggc tggcgccaga tccaggctcc      60
tggaagaacc atgtccggca gctactggtc atgccaggca cacactgctg cccaagagga      120
gctgctgttt gaattatctg tgaatgttgg gaagaggaat gccagagctg cgggctgaaa      180
attaccaac caagagaaat ctgcagg atg gac ttt ctg gtc ctc ttc ttg ttc      234
                               Met Asp Phe Leu Val Leu Phe Leu Phe
                               -25
tac ctg gct tcg gtg ctg atg ggt ctt gtt ctt atc tgc gtc tgc tcg      282
Tyr Leu Ala Ser Val Leu Met Gly Leu Val Leu Ile Cys Val Cys Ser
-20                               -15                               -10                               -5
aaa acc cat agc ttg aaa ggc ctg gcc agg gga gga gca cag ata ttt      330
Lys Thr His Ser Leu Lys Gly Leu Ala Arg Gly Gly Ala Gln Ile Phe
                               1                               5                               10
tcc tgt ata att cca gaa tgt ctt cag aga gcc gtg cat gga ttg ctt      378
Ser Cys Ile Ile Pro Glu Cys Leu Gln Arg Ala Val His Gly Leu Leu
                               15                               20                               25
cat tac ctt ttc cat acg aga aac cac acc ttc att gtc ctg cac ctg      426
His Tyr Leu Phe His Thr Arg Asn His Thr Phe Ile Val Leu His Leu
                               30                               35                               40
gtc ttg caa ggg atg gtt tat act gag tac acc tgg gaa gta ttt ggc      474
Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr Trp Glu Val Phe Gly
45                               50                               55                               60
tac tgt cag gag ctg gag ttg tcc ttg cat tac ctt ctt ctg ccc tat      522
Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr Leu Leu Leu Pro Tyr
                               65                               70                               75
ctg ctg cta ggt gta aac ctg ttt ttt ttc acc ctg act tgt gga acc      570
Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr Leu Thr Cys Gly Thr
                               80                               85                               90
aat cct ggc att ata aca aaa gca aat gaa tta tta ttt ctt cat gtt      618
Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu Leu Phe Leu His Val
95                               100                               105
tat gaa ttt gat gaa gtg atg ttt cca aag aac gtg agg tgc tct act      666
Tyr Glu Phe Asp Glu Val Met Phe Pro Lys Asn Val Arg Cys Ser Thr
110                               115                               120
tgt gat tta agg aaa cca gct cga tcc aag cac tgc agt gtg tgt aac      714
Cys Asp Leu Arg Lys Pro Ala Arg Ser Lys His Cys Ser Val Cys Asn
125                               130                               135                               140
tgg tgt gtg cac cgt ttc gac cat cac tgt gtt tgg gtg aac aac tgc      762
Trp Cys Val His Arg Phe Asp His His Cys Val Trp Val Asn Asn Cys
145                               150                               155
atc ggg gcc tgg aac atc agg tac ttc ctc atc tac gtc ttg acc ttg      810
Ile Gly Ala Trp Asn Ile Arg Tyr Phe Leu Ile Tyr Val Leu Thr Leu
160                               165                               170
acg gcc tcg gct gcc acc gtc gcc att gtg agc acc act ttt ctg gtc      858
Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser Thr Thr Phe Leu Val
175                               180                               185
cac ttg gtg gtg atg tca gat tta tac cag gag act tac atc gat gac      906
His Leu Val Val Met Ser Asp Leu Tyr Gln Glu Thr Tyr Ile Asp Asp
190                               195                               200
ctt gga cac ctc cat gtt atg gac acg gtc ttt ctt att cag tac ctg      954
Leu Gly His Leu His Val Met Asp Thr Val Phe Leu Ile Gln Tyr Leu

```

205		210		215		220	
ttc ctg act ttt cca cgg att gtc ttc atg ctg ggc ttt gtc gtg gtt	1002						
Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu Gly Phe Val Val Val							
ctg agc ttc ctc ctg ggt ggc tac ctg ttg ttt gtc ctg tat ctg gcg	1050						
Leu Ser Phe Leu Leu Gly Gly Tyr Leu Leu Phe Val Leu Tyr Leu Ala							
gcc acc aac cag act act aac gag tgg tac aga ggt gac tgg gcc tgg	1098						
Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg Gly Asp Trp Ala Trp							
tgc cag cgt tgt ccc ctt gtg gcc tgg cct ccg tca gca gag ccc caa	1146						
Cys Gln Arg Cys Pro Leu Val Ala Trp Pro Pro Ser Ala Glu Pro Gln							
gtc cac cgg aac att cac tcc cat ggg ctt cgg agc aac ctt caa gag	1194						
Val His Arg Asn Ile His Ser His Gly Leu Arg Ser Asn Leu Gln Glu							
atc ttt cta cct gcc ttt cca tgt cat gag agg aag aaa caa gaa	1239						
Ile Phe Leu Pro Ala Phe Pro Cys His Glu Arg Lys Lys Gln Glu							
tgacaagtgt atgactgcct ttgagctgta gttcccgttt atttacacat gtggatcctc	1299						
gttttccaaa aaaaaaaaaa aaaa	1323						

<210> 37
 <211> 1945
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 60..1682

<220>
 <221> sig_peptide
 <222> 60..143
 <223> Von Heijne matrix
 score 3.75144398608723
 seq SGLLLQVLFRLIT/FV

<400> 37	
atcgcgacta aacggagtgg cggcggcatt tcttggtgtc tgagcctggc gcggaggct	59
atg ggc agc cag gag gtg ctg ggc cac gcg gcc cgg ctg tcc tcc tcc	107
Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ser Ser Ser	
ggt ctc ctc ctg cag gtg ttg ttt cgg ttg atc acc ttt gtc ttg aat	155
Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn	
gca ttt att ctt cgc ttc ctg tca aag gaa atc gtt ggc gta gta aat	203
Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn	
gta aga cta acg ctg ctt tac tca acc acc ctc ttc ctg gcc aga gag	251
Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu	
gcc ttc cgc aga gca tgt ctc agt ggg ggc acc cag cga gac tgg agc	299
Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser	

cag	acc	ctc	aac	ctg	ctg	tgg	cta	aca	gtc	ccc	ctg	ggg	gtg	ttt	tgg	347
Gln	Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp	
		55					60					65				
tcc	tta	ttc	ctg	ggc	tgg	atc	tgg	ttg	cag	ctg	ctt	gaa	gtg	cct	gat	395
Ser	Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp	
	70					75					80					
cct	aat	gtt	gtc	cct	cac	tat	gca	act	gga	gtg	gtg	ctg	ttt	ggg	ctc	443
Pro	Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu	
	85				90				95						100	
tcg	gca	gtg	gtg	gag	ctt	cta	gga	gag	ccc	ttt	tgg	gtc	ttg	gca	caa	491
Ser	Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln	
				105				110						115		
gca	cat	atg	ttt	gtg	aag	ctc	aag	gtg	att	gca	gag	agc	ctg	tcg	gta	539
Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val	
			120					125						130		
att	ctt	aag	acc	gtt	ctg	aca	gct	ttt	ctc	gtg	ctg	tgg	ttg	cct	cac	587
Ile	Leu	Lys	Thr	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His	
		135					140					145				
tgg	gga	ttg	tac	att	ttc	tct	ttg	gcc	cag	ctt	ttc	tat	acc	aca	gtt	635
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val	
	150					155					160					
ctg	gtg	ctc	tgc	tat	gtt	att	tat	ttc	aca	aag	tta	ctg	ggg	tcc	cca	683
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro	
	165				170					175					180	
gaa	tca	acc	aag	ctt	caa	act	ctt	cct	gtc	tcc	aga	ata	aca	gat	ctg	731
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	
				185					190					195		
tta	ccc	aat	att	aca	aga	aat	gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	779
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	
		200					205						210			
aaa	ctg	act	tgg	agt	ttt	ttc	aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	827
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	
		215					220					225				
aca	gaa	ggc	gag	cga	tat	gtg	atg	aca	ttt	ttg	aat	gta	ttg	aac	ttt	875
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	
	230					235					240					
ggg	gat	cag	ggg	gtg	tat	gat	ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	923
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val	
	245				250				255						260	
gcc	aga	tta	att	ttc	cag	cca	ata	gag	gaa	agt	ttt	tat	ata	ttt	ttt	971
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	
				265					270					275		
gct	aag	gtg	ctg	gag	agg	gga	aag	gat	gcc	aca	ctt	cag	aag	cag	gag	1019
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	
			280				285							290		
gac	gtt	gct	gtg	gct	gct	gca	gtc	ttg	gag	tcc	ctg	ctc	aag	ctg	gcc	1067
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	
		295					300					305				
ctg	ctg	gcc	ggc	ctg	acc	atc	act	gtt	ttt	ggc	ttt	gcc	tat	tct	cag	1115
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	
		310				315					320					
ctg	gct	ctg	gat	atc	tac	gga	ggg	acc	atg	ctt	agc	tca	gga	tcc	ggg	1163
Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	

325		330		335		340	
cct gtt ttg ctg cgt tcc tac tgt ctc tat gtt ctc ctg ctt gcc atc							1211
Pro Val Leu Leu Arg Ser Tyr Cys Leu Tyr Val Leu Leu Leu Ala Ile							
	345		350		355		
aat gga gtg aca gag tgt ttc aca ttt gct gcc atg agc aaa gag gag							1259
Asn Gly Val Thr Glu Cys Phe Thr Phe Ala Ala Met Ser Lys Glu Glu							
	360		365		370		
gtc gac agg tac aat ttt gtg atg ctg gcc ctg tcc tcc tca ttc ctg							1307
Val Asp Arg Tyr Asn Phe Val Met Leu Ala Leu Ser Ser Ser Phe Leu							
	375		380		385		
gtg tta tcc tat ctc ttg acc cgt tgg tgt ggc agc gtg ggc ttc atc							1355
Val Leu Ser Tyr Leu Leu Thr Arg Trp Cys Gly Ser Val Gly Phe Ile							
	390		395		400		
ttg gcc aac tgc ttt aac atg ggc att cgg atc acg cag agc ctt tgc							1403
Leu Ala Asn Cys Phe Asn Met Gly Ile Arg Ile Thr Gln Ser Leu Cys							
	405		410		415		420
ttc atc cac cgc tac tac cga agg agc ccc cac agg ccc ctg gct ggc							1451
Phe Ile His Arg Tyr Tyr Arg Arg Ser Pro His Arg Pro Leu Ala Gly							
	425		430		435		
ctg cac cta tcg cca gtc ctg ctc ggg aca ttt gcc ctc agt ggt ggg							1499
Leu His Leu Ser Pro Val Leu Leu Gly Thr Phe Ala Leu Ser Gly Gly							
	440		445		450		
gtt act gct gtt tcg gag gta ttc ctc tgc tgt gag cag ggc tgg cca							1547
Val Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro							
	455		460		465		
gcc aga ctg gca cac att gct gtg ggg gcc ttc tgt ctg gga gca act							1595
Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr							
	470		475		480		
ctc ggg aca gca ttc ctc aca gag acc aag ctg atc cat ttc ctc agg							1643
Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg							
	485		490		495		500
act cag tta ggt gtg ccc aga cgc act gac aaa atg aca tgacttcagg							1692
Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr							
	505		510				
gaagcctgga caccgaggc acctggacca gctatgggta gttctgtggg tggaacacat							1752
tctgtgtaag agccccactg agggctctgc agcggagtga cagcaacccc agagatgagg							1812
caccagagag tgccactgca tgagacacct gtgaccattc gaagtctgaa atgcgggggg							1872
ggagtttcat ttttaagtga agaccaaag ccctttaaaa ataatagttt tttatcaaaa							1932
aaaaaaaaaa aaa							1945

<210> 38
 <211> 1330
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 198..998

<220>
 <221> sig_peptide
 <222> 198..269
 <223> Von Heijne matrix
 score 9.08017839002281

seq LLLGPGLLATVRA/EC

<400> 38

```

agaaatcagc cctttgcaga gggcgagag ggccctgaaa cctctgggac cttttcccag      60
gaactgttta tggtttcccc ctaggtctag gagacgtaga tgcataaggtag gattggatac      120
atcgatggta gctataagag tcgtgtctga acccggtttt tccaattggc ctgctccatc      180
cgaacagcgt caactcc atg gcg cgg ttc ctg aca ctt tgc act tgg ctg      230
          Met Ala Arg Phe Leu Thr Leu Cys Thr Trp Leu
                    -20                                -15
ctg ttg ctc ggc ccc ggg ctc ctg gcg acc gtg cgg gcc gaa tgc agc      278
Leu Leu Leu Gly Pro Gly Leu Leu Ala Thr Val Arg Ala Glu Cys Ser
          -10                                -5                                1
cag gat tgc gcg acg tgc agc tac cgc cta gtg cgc ccg gcc gac atc      326
Gln Asp Cys Ala Thr Cys Ser Tyr Arg Leu Val Arg Pro Ala Asp Ile
          5                                10                                15
aac ttc ctg gct tgc gta atg gaa tgt gaa ggt aaa ctg cct tct ctg      374
Asn Phe Leu Ala Cys Val Met Glu Cys Glu Gly Lys Leu Pro Ser Leu
          20                                25                                30                                35
aaa att tgg gaa acc tgc aag gag ctc ctg cag ctg tcc aaa cca gat      422
Lys Ile Trp Glu Thr Cys Lys Glu Leu Leu Gln Leu Ser Lys Pro Asp
          40                                45                                50
ctt cct caa gat ggc acc agc acc ctc aga gaa aat agc aaa ccg gaa      470
Leu Pro Gln Asp Gly Thr Ser Thr Leu Arg Glu Asn Ser Lys Pro Glu
          55                                60                                65
gaa agc cat ttg cta gcc aaa agg tat ggg ggc ttc atg aaa agg tat      518
Glu Ser His Leu Leu Ala Lys Arg Tyr Gly Gly Phe Met Lys Arg Tyr
          70                                75                                80
gga ggc ttc atg aag aaa atg gat gag ctt tat ccc atg gag cca gaa      566
Gly Gly Phe Met Lys Lys Met Asp Glu Leu Tyr Pro Met Glu Pro Glu
          85                                90                                95
gaa gag gcc aat gga agt gag atc ctc gcc aag cgg tat ggg ggc ttc      614
Glu Glu Ala Asn Gly Ser Glu Ile Leu Ala Lys Arg Tyr Gly Gly Phe
          100                                105                                110                                115
atg aag aag gat gca gag gag gac gac tcg ctg gcc aat tcc tca gac      662
Met Lys Lys Asp Ala Glu Glu Asp Asp Ser Leu Ala Asn Ser Ser Asp
          120                                125                                130
ctg cta aaa gag ctt ctg gaa aca ggg gac aac cga gag cgt agc cac      710
Leu Leu Lys Glu Leu Leu Glu Thr Gly Asp Asn Arg Glu Arg Ser His
          135                                140                                145
cac cag gat ggc agt gat aat gag gaa gaa gtg agc aag aga tat ggg      758
His Gln Asp Gly Ser Asp Asn Glu Glu Glu Val Ser Lys Arg Tyr Gly
          150                                155                                160
ggc ttc atg aga ggc tta aag aga agc ccc caa ctg gaa gat gaa gcc      806
Gly Phe Met Arg Gly Leu Lys Arg Ser Pro Gln Leu Glu Asp Glu Ala
          165                                170                                175
aaa gag ctg cag aag cga tat ggg ggc ttc atg aga aga gta ggt cgc      854
Lys Glu Leu Gln Lys Arg Tyr Gly Gly Phe Met Arg Arg Val Gly Arg
          180                                185                                190                                195
cca gag tgg tgg atg gac tac cag aaa cgg tat gga ggt ttc ctg aag      902
Pro Glu Trp Trp Met Asp Tyr Gln Lys Arg Tyr Gly Gly Phe Leu Lys
          200                                205                                210
cgc ttt gcc gag gct ctg ccc tcc gac gaa gaa ggc gaa agt tac tcc      950
Arg Phe Ala Glu Ala Leu Pro Ser Asp Glu Glu Gly Glu Ser Tyr Ser
          215                                220                                225

```

aaa gaa gtt cct gaa atg gaa aaa aga tac gga gga ttt atg aga ttt	998
Lys Glu Val Pro Glu Met Glu Lys Arg Tyr Gly Gly Phe Met Arg Phe	

230	235	240	
taatattttt	cccactagtg	gccccaggcc	ccagcaagcc
aaactggtga	tggtgtttta	ttgtcatgtg	ttgcttgcc
ctggataact	atacaacctg	aaaactgtca	tttcagggtc
taagctcagt	attagtctat	tgcagctatc	tcgttttcac
cttgtctctt	atTTTTgaca	aacatcaata	aatgcttact
ctattacccc	aagtgcacaaa	aaaaaaaaaa	aa

<210> 39
 <211> 2124
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 505..1590

<220>
 <221> sig_peptide
 <222> 505..624
 <223> Von Heijne matrix
 score 8.5056444915604
 seq VVMLMLLTLLVLG/MV

<400> 39	
cctggcataa ctgataggca tgtatgggag gaccacattc ctggggacag cctgggtatg	60
tgacatggca ggtgaccagg ttcccatgaa tgcccaggcc tgtgcccac	120
gggcttcctt ggaggtaaag agctaggggtg gggtaggacg cagctggac	180
agctccttcc ttagctctgt gattgctaca gctggttctg gaagccacag gcgcccctcag	240
gacaaatggg gcttcttcag cacagggtag tgagtgtga gctaagcaag gacactgtcc	300
ccttctctgc ccaggctcga gctgtgcacc tttaccctgg caattgccct ggggtgctgtc	360
ctgctcctgc ccttctccat catcagcaat gaggtgctgc tctccctgcc tcggaactac	420
tacatccagt ggctcaacgg ctccctcatc catggcctct ggaaccttgt ttttctcttc	480
tccaacctgt ccctcatctt cctc atg ccc ttt gca tat ttc ttc act gag	531

Met Pro Phe Ala Tyr Phe Phe Thr Glu	
-40	-35

tct gag ggc ttt gct ggc tcc aga aag ggt gtc ctg ggc cgg gtc tat	579
Ser Glu Gly Phe Ala Gly Ser Arg Lys Gly Val Leu Gly Arg Val Tyr	
-30	-25

gag aca gtg gtg atg ttg atg ctc ctc act ctg ctg gtg cta ggt atg	627
Glu Thr Val Val Met Leu Met Leu Leu Thr Leu Leu Val Leu Gly Met	
-15	-10

gtg tgg gtg gca tca gcc att gtg gac aag aac aag gcc aac aga gag	675
Val Trp Val Ala Ser Ala Ile Val Asp Lys Asn Lys Ala Asn Arg Glu	
5	10

tca ctc tat gac ttt tgg gag tac tat ctc ccc tac ctc tac tca tgc	723
Ser Leu Tyr Asp Phe Trp Glu Tyr Tyr Leu Pro Tyr Leu Tyr Ser Cys	
20	25

atc tcc ttc ctt ggg gtt ctg ctg ctc ctg gtg tgt act cca ctg ggt	771
Ile Ser Phe Leu Gly Val Leu Leu Leu Leu Val Cys Thr Pro Leu Gly	
35	40

ctc gcc cgc atg ttc tcc gtc act ggg aag ctg cta gtc aag ccc cgg	819
---	-----

Leu	Ala	Arg	Met	Phe	Ser	Val	Thr	Gly	Lys	Leu	Leu	Val	Lys	Pro	Arg	
50					55					60					65	
ctg	ctg	gaa	gac	ctg	gag	gag	cag	ctg	tac	tgc	tca	gcc	ttt	gag	gag	867
Leu	Leu	Glu	Asp	Leu	Glu	Glu	Gln	Leu	Tyr	Cys	Ser	Ala	Phe	Glu	Glu	
				70					75					80		
gca	gcc	ctg	acc	cgc	agg	atc	tgt	aat	cct	act	tcc	tgc	tgg	ctg	cct	915
Ala	Ala	Leu	Thr	Arg	Arg	Ile	Cys	Asn	Pro	Thr	Ser	Cys	Trp	Leu	Pro	
			85					90						95		
tta	gac	atg	gag	ctg	cta	cac	aga	cag	gtc	ctg	gct	ctg	cag	aca	cag	963
Leu	Asp	Met	Glu	Leu	Leu	His	Arg	Gln	Val	Leu	Ala	Leu	Gln	Thr	Gln	
		100						105				110				
agg	gtc	ctg	ctg	gag	aag	agg	cgg	aag	gct	tca	gcc	tgg	caa	cgg	aac	1011
Arg	Val	Leu	Leu	Glu	Lys	Arg	Arg	Lys	Ala	Ser	Ala	Trp	Gln	Arg	Asn	
		115				120					125					
ctg	ggc	tac	ccc	ctg	gct	atg	ctg	tgc	ttg	ctg	gtg	ctg	acg	ggc	ctg	1059
Leu	Gly	Tyr	Pro	Leu	Ala	Met	Leu	Cys	Leu	Leu	Val	Leu	Thr	Gly	Leu	
130					135				140					145		
tct	gtg	ctc	att	gtg	gcc	atc	cac	atc	ctg	gag	ctg	ctc	atc	gat	gag	1107
Ser	Val	Leu	Ile	Val	Ala	Ile	His	Ile	Leu	Glu	Leu	Leu	Ile	Asp	Glu	
				150					155					160		
gct	gcc	atg	ccc	cga	ggc	atg	cag	ggt	acc	tcc	tta	ggc	cag	gtc	tcc	1155
Ala	Ala	Met	Pro	Arg	Gly	Met	Gln	Gly	Thr	Ser	Leu	Gly	Gln	Val	Ser	
			165					170					175			
ttc	tcc	aag	ctg	ggc	tcc	ttt	ggt	gcc	gtc	att	cag	gtt	gta	ctc	atc	1203
Phe	Ser	Lys	Leu	Gly	Ser	Phe	Gly	Ala	Val	Ile	Gln	Val	Val	Leu	Ile	
		180					185					190				
ttt	tac	cta	atg	gtg	tcc	tca	gtt	gtg	ggc	ttc	tat	agc	tct	cca	ctc	1251
Phe	Tyr	Leu	Met	Val	Ser	Ser	Val	Val	Gly	Phe	Tyr	Ser	Ser	Pro	Leu	
		195				200					205					
ttc	cgg	agc	ctg	cgg	ccc	aga	tgg	cac	gac	act	gcc	atg	acg	cag	ata	1299
Phe	Arg	Ser	Leu	Arg	Pro	Arg	Trp	His	Asp	Thr	Ala	Met	Thr	Gln	Ile	
210					215					220				225		
att	ggg	aac	tgt	gtc	tgt	ctc	ctg	gtc	cta	agc	tca	gca	ctt	cct	gtc	1347
Ile	Gly	Asn	Cys	Val	Cys	Leu	Leu	Val	Leu	Ser	Ser	Ala	Leu	Pro	Val	
				230					235					240		
ttc	tct	cga	acc	ctg	ggg	ctc	act	cgc	ttt	gac	ctg	ctg	ggt	gac	ttt	1395
Phe	Ser	Arg	Thr	Leu	Gly	Leu	Thr	Arg	Phe	Asp	Leu	Leu	Gly	Asp	Phe	
			245					250					255			
gga	cgc	ttc	aac	tgg	ctg	ggc	aat	ttc	tac	att	gtg	ttc	ctc	tac	aac	1443
Gly	Arg	Phe	Asn	Trp	Leu	Gly	Asn	Phe	Tyr	Ile	Val	Phe	Leu	Tyr	Asn	
		260					265					270				
gca	gcc	ttt	gca	ggc	ctc	acc	aca	ctc	tat	ctg	gtg	aag	acc	ttc	act	1491
Ala	Ala	Phe	Ala	Gly	Leu	Thr	Thr	Leu	Tyr	Leu	Val	Lys	Thr	Phe	Thr	
		275				280					285					
gca	gct	gtg	cgg	gca	gag	ctg	atc	cgg	gcc	ttt	ggg	ctg	gac	aga	ctg	1539
Ala	Ala	Val	Arg	Ala	Glu	Leu	Ile	Arg	Ala	Phe	Gly	Leu	Asp	Arg	Leu	
290					295				300					305		
ccg	ctg	ccc	gtc	tcc	ggt	ttc	ccc	cag	gca	tct	agg	aag	acc	cag	cac	1587
Pro	Leu	Pro	Val	Ser	Gly	Phe	Pro	Gln	Ala	Ser	Arg	Lys	Thr	Gln	His	
				310					315					320		
cag	tgacctccag	ctgggggtgg	gaagaaaaaa	actggacact	gccatctgct											1640
Gln																
gcctaggcct	ggaggggaagc	ccaaggctac	ttggacctca	ggacctggaa	tctgagaggg											1700
tgggtggcag	aggggagcag	agccatctgc	actattgcat	aatctgagcc	agagtttggg											1760

accaggacct	cctgcttttc	cataacttaac	tgtggcctca	gcatggggta	gggctgggtg	1820
actgggtcta	gcccctgatc	ccaaatctgt	ttacacatca	atctgcctca	ctgctgttct	1880
gggccatccc	catagccatg	tttacatgat	ttgatgtgca	ataggggtggg	gtaggggcag	1940
ggaaaggact	gggccagggc	aggctcggga	gatagattgt	ctcccttgcc	tctggcccag	2000
cagagcctaa	gcaactgtgt	atcctggagg	ggctttggac	cacctgaaag	accaagggga	2060
tagggaggag	gaggcttcag	ccatcagcaa	taaagttgat	cccaggcaaa	aaaaaaaaaa	2120
aaaa						2124

<210> 40
 <211> 1159
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..326

<220>
 <221> sig_peptide
 <222> 84..146
 <223> Von Heijne matrix
 score 6.39000252120129
 seq LGLSVLLTAATVA/GV

<400> 40						
agtacaggcg	gcggtgcgca	ctctgcggcg	gcctctgcgc	ctcgggcggg	cgggagagag	60
aggccgcggc	cgccagcgtg	ggg atg tct	agg agc tgc	aag gtg gtg	ctg ggc	113
		Met Ser Arg	Ser Ser Lys	Val Val Leu	Gly	
		-20		-15		
ctc tgc	gtg ctg	ctg acg	gcg gcc	aca gtg	gcc ggc	gta cat
Leu Ser	Val Leu	Leu Thr	Ala Ala	Thr Val	Ala Gly	Val His
-10		-5		1		5
cag cag	tgg gac	cag cag	agg ctt	cgt gac	gga gtt	atc aga
Gln Gln	Trp Asp	Gln Gln	Arg Leu	Arg Asp	Gly Val	Ile Arg
	10		15		20	
gag agg	caa att	cgg aaa	aaa gaa	aac att	cgt ctt	ttg gga
Glu Arg	Gln Ile	Arg Lys	Lys Glu	Asn Ile	Arg Leu	Leu Gly
	25		30		35	
att att	ttg act	gag caa	ctt gaa	gca gaa	aga gag	aag atg
Ile Ile	Leu Thr	Glu Gln	Leu Glu	Ala Glu	Arg Glu	Lys Met
	40		45		50	
gca aaa	gga tct	caa aaa	tca tgact	tgaat gtg	aaatattc	tgattggacag
Ala Lys	Gly Ser	Gln Lys	Ser			
55		60				
acaacacgag	tttgtgtgtg	tgtgttgatg	gagagtagct	tagtagtatc	ttcatctttt	416
tttttggtca	ctgtcctttt	aaacttgatc	aaataaagga	cagtgggtca	tataagttac	476
tgcttttcagg	gtcccttata	tctgaataaa	ggagtgtggg	cagacacttt	ttggaagagt	536
ctgtctgggt	gatcctggta	gaagcccat	tagggtcact	gtccagtgc	tagggttgtt	596
actgagaagc	actgccgagc	ttgtgagaag	gaagggatgg	atagtagcat	ccacctgagt	656
agtctgatca	gtcggcatga	tgacgaagcc	acgagaacat	cgacctcaga	aggactggag	716
gaaggtgaaa	gtggagggag	agacgctcct	gatcgtcgaa	tyccgaggat	caggkcatca	776
gtggacttat	cgcacgacca	gagtggggat	tccctcaaca	gtgatgaagg	agacgtgtct	836
tggtatggagg	agcagctgtc	ctacttctgt	gacaagtgcc	aaaaatggat	accagccagt	896
aaggagcttc	tcaattcctt	tgatttgtca	attcctgtgt	gaaggtttgt	ttttccaacc	956

tgtgaaagaa acgtgaatgt aaaagagacc taaataaaag gataattata tttattctct	1016
agttgatcag ctataaatTT atataaaaca taggcatgtt tgtactaatg aaacgtactg	1076
tcaacctcta tcacattgtt aaattaacac ttttgggtgt aactcaataa aattgagaaa	1136
attgcaaaaa aaaaaaaaaa aaa	1159

<210> 41
 <211> 1953
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 56..1678

<220>
 <221> sig_peptide
 <222> 56..139
 <223> Von Heijne matrix
 score 3.75144398608723
 seq SGLLLQVLFRLIT/FV

<400> 41	
agactaaacg gagtggcggc ggcatttcct ggtgtctgag cctggcgcgg aggct atg	58
	Met
ggc agc cag gag gtg ctg ggc cac gcg gcc cgg ctg gcc tcc tcc ggt	106
Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser Gly	
-25 -20 -15	
ctc ctc ctg cag gtg ttg ttt cgg ttg atc acc ttt gtc ttg aat gca	154
Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn Ala	
-10 -5 1 5	
ttt att ctt cgc ttc ctg tca aag gaa atc gtt ggc gta gta aat gta	202
Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn Val	
10 15 20	
aga cta acg ctg ctt tac tca acc acc ctc ttc ctg gcc aga gag gcc	250
Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala	
25 30 35	
ttc cgc aga gca tgt ctc agt ggg ggc acc cag cga gac tgg agc cag	298
Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser Gln	
40 45 50	
acc ctc aac ctg ctg tgg cta aca gtc ccc ctg ggt gtg ttt tgg tcc	346
Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp Ser	
55 60 65	
tta ttc ctg ggc tgg atc tgg ttg cag ctg ctt gaa gtg cct gat cct	394
Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp Pro	
70 75 80 85	
aat gtt gtc cct cac tat gca act gga gtg gtg ctg ttt ggt ctc tcg	442
Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu Ser	
90 95 100	
gca gtg gtg gag ctt cta gga gag ccc ttt tgg gtc ttg gca caa gca	490
Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln Ala	
105 110 115	
cat atg ttt gtg aag ctc aag gtg att gca gag agc ctg tcg gta att	538
His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val Ile	
120 125 130	

ctt aag agc gtt ctg aca gct ttt ctc gtg ctg tgg ttg cct cac tgg	586
Leu Lys Ser Val Leu Thr Ala Phe Leu Val Leu Trp Leu Pro His Trp	
135 140 145	
gga ttg tac att ttc tct ttg gcc cag ctt ttc tat acc aca gtt ctg	634
Gly Leu Tyr Ile Phe Ser Leu Ala Gln Leu Phe Tyr Thr Thr Val Leu	
150 155 160 165	
gtg ctc tgc tat gtt att tat ttc aca aag tta ctg ggt tcc cca gaa	682
Val Leu Cys Tyr Val Ile Tyr Phe Thr Lys Leu Leu Gly Ser Pro Glu	
170 175 180	
tca acc aag ctt caa act ctt cct gtc tcc aga ata aca gat ctg tta	730
Ser Thr Lys Leu Gln Thr Leu Pro Val Ser Arg Ile Thr Asp Leu Leu	
185 190 195	
ccc aat att aca aga aat gga gcg ttt ata aac tgg aaa gag gct aaa	778
Pro Asn Ile Thr Arg Asn Gly Ala Phe Ile Asn Trp Lys Glu Ala Lys	
200 205 210	
ctg act tgg agt ttt ttc aaa cag tct ttc ttg aaa cag att ttg aca	826
Leu Thr Trp Ser Phe Phe Lys Gln Ser Phe Leu Lys Gln Ile Leu Thr	
215 220 225	
gaa ggc gag cga tat gtg atg aca ttt ttg aat gta ttg aac ttt ggt	874
Glu Gly Glu Arg Tyr Val Met Thr Phe Leu Asn Val Leu Asn Phe Gly	
230 235 240 245	
gat cag ggt gtg tat gat ata gtg aat aat ctt ggc tcc ctt gtg gcc	922
Asp Gln Gly Val Tyr Asp Ile Val Asn Asn Leu Gly Ser Leu Val Ala	
250 255 260	
aga tta att ttc cag cca ata gag gaa agt ttt tat ata ttt ttt gct	970
Arg Leu Ile Phe Gln Pro Ile Glu Ser Phe Tyr Ile Phe Phe Ala	
265 270 275	
aag gtg ctg gag agg gga aag gat gcc aca ctt cag aag cag gag gac	1018
Lys Val Leu Glu Arg Gly Lys Asp Ala Thr Leu Gln Lys Gln Glu Asp	
280 285 290	
gtt gct gtg gct gct gca gtc ttg gag tcc ctg ctc aag ctg gcc ctg	1066
Val Ala Val Ala Ala Ala Val Leu Glu Ser Leu Leu Lys Leu Ala Leu	
295 300 305	
ctg gcc ggc ctg acc atc act gtt ttt ggc ttt gcc tat tct cag ctg	1114
Leu Ala Gly Leu Thr Ile Thr Val Phe Gly Phe Ala Tyr Ser Gln Leu	
310 315 320 325	
gct ctg gat atc aac gga ggg acc atg ctt agc tca gga tcc ggt cct	1162
Ala Leu Asp Ile Asn Gly Gly Thr Met Leu Ser Ser Gly Ser Gly Pro	
330 335 340	
gtt ttg ctg cgt tcc tac tgt ctc tat gtt ctc ctg ctt gcc atc aat	1210
Val Leu Leu Arg Ser Tyr Cys Leu Tyr Val Leu Leu Leu Ala Ile Asn	
345 350 355	
gga gtg aca gag tgt ttc aca ttt gct gcc atg agc aaa gag gag gtc	1258
Gly Val Thr Glu Cys Phe Thr Phe Ala Ala Met Ser Lys Glu Glu Val	
360 365 370	
gac agg tac aat ttt gtg atg ctg gcc ctg tcc tcc tca ttc ctg gtg	1306
Asp Arg Tyr Asn Phe Val Met Leu Ala Leu Ser Ser Ser Phe Leu Val	
375 380 385	
tta tcc tat ctc ttg acc cgt tgg tgt ggc agc gtg ggc ttc atc ttg	1354
Leu Ser Tyr Leu Leu Thr Arg Trp Cys Gly Ser Val Gly Phe Ile Leu	
390 395 400 405	
gcc aac tgc ttt aac atg ggc att cgg atc acg cag agc ctt tgc ttc	1402
Ala Asn Cys Phe Asn Met Gly Ile Arg Ile Thr Gln Ser Leu Cys Phe	
410 415 420	

atc cac cgc tac tac cga agg agc ccc cac agg ccc ctg gct ggc ctg	1450
Ile His Arg Tyr Tyr Arg Arg Ser Pro His Arg Pro Leu Ala Gly Leu	
425 430 435	
cac cta tcg cca gtc ctg ctc ggg aca ttt gcc ctc agt ggt ggg gtt	1498
His Leu Ser Pro Val Leu Leu Gly Thr Phe Ala Leu Ser Gly Gly Val	
440 445 450	
act gct gtt tcg gag gta ttc ctc tgc tgt gag cag ggc tgg cca gcc	1546
Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro Ala	
455 460 465	
aga ctg gca cac att gct gtg ggg gcc ttc tgt ctg gga gca act ctc	1594
Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr Leu	
470 475 480 485	
ggg aca gca ttc ctc aca gag acc aag ctg atc cat ttc ctc agg act	1642
Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg Thr	
490 495 500	
cag tta ggt gtg ccc aga cgc act gac aaa atg acg tgacttcagg	1688
Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr	
505 510	
gaagcctgga caccgaggc acctggacca gctatgggta gttctgtggg tggaacacat	1748
tctgtgtaag agccccactg agggctctgc agcggagtga cagcaacccc agagatgagg	1808
caccagagag tgccactgca tgagacacct gtgaccattc gaagtctgaa atgcgggggg	1868
ggagtttcat ttttaagtga agaccaaag ccctttaaaa ataatagttt tttatcattt	1928
tatagtgaag aaaaaaaaaa aaaaa	1953

<210> 42
 <211> 1688
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 119..1522

<220>
 <221> sig_peptide
 <222> 119..181
 <223> Von Heijne matrix
 score 11.6921972463885
 seq LLLCLALSGAAET/KP

<400> 42	
aaaaggctgc aggctgccag gtgtgcttgg agagccccct tcttccgccc ggcctcgcaa	60
gcagcgtagg actgtggaga agggcggtgg gcaaggaggg aactcgagag cagcctcc	118
atg ggc aca cag gag ggc tgg tgc ctg ctg ctc tgc ctg gct cta tct	166
Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser	
-20 -15 -10	
gga gca gca gaa acc aag ccc cac cca gca gag ggg cag tgg cgg gca	214
Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala	
-5 1 5 10	
gtg gac gtg gtc cta gac tgt ttc ctg gtg aag gac ggt gcg cac cgt	262
Val Asp Val Val Leu Asp Cys Phe Leu Val Lys Asp Gly Ala His Arg	
15 20 25	
gga gct ctc gcc agc agt gag gac agg gca agg gcc tcc ctt gtg ctg	310
Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu	

	30		35		40											
aag	cag	gtg	cca	gtg	ctg	gac	gat	ggc	tcc	ctg	gag	gac	ttc	acc	gat	358
Lys	Gln	Val	Pro	Val	Leu	Asp	Asp	Gly	Ser	Leu	Glu	Asp	Phe	Thr	Asp	
	45					50					55					
ttc	caa	ggg	ggc	aca	ctg	gcc	caa	gat	gac	cca	cct	att	atc	ttt	gag	406
Phe	Gln	Gly	Gly	Thr	Leu	Ala	Gln	Asp	Asp	Pro	Pro	Ile	Ile	Phe	Glu	
60					65					70					75	
gcc	tca	gtg	gac	ctg	gtc	cag	att	ccc	cag	gcc	gag	gcc	ttg	ctc	cat	454
Ala	Ser	Val	Asp	Leu	Val	Gln	Ile	Pro	Gln	Ala	Glu	Ala	Leu	Leu	His	
				80					85						90	
gct	gac	tgc	agt	ggg	aag	gag	gtg	acc	tgt	gag	atc	tcc	cgc	tac	ttt	502
Ala	Asp	Cys	Ser	Gly	Lys	Glu	Val	Thr	Cys	Glu	Ile	Ser	Arg	Tyr	Phe	
			95					100					105			
ctc	cag	atg	aca	gag	acc	act	gtt	aag	aca	gca	gct	tgg	ttc	atg	gcc	550
Leu	Gln	Met	Thr	Glu	Thr	Thr	Val	Lys	Thr	Ala	Ala	Trp	Phe	Met	Ala	
		110					115					120				
aac	gtg	cag	gtc	tct	gga	ggg	gga	cct	agc	atc	tcc	ttg	gtg	atg	aag	598
Asn	Val	Gln	Val	Ser	Gly	Gly	Gly	Pro	Ser	Ile	Ser	Leu	Val	Met	Lys	
	125					130					135					
act	ccc	agg	gtc	gcc	aag	aat	gag	gtg	ctc	tgg	cac	cca	acg	ctg	aac	646
Thr	Pro	Arg	Val	Ala	Lys	Asn	Glu	Val	Leu	Trp	His	Pro	Thr	Leu	Asn	
	140				145					150					155	
ttg	cca	ctg	agc	ccc	cag	ggg	act	gtg	cga	act	gca	gtg	gag	ttc	cag	694
Leu	Pro	Leu	Ser	Pro	Gln	Gly	Thr	Val	Arg	Thr	Ala	Val	Glu	Phe	Gln	
			160						165						170	
gtg	atg	aca	cag	acc	caa	tcc	ctg	agc	ttc	ctg	ctg	ggg	tcc	tca	gcc	742
Val	Met	Thr	Gln	Thr	Gln	Ser	Leu	Ser	Phe	Leu	Leu	Gly	Ser	Ser	Ala	
			175					180					185			
tcc	ttg	gac	tgt	ggc	ttc	tcc	atg	gca	ccg	ggc	ttg	gac	ctc	atc	agt	790
Ser	Leu	Asp	Cys	Gly	Phe	Ser	Met	Ala	Pro	Gly	Leu	Asp	Leu	Ile	Ser	
	190						195					200				
gtg	gag	tgg	cga	ctg	cag	cac	aag	ggc	agg	ggt	cag	ttg	gtg	tac	agc	838
Val	Glu	Trp	Arg	Leu	Gln	His	Lys	Gly	Arg	Gly	Gln	Leu	Val	Tyr	Ser	
	205					210					215					
tgg	acc	gca	ggg	cag	ggg	cag	gct	gtg	cgg	aag	ggc	gct	acc	ctg	gag	886
Trp	Thr	Ala	Gly	Gln	Gly	Gln	Ala	Val	Arg	Lys	Gly	Ala	Thr	Leu	Glu	
	220				225					230					235	
cct	gca	caa	ctg	ggc	atg	gcc	agg	gat	gcc	tcc	ctc	acc	ctg	ccc	ggc	934
Pro	Ala	Gln	Leu	Gly	Met	Ala	Arg	Asp	Ala	Ser	Leu	Thr	Leu	Pro	Gly	
			240						245					250		
ctc	act	ata	cag	gac	gag	ggg	acc	tac	att	tgc	cag	atc	acc	acc	tct	982
Leu	Thr	Ile	Gln	Asp	Glu	Gly	Thr	Tyr	Ile	Cys	Gln	Ile	Thr	Thr	Ser	
			255					260					265			
ctg	tac	cga	gct	cag	cag	atc	atc	cag	ctc	aac	atc	caa	gct	tcc	cct	1030
Leu	Tyr	Arg	Ala	Gln	Gln	Ile	Ile	Gln	Leu	Asn	Ile	Gln	Ala	Ser	Pro	
	270					275						280				
aaa	gta	cga	ctg	agc	ttg	gca	aac	gaa	gct	ctg	ctg	ccc	acc	ctc	atc	1078
Lys	Val	Arg	Leu	Ser	Leu	Ala	Asn	Glu	Ala	Leu	Leu	Pro	Thr	Leu	Ile	
	285					290					295					
tgc	gac	att	gct	ggc	tat	tac	cct	ctg	gat	gtg	gtg	gtg	acg	tgg	acc	1126
Cys	Asp	Ile	Ala	Gly	Tyr	Tyr	Pro	Leu	Asp	Val	Val	Val	Thr	Trp	Thr	
	300				305					310					315	
cga	gag	gag	ctg	ggt	gga	tcc	cca	gcc	caa	gtc	tct	ggt	gcc	tcc	ttc	1174
Arg	Glu	Glu	Leu	Gly	Gly	Ser	Pro	Ala	Gln	Val	Ser	Gly	Ala	Ser	Phe	

	320	325	330	
tcc agc ctc agg caa agc gtg gca ggc acc tac agc atc tcc tcc tct				1222
Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser				
	335	340	345	
ctc acc gca gaa cct ggc tct gca ggt gcc act tac acc tgc cag gtc				1270
Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val				
	350	355	360	
aca cac atc tct ctg gag gag ccc ctt ggg gcc agc acc cag gtt gtc				1318
Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val				
	365	370	375	
cca cca gag cgg aga aca gcc ttg gga gtc atc ttt gcc agc agt ctc				1366
Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu				
	380	385	390	
ttc ctt ctt gca ctg atg ttc ctg ggg ctt cag aga cgg caa gca cct				1414
Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro				
	400	405	410	
aca gga ctt ggg ctg ctt cag gct gaa cgc tgg gag acc act tcc tgt				1462
Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys				
	415	420	425	
gct gac aca cag agc tcc cat ctc cat gaa gac cgc aca gcg cgt gta				1510
Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val				
	430	435	440	
agc cag ccc agc tgacctaaag cgacatgaga ctactagaaa gaaacgacac				1562
Ser Gln Pro Ser				
	445			
ccttccccaa gccccacag ctactccaac ccaaacaaca accaagccag tttaatggta				1622
ggaatttgta ttttttgctt ttgttcagaa tacatgacat tggtaaataa aaaaaaaaaa				1682
aaaaaa				1688

<210> 43
 <211> 1942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 334..1551

<220>
 <221> sig_peptide
 <222> 334..426
 <223> Von Heijne matrix
 score 4.0554926521937
 seq TVFLLVTLQALDT/VE

<400> 43	
gctcataggg agaaaggaag ctgcgctgcg ttctgcggga cgaaccctgc tccgcgcgag	60
aatttttttg attccttctt atttgagaaa atctccagct gctctgatca tagcctaaga	120
agactgcatg ctgcttcctc tcgatgccaa gccagaccct ctcacaacct cggatctcag	180
tccttcatgg agacctgggc ccagcaggaa tggcagtgca ggaaattggc gccagatgg	240
ttcttccatg tgaagttgtc tcgggctctg ggctgacgag agaacacctg gtaaccaggt	300
tagccctctg tcagtcaccc agggcagggc agc atg gtg cgg att cag agg agg	354
Met Val Arg Ile Gln Arg Arg	
-30 -25	

aag ctt ttg gca tct tgc ctg tgc gtc	aca gcc acc gtc ttt ctg ctt	402
Lys Leu Leu Ala Ser Cys Leu Cys Val Thr Ala Thr Val Phe Leu Leu		
-20	-15	-10
gtc aca ctc cag gcc ttg gat acc gtt gag aat cta atg aaa gtc acg	450	
Val Thr Leu Gln Ala Leu Asp Thr Val Glu Asn Leu Met Lys Val Thr		
-5	1	5
ggc cct ccc cag gga gtt aca gac tcc atg caa tgc ttc aat gat cag	498	
Gly Pro Pro Gln Gly Val Thr Asp Ser Met Gln Cys Phe Asn Asp Gln		
10	15	20
tgg cct tta tct aac acc agg agc agc gag cac ata aaa gag gtc atg	546	
Trp Pro Leu Ser Asn Thr Arg Ser Ser Glu His Ile Lys Glu Val Met		
25	30	35
gtt gag ctg ggg aag ttt gaa agg aag gag ttt aaa agt tcc agt ttg	594	
Val Glu Leu Gly Lys Phe Glu Arg Lys Glu Phe Lys Ser Ser Ser Leu		
45	50	55
caa gat gga cat aca aaa atg gag gaa gca cct acg cat ctt aat tca	642	
Gln Asp Gly His Thr Lys Met Glu Glu Ala Pro Thr His Leu Asn Ser		
60	65	70
ttt ctt aag aaa gaa gga ttg acc ttc aac agg aaa aga aaa tgg gaa	690	
Phe Leu Lys Lys Glu Gly Leu Thr Phe Asn Arg Lys Arg Lys Trp Glu		
75	80	85
ttg gac agc tac ccc att atg ctc tgg tgg tcc ccg ctg acg ggg gag	738	
Leu Asp Ser Tyr Pro Ile Met Leu Trp Trp Ser Pro Leu Thr Gly Glu		
90	95	100
act ggg agg tta ggc caa tgt gga gca gat gct tgt ttc ttc acc atc	786	
Thr Gly Arg Leu Gly Gln Cys Gly Ala Asp Ala Cys Phe Phe Thr Ile		
105	110	115
aac cgg acc tac ctc cat cat cac atg acc aaa gca ttc ctc ttc tat	834	
Asn Arg Thr Tyr Leu His His His Met Thr Lys Ala Phe Leu Phe Tyr		
125	130	135
ggt act gac ttt aac ata gat agc tta cct ctg cct cgg aaa gcc cat	882	
Gly Thr Asp Phe Asn Ile Asp Ser Leu Pro Leu Pro Arg Lys Ala His		
140	145	150
cat gac tgg gct gtt ttt cat gaa gag tcc ccg aaa aac aat tat aag	930	
His Asp Trp Ala Val Phe His Glu Glu Ser Pro Lys Asn Asn Tyr Lys		
155	160	165
ctc ttt cat aaa cca gtg atc acc ttg ttc aac tac act gcc acg ttc	978	
Leu Phe His Lys Pro Val Ile Thr Leu Phe Asn Tyr Thr Ala Thr Phe		
170	175	180
agc agg cat tcc cac ttg cca cta act acc caa tac ttg gag agc att	1026	
Ser Arg His Ser His Leu Pro Leu Thr Thr Gln Tyr Leu Glu Ser Ile		
185	190	195
gaa gtc ctg aag tca ctc cga tac cta gtt cct ttg cag tcc aaa aac	1074	
Glu Val Leu Lys Ser Leu Arg Tyr Leu Val Pro Leu Gln Ser Lys Asn		
205	210	215
aag ctt aga aaa aga ctt gct ccg ctg gtg tat gta cag tca tac tgt	1122	
Lys Leu Arg Lys Arg Leu Ala Pro Leu Val Tyr Val Gln Ser Tyr Cys		
220	225	230
gac cca cca tca gac agg gac agc tat gtt cgc gag ctg atg act tac	1170	
Asp Pro Pro Ser Asp Arg Asp Ser Tyr Val Arg Glu Leu Met Thr Tyr		
235	240	245
atc gag gtc gat tcc tat ggt gaa tgt tta cga aac aaa gac ctc cct	1218	
Ile Glu Val Asp Ser Tyr Gly Glu Cys Leu Arg Asn Lys Asp Leu Pro		
250	255	260

Val	Arg	Arg	Ser	Arg	Arg	Pro	Gln	Val	Thr	Leu	Leu	Asp	Pro	Asn	Glu	
5						10					15					
aag	tac	ctg	cta	cga	ctg	cta	gac	aag	acg	act	gtg	agc	cac	aac	acc	254
Lys	Tyr	Leu	Leu	Arg	Leu	Leu	Asp	Lys	Thr	Thr	Val	Ser	His	Asn	Thr	
20					25					30					35	
aag	agg	ttc	cgc	ttt	gcc	ctg	ccc	acc	gcc	cac	cac	act	ctg	ggg	ctg	302
Lys	Arg	Phe	Arg	Phe	Ala	Leu	Pro	Thr	Ala	His	His	Thr	Leu	Gly	Leu	
			40						45					50		
cct	gtg	ggc	aaa	cat	atc	tac	ctc	tcc	acc	cga	att	gat	ggc	agc	ctg	350
Pro	Val	Gly	Lys	His	Ile	Tyr	Leu	Ser	Thr	Arg	Ile	Asp	Gly	Ser	Leu	
			55					60					65			
gtc	atc	agg	cca	tac	act	cct	gtc	acc	agt	gat	gag	gat	caa	ggc	tat	398
Val	Ile	Arg	Pro	Tyr	Thr	Pro	Val	Thr	Ser	Asp	Glu	Asp	Gln	Gly	Tyr	
	70						75					80				
gtg	gat	ctt	gtc	atc	aag	gtc	tac	ctg	aag	ggg	gtg	cac	ccc	aaa	ttt	446
Val	Asp	Leu	Val	Ile	Lys	Val	Tyr	Leu	Lys	Gly	Val	His	Pro	Lys	Phe	
	85					90					95					
cct	gag	gga	ggg	aag	atg	tct	cag	tac	ctg	gat	agc	ctg	aag	gtt	ggg	494
Pro	Glu	Gly	Gly	Lys	Met	Ser	Gln	Tyr	Leu	Asp	Ser	Leu	Lys	Val	Gly	
				105						110					115	
gat	gtg	gtg	gag	ttt	cgg	ggg	cca	agc	ggg	ttg	ctc	act	tac	act	gga	542
Asp	Val	Val	Glu	Phe	Arg	Gly	Pro	Ser	Gly	Leu	Leu	Thr	Tyr	Thr	Gly	
				120					125					130		
aaa	ggg	cat	ttt	aac	att	cag	ccc	aac	aag	aaa	tct	cca	cca	gaa	ccc	590
Lys	Gly	His	Phe	Asn	Ile	Gln	Pro	Asn	Lys	Lys	Ser	Pro	Pro	Glu	Pro	
			135					140					145			
cga	gtg	gcg	aag	aaa	ctg	gga	atg	att	gcc	ggc	ggg	aca	gga	atc	acc	638
Arg	Val	Ala	Lys	Lys	Leu	Gly	Met	Ile	Ala	Gly	Gly	Thr	Gly	Ile	Thr	
		150					155					160				
cca	atg	cta	cag	ctg	atc	cgg	gcc	atc	ctg	aaa	gtc	cct	gaa	gat	cca	686
Pro	Met	Leu	Gln	Leu	Ile	Arg	Ala	Ile	Leu	Lys	Val	Pro	Glu	Asp	Pro	
		165				170					175					
acc	cag	tgc	ttt	ctg	ctt	ttt	gcc	aac	cag	aca	gaa	aag	gat	atc	atc	734
Thr	Gln	Cys	Phe	Leu	Leu	Phe	Ala	Asn	Gln	Thr	Glu	Lys	Asp	Ile	Ile	
				185						190					195	
ttg	cgg	gag	gac	tta	gag	gaa	ctg	cag	gcc	cgc	tat	ccc	aat	cgc	ttt	782
Leu	Arg	Glu	Asp	Leu	Glu	Glu	Leu	Gln	Ala	Arg	Tyr	Pro	Asn	Arg	Phe	
			200						205					210		
aag	ctc	tgg	ttc	act	ctg	gat	cat	ccc	cca	aaa	gat	tgg	gcc	tac	agc	830
Lys	Leu	Trp	Phe	Thr	Leu	Asp	His	Pro	Pro	Lys	Asp	Trp	Ala	Tyr	Ser	
			215					220					225			
aag	ggc	ttt	gtg	act	gcc	gac	atg	atc	cgg	gaa	cac	ctg	ccc	gct	cca	878
Lys	Gly	Phe	Val	Thr	Ala	Asp	Met	Ile	Arg	Glu	His	Leu	Pro	Ala	Pro	
		230				235						240				
ggg	gat	gat	gtg	ctg	gta	ctg	ctt	tgt	ggg	cca	ccc	cca	atg	gtg	cag	926
Gly	Asp	Asp	Val	Leu	Val	Leu	Leu	Cys	Gly	Pro	Pro	Pro	Met	Val	Gln	
		245				250					255					
ctg	gcc	tgc	cat	ccc	aac	ttg	gac	aaa	ctg	ggc	tac	tca	caa	aag	atg	974
Leu	Ala	Cys	His	Pro	Asn	Leu	Asp	Lys	Leu	Gly	Tyr	Ser	Gln	Lys	Met	
			265						270						275	
cga	ttc	acc	tac	tgagcatcct	ccagcttccc	tggtgctggt	cgctgcagtt									1026
Arg	Phe	Thr	Tyr													
gttccccatc	agtactcaag	cactataagc	cttagattcc	tttcctcaga	gtttcaggtt											1086
ttttcagtta	catctagagc	tgaaatctgg	atagtagctg	caggaacaat	attcctgtag											1146

c	c	t	c	t	t	1206
a	a	a	a	a	a	1266
t	t	t	t	t	t	1326
g	g	g	g	g	g	1386
a	a	a	a	a	a	1446
t	t	t	t	t	t	1506
a	a	a	a	a	a	1566
t	t	t	t	t	t	1626
c	c	c	c	c	c	1657

```
<220>
<221> CDS
<222> 157..1482
```

<400> 45																
aaagaaaagt	cggcagcaga	gggaacaggg	aagaaaccta	aaggctgcag	gctgccaggt											60
gtgcttgag	agcccccttc	ttccgccggg	cctcgcaagc	agcgtaggac	tgtggagaag											120
ggcggtgggc	aaggagggaa	ctcgagagca	gcctcc	atg	ggc	aca	cag	gag	ggc							174
				Met	Gly	Thr	Gln	Glu	Gly							
-20																
tgg	tgc	ctg	ctg	ctc	tgc	ctg	gct	cta	tct	gga	gca	gca	gaa	acc	aag	222
Trp	Cys	Leu	Leu	Leu	Cys	Leu	Ala	Leu	Ser	Gly	Ala	Ala	Glu	Thr	Lys	
-15				-10				-5				1				
ccc	cac	cca	gca	gag	ggg	cag	ttg	cgg	gca	gtg	gac	gtg	gtc	cta	gac	270
Pro	His	Pro	Ala	Glu	Gly	Gln	Leu	Arg	Ala	Val	Asp	Val	Val	Leu	Asp	
5				10				15								
tgc	ttc	ctg	gcg	aag	gac	ggg	gcg	cac	cgt	gga	gct	ctc	gcc	agc	agt	318
Cys	Phe	Leu	Ala	Lys	Asp	Gly	Ala	His	Arg	Gly	Ala	Leu	Ala	Ser	Ser	
20				25				30								
gag	gac	agg	gca	agg	gcc	tcc	ctt	gtg	ctg	aag	cag	gtg	cca	gtg	ctg	366
Glu	Asp	Arg	Ala	Arg	Ala	Ser	Leu	Val	Leu	Lys	Gln	Val	Pro	Val	Leu	
35				40				45								
gac	gat	ggc	tcc	ctg	gag	gac	ttc	acc	gat	ttc	caa	ggg	ggc	aca	ctg	414
Asp	Asp	Gly	Ser	Leu	Glu	Asp	Phe	Thr	Asp	Phe	Gln	Gly	Gly	Thr	Leu	
50				55				60				65				
gcc	caa	gat	gac	cca	cct	att	atc	ttt	gag	gcc	tca	gtg	gac	ctg	gtc	462
Ala	Gln	Asp	Asp	Pro	Pro	Ile	Ile	Phe	Glu	Ala	Ser	Val	Asp	Leu	Val	
70				75				80								
cag	att	ccc	cag	gcc	gag	gcc	ttg	ctc	cat	gct	gac	tgc	agt	ggg	aag	510
Gln	Ile	Pro	Gln	Ala	Glu	Ala	Leu	Leu	His	Ala	Asp	Cys	Ser	Gly	Lys	
85				90				95								
gaq	gtg	acc	tgt	gaq	atc	tcc	cgc	tac	ttt	ctc	cag	atg	aca	gaq	acc	558

Glu	Val	Thr	Cys	Glu	Ile	Ser	Arg	Tyr	Phe	Leu	Gln	Met	Thr	Glu	Thr		
		100					105					110					
act	ggt	aag	aca	gca	gct	tgg	ttc	atg	gcc	aac	atg	cag	gtc	tct	gga	606	
Thr	Val	Lys	Thr	Ala	Ala	Trp	Phe	Met	Ala	Asn	Met	Gln	Val	Ser	Gly		
		115					120					125					
ggg	gga	cst	agc	atc	tcc	ttg	gtg	atg	aag	act	ccc	agg	gtc	acc	aag	654	
Gly	Gly	Xaa	Ser	Ile	Ser	Leu	Val	Met	Lys	Thr	Pro	Arg	Val	Thr	Lys		
130					135					140					145		
aat	gag	gcg	ctc	tgg	cac	ccg	acg	ctg	aac	ttg	cca	ctg	agc	ccc	cag	702	
Asn	Glu	Ala	Leu	Trp	His	Pro	Thr	Leu	Asn	Leu	Pro	Leu	Ser	Pro	Gln		
				150					155					160			
ggg	act	gtg	cga	act	gca	gtg	gag	ttc	cag	gtg	atg	aca	cag	acc	caa	750	
Gly	Thr	Val	Arg	Thr	Ala	Val	Glu	Phe	Gln	Val	Met	Thr	Gln	Thr	Gln		
			165					170					175				
tcc	ctg	agc	ttc	ctg	ctg	ggg	tcc	tca	gcc	tcc	ttg	gac	tgt	ggc	ttc	798	
Ser	Leu	Ser	Phe	Leu	Leu	Gly	Ser	Ser	Ala	Ser	Leu	Asp	Cys	Gly	Phe		
		180					185					190					
tcc	atg	gca	ccg	ggc	ttg	gac	ctc	atc	agt	gtg	gag	tgg	cga	ctg	cag	846	
Ser	Met	Ala	Pro	Gly	Leu	Asp	Leu	Ile	Ser	Val	Glu	Trp	Arg	Leu	Gln		
		195				200					205						
cac	aag	ggc	agg	ggt	cag	ttg	gtg	tac	agc	tgg	acc	gca	ggg	cag	ggg	894	
His	Lys	Gly	Arg	Gly	Gln	Leu	Val	Tyr	Ser	Trp	Thr	Ala	Gly	Gln	Gly		
210					215					220					225		
cag	gct	gtg	cgg	aag	ggc	gct	acc	ctg	gag	cct	gca	caa	ctg	ggc	atg	942	
Gln	Ala	Val	Arg	Lys	Gly	Ala	Thr	Leu	Glu	Pro	Ala	Gln	Leu	Gly	Met		
			230						235				240				
gcc	agg	gat	gcc	tcc	ctc	acc	ctg	ccc	ggc	ctc	act	ata	cag	gac	gag	990	
Ala	Arg	Asp	Ala	Ser	Leu	Thr	Leu	Pro	Gly	Leu	Thr	Ile	Gln	Asp	Glu		
		245						250				255					
ggg	acc	tac	att	tgc	cag	atc	acc	acc	tct	ctg	tac	cga	gct	cag	cag	1038	
Gly	Thr	Tyr	Ile	Cys	Gln	Ile	Thr	Thr	Ser	Leu	Tyr	Arg	Ala	Gln	Gln		
		260					265					270					
atc	atc	cag	ctc	aac	atc	caa	gct	tcc	cct	aaa	gta	cga	ctg	agc	ttg	1086	
Ile	Ile	Gln	Leu	Asn	Ile	Gln	Ala	Ser	Pro	Lys	Val	Arg	Leu	Ser	Leu		
		275				280					285						
gca	aac	gaa	gct	ctg	ctg	ccc	acc	ctc	atc	tgc	gac	att	gct	ggc	tat	1134	
Ala	Asn	Glu	Ala	Leu	Leu	Pro	Thr	Leu	Ile	Cys	Asp	Ile	Ala	Gly	Tyr		
290					295					300					305		
tac	cct	ctg	gat	gtg	gtg	gtg	acg	tgg	acc	cga	gag	gag	ctg	ggt	gga	1182	
Tyr	Pro	Leu	Asp	Val	Val	Val	Thr	Trp	Thr	Arg	Glu	Glu	Leu	Gly	Gly		
			310						315				320				
tcc	cca	gcc	caa	gtc	tct	ggt	gcc	tcc	ttc	tcc	agc	ctc	agg	caa	agc	1230	
Ser	Pro	Ala	Gln	Val	Ser	Gly	Ala	Ser	Phe	Ser	Ser	Leu	Arg	Gln	Ser		
			325				330						335				
gtg	gca	ggc	acc	tac	agc	atc	tcc	tcc	tct	ctc	acc	gca	gaa	cct	ggc	1278	
Val	Ala	Gly	Thr	Tyr	Ser	Ile	Ser	Ser	Ser	Leu	Thr	Ala	Glu	Pro	Gly		
		340					345					350					
tct	gca	ggt	gcc	act	tac	acc	tgc	cag	gtc	aca	cac	atc	tct	ctg	gag	1326	
Ser	Ala	Gly	Ala	Thr	Tyr	Thr	Cys	Gln	Val	Thr	His	Ile	Ser	Leu	Glu		
		355				360					365						
gag	ccc	ctt	ggg	gcc	agc	acc	cag	gtt	gtc	cca	cca	gag	cgg	aga	aca	1374	
Glu	Pro	Leu	Gly	Ala	Ser	Thr	Gln	Val	Val	Pro	Pro	Glu	Arg	Arg	Thr		
370					375					380					385		
gcc	ttg	gga	gtc	atc	ttt	gcc	agc	agt	ctc	ttc	ctt	ctt	gca	ctg	atg	1422	

Ala Leu Gly Val Ile Phe Ala Ser Ser Leu Phe Leu Leu Ala Leu Met	
390 395 400	
ttc ctg ggg ctt cag aga cgg caa gca cct aca gga ctt ggg ctg ctt	1470
Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro Thr Gly Leu Gly Leu Leu	
405 410 415	
cag gct gaa cgc taggagacca cttcctgtgc tgacacacag agctcccatc	1522
Gln Ala Glu Arg	
420	
tccatgaaga ccgcacagcg cgtgtaagcc agcccagctg acctaaagcg acatgagact	1582
actagaaaga aacgacaccc ttccccaagc cccacagct actccaacc aaacaacaac	1642
caagccagtt taatggtagg aatttgatt ttttgccttt gttcagaata catgacattg	1702
gtaaatatgc cacaaaaaaaa a	1733

<210> 46
 <211> 1871
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 195..1052

<220>
 <221> sig_peptide
 <222> 195..338
 <223> Von Heijne matrix
 score 3.50178852790004
 seq LGV FV VCHQLSSS/LN

<400> 46	
agtgactgcc gggagtcctg caggggcggg gcggcgccaa gcgcagggag cccggctgag	60
tggcagccca gattgaagat ggatacgtga caatcccagg gaccgctgca ctgacttcat	120
ttccttagac aagacacagt gtagggcccg gcccggtgtg gcccaggac tcctttggaa	180
tatagctgtg gaca atg aat cct gcg agc gat ggg ggc aca tca gag agc	230
Met Asn Pro Ala Ser Asp Gly Gly Thr Ser Glu Ser	
-45 -40	
att ttt gac ctg gac tat gca tcc tgg ggg atc cgc tcc acg ctg atg	278
Ile Phe Asp Leu Asp Tyr Ala Ser Trp Gly Ile Arg Ser Thr Leu Met	
-35 -30 -25	
gtc gct ggc ttt gtc ttc tac ttg ggc gtc ttt gtg gtc tgc cac cag	326
Val Ala Gly Phe Val Phe Tyr Leu Gly Val Phe Val Val Cys His Gln	
-20 -15 -10 -5	
ctg tcc tct tcc ctg aat gcc act tac cgt tct ttg gtg gcc aga gag	374
Leu Ser Ser Ser Leu Asn Ala Thr Tyr Arg Ser Leu Val Ala Arg Glu	
1 5 10	
aag gtc ttc tgg gac ctg gcg gcc acg cgt gca gtc ttt ggt gtt cag	422
Lys Val Phe Trp Asp Leu Ala Ala Thr Arg Ala Val Phe Gly Val Gln	
15 20 25	
agc aca gcc gca ggc ctg tgg gct ctg ctg ggg gac cct gtg ctg cat	470
Ser Thr Ala Ala Gly Leu Trp Ala Leu Leu Gly Asp Pro Val Leu His	
30 35 40	
gcc gac aag gcg cgt ggc cag cag aac tgg tgc tgg ttt cac atc acg	518
Ala Asp Lys Ala Arg Gly Gln Gln Asn Trp Cys Trp Phe His Ile Thr	
45 50 55 60	

aca gca acg gga ttc ttt tgc ttt gaa aat gtt gca gtc cac ctg tcc	566
Thr Ala Thr Gly Phe Phe Cys Phe Glu Asn Val Ala Val His Leu Ser	
65 70 75	
aac ttg atc ttc cgg aca ttt gac ttg ttt ctg gtt atc cac cat ctc	614
Asn Leu Ile Phe Arg Thr Phe Asp Leu Phe Leu Val Ile His His Leu	
80 85 90	
ttt gcc ttt ctt ggg ttt ctt ggc tgc ttg gtc aat ctc caa gct ggc	662
Phe Ala Phe Leu Gly Phe Leu Gly Cys Leu Val Asn Leu Gln Ala Gly	
95 100 105	
cac tat cta gct atg acc acg ttg ctc ctg gag atg agc acg ccc ttt	710
His Tyr Leu Ala Met Thr Thr Leu Leu Leu Glu Met Ser Thr Pro Phe	
110 115 120	
acc tgc gtt tcc tgg atg ctc tta aag gcg ggc tgg tcc gag tct ctg	758
Thr Cys Val Ser Trp Met Leu Leu Lys Ala Gly Trp Ser Glu Ser Leu	
125 130 135 140	
ttt tgg aag ctc aac cag tgg ctg atg att cac atg ttt cac tgc cgc	806
Phe Trp Lys Leu Asn Gln Trp Leu Met Ile His Met Phe His Cys Arg	
145 150 155	
atg gtt cta acc tac cac atg tgg tgg gtg tgt ttc tgg cac tgg gac	854
Met Val Leu Thr Tyr His Met Trp Trp Val Cys Phe Trp His Trp Asp	
160 165 170	
ggc ctg gtc agc agc ctg tat ctg cct cat ttg aca ctg ttc ctt gtc	902
Gly Leu Val Ser Ser Leu Tyr Leu Pro His Leu Thr Leu Phe Leu Val	
175 180 185	
gga ctg gct ctg ctt acg cta atc att aat cca tat tgg acc cat aag	950
Gly Leu Ala Leu Leu Thr Leu Ile Ile Asn Pro Tyr Trp Thr His Lys	
190 195 200	
aag act cag cag ctt ctg aat ccg gtg gac tgg aac ttc gca cag cca	998
Lys Thr Gln Gln Leu Leu Asn Pro Val Asp Trp Asn Phe Ala Gln Pro	
205 210 215 220	
gaa gcc aag agc agg cca gaa ggc aac ggg cag ctg ctg cgg aag aag	1046
Glu Ala Lys Ser Arg Pro Glu Gly Asn Gly Gln Leu Leu Arg Lys Lys	
225 230 235	
agg cca tagctgctcc agccggggct ccggggcggc agcagagctg gcacaccgat	1102
Arg Pro	
tctgggaagc cccgcgaatg atggcctttg aattaatgag gcagtgaatg ttttgtgttt	1162
acttctaagg gaaatactaa ctttctttcg cattagtatt aattttgaag tagctacaaa	1222
gtatttttaa gaaattataa ttttatgact gtctggcagg ctctgtcagt ttagccgcgc	1282
cggaccgtgt caagcatcta ggagaggagt ccattggtgtc caggcatcgg ggcgtcacac	1342
ctgttgagga gtgggggtggc tttgaatgct ggaaatggct tcatagtga gtgcctccca	1402
cagggcgggt gggtcagcgt tgactctttc cagctgcaca ctcataatgcc gtgtgtctta	1462
ttcagaagtc acattctttt cagttggaga gaattgggct aagatagaaa ataacatgat	1522
ttgttcctta ttaaagtttc ccagcgtatg aaattctaag ctgggtgggg tggctcacac	1582
ccgacgtaat cccagcacgt tgggaggccg aggcaggtgg atcacttgag gccaggagtt	1642
cgagaccagc ctggtcaaga tgggtgaaacc ccatctctac taaaattaca aaaattagcc	1702
gggtgtcgtg gcacacacct gtaatcccag ctattttggga ggccaaggca ggagaattgc	1762
ctgaacccgg gaggcggagg ttgcagttag ctgagatcgc accactgcac tccagcactc	1822
cagcctgggt gacggagcaa cactctctcg caaaaaaaaa aaaaaaaaaa	1871

<210> 47
 <211> 1523
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 217..1410

<220>
 <221> sig_peptide
 <222> 217..279
 <223> Von Heijne matrix
 score 5.8172934575094
 seq ALLWAQEVGQVLA/GR

<400> 47
 acttccccgg gagccggaag tcccgtctca cggttgccct ggcagcgcgc gaggctggtg 60
 agtcggcagc cctgtggcag ccggcgggct ggtttccatg gttgcacgat taggaaccac 120
 cagctgctgc atcccatggc caggggtggc gtccaggtgg cagagcagct aggaacgcaa 180
 ggcctgaacc tggggccaga caccctctc ccggcc atg gtc aac gac cct cca 234
 Met Val Asn Asp Pro Pro
 -20
 gta cct gcc tta ctg tgg gcc cag gag gtg ggc caa gtc ttg gca ggc 282
 Val Pro Ala Leu Leu Trp Ala Gln Glu Val Gly Gln Val Leu Ala Gly
 -15 -10 -5 1
 cgt gcc cgc agg ctg ctg ctg cag ttt ggg gtg ctc ttc tgc acc atc 330
 Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly Val Leu Phe Cys Thr Ile
 5 10 15
 ctc ctt ttg ctc tgg gtg tct gtc ttc ctc tat ggc tcc ttc tac tat 378
 Leu Leu Leu Leu Trp Val Ser Val Phe Leu Tyr Gly Ser Phe Tyr Tyr
 20 25 30
 tcc tat atg ccg aca gtc agc cac ctc agc cct gtg cat ttc tac tac 426
 Ser Tyr Met Pro Thr Val Ser His Leu Ser Pro Val His Phe Tyr Tyr
 35 40 45
 agg acc gac tgt gat tcc tcc acc acc tca ctc tgc tcc ttc cct gtt 474
 Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser Leu Cys Ser Phe Pro Val
 50 55 60 65
 gcc aat gtc tcg ctg act aag ggt gga cgt gat cgg gtg ctg atg tat 522
 Ala Asn Val Ser Leu Thr Lys Gly Gly Arg Asp Arg Val Leu Met Tyr
 70 75 80
 gga cag ccg tat cgt gtt acc tta gag ctt gag ctg cca gag tcc cct 570
 Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu Glu Leu Pro Glu Ser Pro
 85 90 95
 gtg aat caa gat ttg ggc atg ttc ttg gtc acc att tcc tgc tac acc 618
 Val Asn Gln Asp Leu Gly Met Phe Leu Val Thr Ile Ser Cys Tyr Thr
 100 105 110
 aga ggt ggc cga atc atc tcc act tct tcg cgt tcg gtg atg ctg cat 666
 Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser Arg Ser Val Met Leu His
 115 120 125
 tac cgc tca gac ctg ctc cag atg ctg gac aca ctg gtc ttc tct agc 714
 Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp Thr Leu Val Phe Ser Ser
 130 135 140 145
 ctc ctg cta ttt ggc ttt gca gag cag aag cag ctg ctg gag gtg gaa 762
 Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys Gln Leu Leu Glu Val Glu
 150 155 160
 ctc tac gca gac tat aga gag aac tcg tac gtg ccg acc act gga gcg 810
 Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr Val Pro Thr Thr Gly Ala
 165 170 175

```

atc att gag atc cac agc aag cgc atc cag ctg tat gga gcc tac ctc      858
Ile Ile Glu Ile His Ser Lys Arg Ile Gln Leu Tyr Gly Ala Tyr Leu
      180                      185                      190
cgc atc cac gcg cac ttc act ggg ctc aga tac ctg cta tac aac ttc      906
Arg Ile His Ala His Phe Thr Gly Leu Arg Tyr Leu Leu Tyr Asn Phe
      195                      200                      205
ccg atg acc tgc gcc ttc ata ggt gtt gcc agc aac ttc acc ttc ctc      954
Pro Met Thr Cys Ala Phe Ile Gly Val Ala Ser Asn Phe Thr Phe Leu
      210                      215                      220
agc gtc atc gtg ctc ttc agc tac atg cag tgg gtg tgg ggg ggc atc      1002
Ser Val Ile Val Leu Phe Ser Tyr Met Gln Trp Val Trp Gly Gly Ile
      230                      235                      240
tgg ccc cga cac cgc ttc tct ttg cag gtt aac atc cga aaa aga gac      1050
Trp Pro Arg His Arg Phe Ser Leu Gln Val Asn Ile Arg Lys Arg Asp
      245                      250                      255
aat tcc cgg aag gaa gtc caa cga agg atc tct gct cat cag cca ggg      1098
Asn Ser Arg Lys Glu Val Gln Arg Arg Ile Ser Ala His Gln Pro Gly
      260                      265                      270
cct gaa ggc cag gag gag tca act ccg caa tca gat gtt aca gag gat      1146
Pro Glu Gly Gln Glu Glu Ser Thr Pro Gln Ser Asp Val Thr Glu Asp
      275                      280                      285
ggg gag agc cct gaa gat ccc tca ggg aca gag ggt cag ctg tcc gag      1194
Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr Glu Gly Gln Leu Ser Glu
      290                      295                      300
gag gag aaa cca gat cag cag ccc ctg agc gga gaa gag gag cta gag      1242
Glu Glu Lys Pro Asp Gln Gln Pro Leu Ser Gly Glu Glu Glu Leu Glu
      310                      315                      320
cct gag gcc agt gat ggt tca ggc tcc tgg gaa gat gca gct ttg ctg      1290
Pro Glu Ala Ser Asp Gly Ser Gly Ser Trp Glu Asp Ala Ala Leu Leu
      325                      330                      335
acg gag gcc aac ctg cct gct cct gct cct gct tct gct tct gcc cct      1338
Thr Glu Ala Asn Leu Pro Ala Pro Ala Pro Ala Ser Ala Ser Ala Pro
      340                      345                      350
gtc cta gag act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga      1386
Val Leu Glu Thr Leu Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg
      355                      360                      365
cag cgc ccc acc tgc tct agt tcc tgaagaaaag gggcagactc ctcacattcc      1440
Gln Arg Pro Thr Cys Ser Ser Ser
      370                      375
agcactttcc cacctgactc ctctccctc gtttttcctt caataaacta ttttgtgtca      1500
gcttcgaaaa aaaaaaaaaa aaa
      1523

```

```

<210> 48
<211> 832
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 103..492

```

```

<220>
<221> sig_peptide
<222> 103..162

```


<223> Von Heijne matrix
 score 8.21832452871462
 seq LFFCYLLLFTCSG/VE

```

<400> 48
gtttactcgc tgctgtgccc atctatcagc aggctccggg ctgaagattg cttctcttct 60
ctcctccaag gtctagtac ggagcccgcg cgcggcgcca cc atg cgg cag aag 114
                                     Met Arg Gln Lys
                                     -20
gcg gta tcg ctt ttc ttc tgc tac ctg ctg ctc ttc act tgc agt ggg 162
Ala Val Ser Leu Phe Phe Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly
-15 -10 -5
gtg gag gca ggt aag aaa aag tgc tcg gag agc tcg gac agc ggc tcc 210
Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser
1 5 10 15
ggg ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca 258
Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala
20 25 30
gtc gcc ggg ctg ccc gcg ctg ggc ttc acc ggc gcc ggc atc gcg gcc 306
Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala
35 40 45
aac tcg gtg gct gcc tcg ctg atg agc tgg tct gcg atc ctg aat ggg 354
Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly
50 55 60
ggc ggc gtg ccc gcc ggg ggg cta gtg gcc acg ctg cag agc ctc ggg 402
Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu Gln Ser Leu Gly
65 70 75 80
gct ggt ggc agc agc gtc gtc ata ggt aat att ggt gcc ctg atg ggc 450
Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly Ala Leu Met Gly
85 90 95
tac gcc acc cac aag tat ctc gat agt gag gag gat gag gag 492
Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp Glu Glu
100 105 110
tagccagcag ctcccagaac ctcttcttcc ttcttggcct aactcttccā gttaggatct 552
agaactttgc cttttttttt tttttttttt tttttttgag atgggttctc actatattgt 612
ccaggctaga gtgcagtggc tattcacaga tgcgaacata gtacactgca gcctccaact 672
cctagcctca agtgatcctc ctgtctcaac ctccaagta ggattacaag catgcgccga 732
cgatgcccg aatccagaac tttgtctatc actctcccca acaacctaga tgtgaaaaca 792
gaataaactt caccagaaa gcaaaaaaaaa aaaaaaaaaa 832

```

<210> 49
 <211> 831
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 234..491

<220>
 <221> sig_peptide
 <222> 234..293
 <223> Von Heijne matrix
 score 4.85037394589162

seq AVAGLPALGFTGA/GI

```

<400> 49
gtttactcgc tgctgtgccc atctatcagc aggctccggg ctgaagattg cttctcttct 60
ctcctccaag gtctagtac ggagcccgcg cgcggcgcca ccatgaggca gaaggcggta 120
tcgcttttct ctgctacctg ctgctcttca cttgcagtgg ggtggaggca ggtaagaaaa 180
agtgtctgga gagctcggac agcggctccg ggttctggaa ggccctgacc ttc atg 236
                                         Met
                                         -20
gcc gtc gga gga gga ctc gca gtc gcc ggg ctg ccc gcg ctg ggc ttc 284
Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe
                                         -15          -10          -5
acc ggc gcc ggc atc gcg gcc aac tcg gtg gct gcc tcg ctg atg agc 332
Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser
                                         1          5          10
tgg tct gcg atc ctg aat ggg ggc ggc gtg ccc gcc ggg ggg cta gtg 380
Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val
                                         15          20          25
gcc acg ctg cag agc ctc ggg gct ggt ggc agc agc gtc gtc ata ggt 428
Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly
30          35          40          45
aat att ggt gcc ctg atg ggc tac gcc acc cac aag tat ctc gat agt 476
Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser
                                         50          55          60
gag gag gat gag gag tagccagcag ctcccagaac ctcttcttcc ttcttggcct 531
Glu Glu Asp Glu Glu
65
aactcttcca gttaggatct agaactttgc cttttttttt tttttttttt tttttttgag 591
atgggtttct actatatattg ccaggctaga gtgcagtggc tattcacaga tgcgaacata 651
gtacactgca gctccaact cctagcctca agtgatcctc ctgtctcaac ctcccagta 711
ggattacaag catgcgccga cgatgccag aatccagaac tttgtctatc actctcccca 771
acaacctaga tgtgaaaaca gaataaactt caccagaaa gcaaaaaaaaa aaaaaaaaaa 831

<210> 50
<211> 917
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 180..800

<220>
<221> sig_peptide
<222> 180..248
<223> Von Heijne matrix
      score 14.6828672385356
      seq ILLLLWLIAPSRA/CT

<400> 50
acccttggct tctgcactga tgggtgggtgg atgagtaatg catccaggaa gcctggaggc 60
ctgtgggttcc cgcacccgct gccacccccg cccctagcgt ggacatttat cctctagcgc 120
tcaggccctg ccgccatcgc cgcagatcca gcgccagag agacaccaga gaaccacc 179
atg gcc ccc ttt gag ccc ctg gct tct ggc atc ctg ttg ttg ctg tgg 227

```

Met	Ala	Pro	Phe	Glu	Pro	Leu	Ala	Ser	Gly	Ile	Leu	Leu	Leu	Leu	Trp	
		-20						-15					-10			
ctg	ata	gcc	ccc	agc	agg	gcc	tgc	acc	tgt	gtc	cca	ccc	cac	cca	cag	275
Leu	Ile	Ala	Pro	Ser	Arg	Ala	Cys	Thr	Cys	Val	Pro	Pro	His	Pro	Gln	
		-5					1				5					
acg	gcc	ttc	tgc	aat	tcc	gac	ctc	gtc	atc	agg	gcc	aag	ttc	gtg	ggg	323
Thr	Ala	Phe	Cys	Asn	Ser	Asp	Leu	Val	Ile	Arg	Ala	Lys	Phe	Val	Gly	
10				15					20					25		
aca	cca	gaa	gtc	aac	cag	acc	acc	tta	tac	cag	cgt	tat	gag	atc	aag	371
Thr	Pro	Glu	Val	Asn	Gln	Thr	Thr	Leu	Tyr	Gln	Arg	Tyr	Glu	Ile	Lys	
				30				35					40			
atg	acc	aag	atg	tat	aaa	ggg	ttc	caa	gcc	tta	ggg	gat	gcc	gct	gac	419
Met	Thr	Lys	Met	Tyr	Lys	Gly	Phe	Gln	Ala	Leu	Gly	Asp	Ala	Ala	Asp	
		45					50					55				
atc	cgg	ttc	gtc	tac	acc	ccc	gcc	atg	gag	agt	gtc	tgc	gga	tac	ttc	467
Ile	Arg	Phe	Val	Tyr	Thr	Pro	Ala	Met	Glu	Ser	Val	Cys	Gly	Tyr	Phe	
		60					65					70				
cac	agg	tcc	cac	aac	cgc	agc	gag	gag	ttt	ctc	att	gct	gga	aaa	ctg	515
His	Arg	Ser	His	Asn	Arg	Ser	Glu	Glu	Phe	Leu	Ile	Ala	Gly	Lys	Leu	
		75				80					85					
cag	gat	gga	ctc	ttg	cac	atc	act	acc	tgc	agt	ttt	gtg	gct	ccc	tgg	563
Gln	Asp	Gly	Leu	Leu	His	Ile	Thr	Thr	Cys	Ser	Phe	Val	Ala	Pro	Trp	
90				95					100					105		
aac	agc	ctg	agc	tta	gct	cag	cgc	cgg	ggc	ttc	acc	aag	acc	tac	act	611
Asn	Ser	Leu	Ser	Leu	Ala	Gln	Arg	Arg	Gly	Phe	Thr	Lys	Thr	Tyr	Thr	
				110					115				120			
gtt	ggc	tgt	gag	gaa	tgc	aca	gtg	ttt	ccc	tgt	tta	tcc	ttc	ccc	tgc	659
Val	Gly	Cys	Glu	Glu	Cys	Thr	Val	Phe	Pro	Cys	Leu	Ser	Phe	Pro	Cys	
			125				130					135				
aaa	ctg	cag	agt	ggc	act	cat	tgc	ttg	tgg	acg	gac	cag	ctc	ctc	caa	707
Lys	Leu	Gln	Ser	Gly	Thr	His	Cys	Leu	Trp	Thr	Asp	Gln	Leu	Leu	Gln	
		140				145					150					
ggc	tct	gaa	aag	ggc	ttc	cag	tcc	cgt	cac	ctt	gcc	tgc	ctg	cct	cgg	755
Gly	Ser	Glu	Lys	Gly	Phe	Gln	Ser	Arg	His	Leu	Ala	Cys	Leu	Pro	Arg	
		155				160					165					
gag	cca	ggg	ctg	tgc	acc	tgg	cag	tcc	ctg	cgg	tcc	cag	ata	gcc		800
Glu	Pro	Gly	Leu	Cys	Thr	Trp	Gln	Ser	Leu	Arg	Ser	Gln	Ile	Ala		
170					175				180							
tgaatcctgc	ccggagtgga	agctgaagcc	tgacacagtgt	ccaccctgtt	cccactccca											860
tctttcttcc	ggacaatgaa	ataaagagtt	accaccagc	aaaaaaaaa	aaaaaaaaa											917

<210> 51
 <211> 621
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 140..472

<220>
 <221> sig_peptide
 <222> 140..211
 <223> Von Heijne matrix

score 8.44884907465122
seq FVVFSFLICAMA/GD

```

<400> 51
atatttttttt catatctgac atttctatgt cctatgacgg tttcacagct atcctacttt      60
ggagaagatg ctggaaattc agagtttccg ccagagaata tatgcctgaa ctaaaagagg      120
aagtggctcta taggagaaa atg aaa tat gat tgt ccc ttc agt ggg aca tca      172
                Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser
                        -20                                -15
ttt gtg gtc ttc tct ctc ttt ttg atc tgt gca atg gct gga gat gta      220
Phe Val Val Phe Ser Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val
                -10                                -5                                1
gtc tac gct gac atc aaa act gtt cgg act tcc ccg tta gaa ctc gcg      268
Val Tyr Ala Asp Ile Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala
                5                                10                                15
ttt cca ctt cag aga tct gtt tct ttc aac ttt tct act gtc cat aaa      316
Phe Pro Leu Gln Arg Ser Val Ser Phe Asn Phe Ser Thr Val His Lys
                20                                25                                30                                35
tca tgt cct gcc aaa gac tgg aag gtg cat aag gga aaa tgt tac tgg      364
Ser Cys Pro Ala Lys Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp
                40                                45                                50
att gct gaa act aag aaa tct tgg aac aaa agt caa aat gac tgt gcc      412
Ile Ala Glu Thr Lys Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala
                55                                60                                65
ata aac aat tca tat ctc atg gtg att caa gac att act gct atg gtg      460
Ile Asn Asn Ser Tyr Leu Met Val Ile Gln Asp Ile Thr Ala Met Val
                70                                75                                80
aga ttt aac att tagaggtgac agcatccccc acactggcag ttaatttttt      512
Arg Phe Asn Ile
                85
gtctacaaac ttggcaaaag tctgtgaaaa gaagtttcaa cttcatgtgt tattaactat      572
acaaatatta gttgaatgaa ttgttgaatt acaaaaaaaaa aaaaaaaaaa      621

```

<210> 52
<211> 673
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 68..484

<220>
<221> sig_peptide
<222> 68..112
<223> Von Heijne matrix
score 4.93618539864455
seq AVVFVFSLLDCCA/LI

```

<400> 52
ctatcagggg tgggtcgggg catccgagcg ggtttgacgg aaggagcggc ggcgacggag      60
gaggagg atg gag gcg gtg gtg ttc gtc ttc tct ctc ctc gat tgt tgc      109
                Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys
                -15                                -10                                -5

```

gcg ctc atc ttc ctc tcg gtc tac ttc ata att aca ttg tct gat tta	157
Ala Leu Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu	
1 5 10 15	
gaa tgt gat tac att aat gct aga tca tgt tgc tca aaa tta aac aag	205
Glu Cys Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys	
20 25 30	
tgg gta att cca gaa ttg att ggc cat acc att gtc act gta tta ctg	253
Trp Val Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu	
35 40 45	
ctc atg tca ttg cac tgg ttc atc ttc ctt ctc aac tta cct gtt gcc	301
Leu Met Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala	
50 55 60	
act tgg aat ata tat cga tac att atg gtg ccg agt ggt aac atg gga	349
Thr Trp Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly	
65 70 75	
gtg ttt gat cca aca gaa ata cac aat cga ggg cag ctg aag tca cac	397
Val Phe Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His	
80 85 90 95	
atg aaa gaa gcc atg atc aag ctt ggt ttc cac ttg ctc tgc ttc ttc	445
Met Lys Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe	
100 105 110	
atg tat ctt tat agt atg atc tta gct ttg ata aat gac tgaagctgga	494
Met Tyr Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp	
115 120	
gaagccgtgg ttgaagtcag cctacactac agtgcacagt tgaggagcca gagacttctt	554
aaatcatcct tagaaccgtg accatagcag tatatatattt cctcttgga caaaaaacta	614
tttttgctgt attttttacca tataaagtat ttaaaaaaca cgaaaaaaaa aaaaaaaaaa	673

<210> 53
 <211> 897
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 38..517

<220>
 <221> sig_peptide
 <222> 38..118
 <223> Von Heijne matrix
 score 7.20400999800742
 seq VLWLSGLSEPGAA/RQ

<400> 53	
agattgggac agtcgccagg gatggctgag cgtgaag atg cag cgg gtg tcc ggg	55
Met Gln Arg Val Ser Gly	
-25	
ctg ctc tcc tgg acg ctg agc aga gtc ctg tgg ctc tcc ggc ctc tct	103
Leu Leu Ser Trp Thr Leu Ser Arg Val Leu Trp Leu Ser Gly Leu Ser	
-20 -15 -10	
gag ccg gga gct gcc cgg cag ccc cgg atc atg gaa gag aaa gcg cta	151
Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile Met Glu Glu Lys Ala Leu	
-5 1 5 10	

gag gtt tat gat ttg att aga act atc cgg gac cca gaa aag ccc aat	199
Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg Asp Pro Glu Lys Pro Asn	
15 20 25	
act tta gaa gaa ctg gaa gtg gtc tcg gaa agt tgt gtg gaa gtt cag	247
Thr Leu Glu Glu Leu Glu Val Val Ser Glu Ser Cys Val Glu Val Gln	
30 35 40	
gag ata aat gaa gaa gaa tat ctg gtt att atc agg ttc acg cca aca	295
Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile Ile Arg Phe Thr Pro Thr	
45 50 55	
gta cct cat tgc tct ttg gcg act ctt att ggg ctg tgc tta aga gta	343
Val Pro His Cys Ser Leu Ala Thr Leu Ile Gly Leu Cys Leu Arg Val	
60 65 70 75	
aaa ctt cag cga tgt tta cca ttt aaa cat aag ttg gaa atc tac att	391
Lys Leu Gln Arg Cys Leu Pro Phe Lys His Lys Leu Glu Ile Tyr Ile	
80 85 90	
tct gaa gga acc cac tca aca gaa gaa gac atc aat aag cag ata aat	439
Ser Glu Gly Thr His Ser Thr Glu Glu Asp Ile Asn Lys Gln Ile Asn	
95 100 105	
gac aaa gag cga gtg gca gct gca atg gaa aac ccc aac tta cgg gaa	487
Asp Lys Glu Arg Val Ala Ala Ala Met Glu Asn Pro Asn Leu Arg Glu	
110 115 120	
att gtg gaa cag tgt gtc ctt gaa cct gac tgatagctgt tttaagagcc	537
Ile Val Glu Gln Cys Val Leu Glu Pro Asp	
125 130	
actggcctgt aattgtttga tatatttgta actcttttgta taatgtcaga gactcatgtt	597
taatacatag gtgatttgta cctcagagca ttttttaaag gattctttcc aagcgagatt	657
taattataag gtagtaccta atttgttcaa tgtataacat tctcaggatt tgtaacactt	717
aaatgatcag acagaataat attttctagt tattatgtgt aagatgagtt gctatttttc	777
tgatgctcat tctgatacaa ctatttttcg tgtcaaatat ctactgtgcc caaatgtact	837
caattttaaatt cattactctg taaaataaat aagcagatga ttcttataaa aaaaaaaaaa	897

<210> 54
 <211> 1101
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..634

<220>
 <221> sig_peptide
 <222> 92..139
 <223> Von Heijne matrix
 score 7.36306712986597
 seq FLLLTCLFITGTS/VS

<400> 54	
cttaaaaaaaaa aaagtgcttg aaagagaagg ggacaaagga acaccagtat taagaggatt	60
ttccagtgtt tctggcagtt ggtccagaag g atg cct cca ttc ctg ctt ctc	112
Met Pro Pro Phe Leu Leu Leu	
-15 -10	
acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc gtg gcc cta gat	160
Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro Val Ala Leu Asp	

	-5	1	5	
cct tgt tct gct tac atc agc ctg aat gag ccc tgg agg aac act gac				208
Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp Arg Asn Thr Asp				
	10	15	20	
cac cag ttg gat gag tct caa ggt cct cct cta tgt gac aac cat gtg				256
His Gln Leu Asp Glu Ser Gln Gly Pro Pro Leu Cys Asp Asn His Val				
	25	30	35	
aat ggg gag tgg tac cac ttc acg ggc atg gcg gga gat gcc atg cct				304
Asn Gly Glu Trp Tyr His Phe Thr Gly Met Ala Gly Asp Ala Met Pro				
	40	45	50	55
acc ttc tgc ata cca gaa aac cac tgt gga acc cac gca cct gtc tgg				352
Thr Phe Cys Ile Pro Glu Asn His Cys Gly Thr His Ala Pro Val Trp				
	60	65	70	
ctc aat ggc agc cac ccc cta gaa ggc gac ggc att gtg caa cgc cag				400
Leu Asn Gly Ser His Pro Leu Glu Gly Asp Gly Ile Val Gln Arg Gln				
	75	80	85	
gct tgt gcc agc ttc aat ggg aac tgc tgt ctc tgg aac acc acg gtg				448
Ala Cys Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp Asn Thr Thr Val				
	90	95	100	
gaa gtc aag gct tgc cct gga ggc tac tat gtg tat cgt ctg acc aag				496
Glu Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr Arg Leu Thr Lys				
	105	110	115	
ccc agc gtc tgc ttc cac gtc tac tgt ggt cgt gag tac ctt ccc tgt				544
Pro Ser Val Cys Phe His Val Tyr Cys Gly Arg Glu Tyr Leu Pro Cys				
	120	125	130	135
gct ctt ttt ctc cac caa caa ggc cac agg tgg agt cca aaa gtg ccc				592
Ala Leu Phe Leu His Gln Gln Gly His Arg Trp Ser Pro Lys Val Pro				
	140	145	150	
aat tat agg ata tgc agt tac agt ggc aac tat atc tca atc				634
Asn Tyr Arg Ile Cys Ser Tyr Ser Gly Asn Tyr Ile Ser Ile				
	155	160	165	
tgaacaacat tgatgtgggg cttaaagatac tctgatttct gagatctctt cttagaactt				694
ctgaaaaaatt cctgaagaaa tagaagggga aaggagctat gactttgatc agttcttttt				754
aattttgtct gaattccatt caaacaacaa attagaaaat gaaacattgg gccaggcgca				814
gtggctcatg cctgtaatcc cagcactttg ggaggctgag gcgggtggat cacaagatca				874
ggagtttaag accagcctgg ccaatatggt gaaaccctgt ctctactaga aatacaaaaa				934
ttagacaggc gtggtggcag gcaactgtaa cccagctac ccgggaggct gaggcaggag				994
aattgcttga acccgggagg tggacgttgc ggtcaggcga aaatcgtgcc attgcactcc				1054
agcctgggtg acagagtgag actctgattc aaaaaaaaaa aaaaaaa				1101

<210> 55
 <211> 1047
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..767

<220>
 <221> sig_peptide
 <222> 27..80
 <223> Von Heijne matrix
 score 8.96664802487992

seq LFCLAVLAASSFS/KA

<400> 55

```

agcagaggcc ctacacccac cgaggc atg ggg ctc cct ggg ctg ttc tgc ttg      53
                               Met Gly Leu Pro Gly Leu Phe Cys Leu
                               -15                               -10

gcc gtg ctg gct gcc agc agc ttc tcc aag gca cgg gag gaa gaa att      101
Ala Val Leu Ala Ala Ser Ser Phe Ser Lys Ala Arg Glu Glu Glu Ile
                               -5                               5
                               1                               5

acc cct gtg gtc tcc att gcc tac aaa gtc ctg gaa gtt ttc ccc aaa      149
Thr Pro Val Val Ser Ile Ala Tyr Lys Val Leu Glu Val Phe Pro Lys
                               10                               15                               20

ggc cgc tgg gtg ctc ata acc tgc tgt gca ccc cag cca cca ccg ccc      197
Gly Arg Trp Val Leu Ile Thr Cys Cys Ala Pro Gln Pro Pro Pro Pro
                               25                               30                               35

atc acc tat tcc ctc tgt gga acc aag aac atc aag gtg gcc aag aag      245
Ile Thr Tyr Ser Leu Cys Gly Thr Lys Asn Ile Lys Val Ala Lys Lys
40                               45                               50                               55

gtg gtg aag acc cac gag ccg gcc tcc ttc aac ctc aac gtc aca ctc      293
Val Val Lys Thr His Glu Pro Ala Ser Phe Asn Leu Asn Val Thr Leu
                               60                               65                               70

aag tcc agt cca gac ctg ctc acc tac ttc tgc cgg gcg tcc tcc acc      341
Lys Ser Ser Pro Asp Leu Leu Thr Tyr Phe Cys Arg Ala Ser Ser Thr
                               75                               80                               85

tca ggt gcc cat gtg gac agt gcc agg cta cag atg cac tgg gag ctg      389
Ser Gly Ala His Val Asp Ser Ala Arg Leu Gln Met His Trp Glu Leu
                               90                               95                               100

tgg tcc aag cca gtg tct gag ctg cgg gcc aac ttc act ctg cag gac      437
Trp Ser Lys Pro Val Ser Glu Leu Arg Ala Asn Phe Thr Leu Gln Asp
105                               110                               115

aga ggg gca ggc ccc agg gtg gag atg atc tgc cag gcg tcc tcg ggc      485
Arg Gly Ala Gly Pro Arg Val Glu Met Ile Cys Gln Ala Ser Ser Gly
120                               125                               130                               135

agc cca cct atc acc aac agc ctg atc ggg aag gat ggg cag gtc cac      533
Ser Pro Pro Ile Thr Asn Ser Leu Ile Gly Lys Asp Gly Gln Val His
                               140                               145                               150

ctg cag cag aga cca tgc cac agg cag cct gcc aac ttc tcc ttc ctg      581
Leu Gln Gln Arg Pro Cys His Arg Gln Pro Ala Asn Phe Ser Phe Leu
                               155                               160                               165

ccg agc cag aca tcg gac tgg ttc tgg tgc cag gct gca aac aac gcc      629
Pro Ser Gln Thr Ser Asp Trp Phe Trp Cys Gln Ala Ala Asn Asn Ala
170                               175                               180

aat gtc cag cac agc gcc ctc aca gtg gtg ccc cca gga ggg ttg ccc      677
Asn Val Gln His Ser Ala Leu Thr Val Val Pro Pro Gly Gly Leu Pro
185                               190                               195

agg gca ccc acc atc gtg ctg gtt ggc agc ctt gcc tcc act gcg gcc      725
Arg Ala Pro Thr Ile Val Leu Val Gly Ser Leu Ala Ser Thr Ala Ala
200                               205                               210                               215

atc acc tcc agg atg ctg ggc tgg acc acg tgg gcc agg tgg      767
Ile Thr Ser Arg Met Leu Gly Trp Thr Thr Trp Ala Arg Trp
220                               225

tgaccagaag atggaggact ggcagggtcc cctggagagc cccatccttg ccttgccgct      827
ctacaggagc accgcgcgtc tgagtgaaga ggagtttggg gggttcagga tagggaatgg      887
ggaggtcaga ggacgcaaag cagcagccat gtagaatgaa ccgtccagag agccaagcac      947

```


ggcagaggac tgcaggccat cagcgtgcac tgttcgtatt tggagttcat gcaaaatgag 1007
 tgtgttttag ctgctcttgc cacaaaaaaaa aaaaaaaaaa 1047

<210> 56
 <211> 925
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 4..399

<220>
 <221> sig_peptide
 <222> 4..126
 <223> Von Heijne matrix
 score 4.34454795165846
 seq RVVSWLFSIVVFG/SI

<400> 56
 acg atg gaa ggg ggt gcg tac gga gcg ggc aaa gcc ggg ggc gcc ttc 48
 Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe
 -40 -35 -30
 gac ccc tac acc ctg gtc cgg cag ccg cac acc atc ctg cgc gtc gtg 96
 Asp Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val
 -25 -20 -15
 tct tgg ctg ttc tcc ata gtg gtg ttc ggc tcc atc gtg aac gag ggc 144
 Ser Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly
 -10 -5 1 5
 tac ctc aac agc gcc tcc gag ggg gag cag ttc tgc atc tac aac cgc 192
 Tyr Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg
 10 15 20
 aac ccc aac gcc tgc agc tat ggc gtg gcc gtg ggc gtg ctc gcc ttc 240
 Asn Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe
 25 30 35
 ctc acc tgc ctg ctg tac ctg gcc ctg gac gtg tac ttc ccg cag atc 288
 Leu Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile
 40 45 50
 agc agc gtc aag gac cgc aag aaa gcc gtc ctg tcc gac atc ggt gtc 336
 Ser Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val
 55 60 65 70
 tcg ggt gag ccc cac cca gca ggt acc ccc tgc aca gag tct aca gag 384
 Ser Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu
 75 80 85
 ggc tgt ccc ggg cca taggaggcgg ctgccaccct tcttcccatg tttcagatga 439
 Gly Cys Pro Gly Pro
 90
 gggaaatgag ccttctgggc tttcctctgg ttcgtgggat tctgctacct ggccaaccag 499
 tggcaggtct ccaagcccaa ggacaacca ctgaacgaag ggacggacgc agcccgggcc 559
 gccatcgcct tctccttttt ctccatcttc acctggagcc tgaccgcagc cctggcctg 619
 cgagattca aggacctaag cttccaggag gactacagca cactgttccc tgcttcggca 679
 cagccgtagg cctccccggc ttgcagaggc cggcagccct gtatcacccc tggcagtga 739
 gtggcaggag cagcctagtg ccagaaatgt ccaagatgcc agggcatgca gggcagtga 799
 aggctggctt gaggaaccaa ttcaggttct cactgactc attcattcct tcaccgcctc 859

cttcattgat tcttcatgcg ttcattcatt cagtaaacad ttattgagta aaaaaaaaaa 919
 aaaaaa 925

<210> 57
 <211> 1240
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 127..879

<220>
 <221> sig_peptide
 <222> 127..198
 <223> Von Heijne matrix
 score 5.38660866264012
 seq ALCSVCSMSVLRA/YP

<400> 57
 agtctaggat cctcacacca gctacttgca agggagaagg aaaaggccag taaggcctgg 60
 gccaggagag tcccgacagg agtgtcaggt ttcaatctca gcaccagcca ctgagagcag 120
 ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc 168
 Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
 -20 -15
 agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca 216
 Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
 -10 -5 1 5
 ctg ctc ggc tcc agc tgg ggt gcc ctg atc cac ctg tac aca gcc aca 264
 Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
 10 15 20
 gcc agg aac agc tac cac ctg cag atc cac aag aat gcc cat gtg gat 312
 Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
 25 30 35
 ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag 360
 Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
 40 45 50
 gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc 408
 Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
 55 60 65 70
 tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg 456
 Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
 75 80 85
 gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc 504
 Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
 90 95 100
 tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag 552
 Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
 105 110 115
 aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg 600
 Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu
 120 125 130
 tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca 648
 Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro

135		140		145		150	
cgg cgg cac acc cgg agc gcc gag gac gac tcg gag cgg gac ccc ctg							696
Arg Arg His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu							
	155		160		165		
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt							744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys							
	170		175		180		
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac							792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp							
	185		190		195		
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga							840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly							
	200		205		210		
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggtcgct							889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile							
215		220		225			
ggaagggcac cctctttaac ccatccctca gcaaacgcag ctcttcccaa ggaccaggtc							949
ccttgacgtt ccgaggatgg gaaaggtgac aggggcatgt atggaatttg ctgcttctct							1009
gggggtccctt ccacaggagg tcctgtgaga accaaccttt gaggcccaag tcatgggggtt							1069
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaa							1129
ctagaaattt ccccttcctg aaggtagaga gaaggggtct ctcccaacat atttctcttc							1189
cttgtgcctc tcctctttat cacttttaag catgaaaaaa aaaaaaaaaa a							1240

<210> 58
 <211> 902
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 156..566

<220>
 <221> sig_peptide
 <222> 156..221
 <223> Von Heijne matrix
 score 5.67458379966095
 seq LVSMAGRVCLCQG/SA

<400> 58	
atttcccagc gtgcctcagg aagggcgcca ggactgcatt ttgctccgga gcgtccagag	60
tcctggccct gacgaggaat cgcagtggcc gaggtgagc ggcaggcgga tcgccccgac	120
cctcactcct ggcgtctgag tctctggcgt agccc atg ctg agt ggg cgg ctg	173
Met Leu Ser Gly Arg Leu	
-20	
gtc ctg ggt ctg gtc tcc atg gct ggc cgc gtt tgt ttg tgc cag ggc	221
Val Leu Gly Leu Val Ser Met Ala Gly Arg Val Cys Leu Cys Gln Gly	
-15 -10 -5	
agc gcg gga tcc ggg gcc atc ggt ccg gtg gag gcc gcc att cgc acg	269
Ser Ala Gly Ser Gly Ala Ile Gly Pro Val Glu Ala Ala Ile Arg Thr	
1 5 10 15	
aag ttg gag gag gcc ctg agc ccc gag gtg cta gag ctt cgc aac gag	317
Lys Leu Glu Glu Ala Leu Ser Pro Glu Val Leu Glu Leu Arg Asn Glu	
20 25 30	

```

agc ggt ggc cac gcg gtc ccg cca ggc agt gag act cac ttc cgc gtg      365
Ser Gly Gly His Ala Val Pro Pro Gly Ser Glu Thr His Phe Arg Val
      35              40              45

gct gtg gtg agc tct cgt ttc gag gga ctg agc ccc cta caa cga cac      413
Ala Val Val Ser Ser Arg Phe Glu Gly Leu Ser Pro Leu Gln Arg His
      50              55              60

cgg ctg gtc cac gca gcg ctg gcc gag gag ctg gga ggt ccg gtc cat      461
Arg Leu Val His Ala Ala Leu Ala Glu Glu Leu Gly Gly Pro Val His
      65              70              75              80

gcg ctg gcc atc cag gca cgg acc ccc gcc cag tgg aga gag aac tct      509
Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala Gln Trp Arg Glu Asn Ser
      85              90              95

cag ctg gac act agc ccc cca tgc ctg ggt ggg aac aag aaa act cta      557
Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly Gly Asn Lys Lys Thr Leu
      100              105              110

gga acc ccc tgaaccccaa gagagggagg accaggatcc gaatgggctg      606
Gly Thr Pro
      115

ggtgagcacg aattaccgag gccttcctt tgatacagtc caggatttgt aagggatgaa      666
gaccctggg cccattctg ttgggggtcca tacatactct ccgaagatag caacttgctt      726
cagggtcaaag tgaacccgag aaaagagaag aatcactcac tactgctctt gccctggact      786
attcaggaag ggcagcccg atgttccatg ttaaattcgtg acagaattgc accagacctg      846
atgagttgga aacaatccta tacattaaaa gaaattacac taaaaaaaaa aaaaaa      902

<210> 59
<211> 1969
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 35..1657

<220>
<221> sig_peptide
<222> 35..118
<223> Von Heijne matrix
      score 3.75144398608723
      seq SGLLLQVLFRLIT/FV

<400> 59
atttttcctg gtgtctgagc ctggcgcgga ggct atg ggc agc cag gag gtg ctg      55
                        Met Gly Ser Gln Glu Val Leu
                        -25

ggc cac gcg gcc cgg ctg gcc tcc tcc ggt ctc ctc ctg cag gtg ttg      103
Gly His Ala Ala Arg Leu Ala Ser Ser Gly Leu Leu Leu Gln Val Leu
      -20              -15              -10

ttt cgg ttg atc acc ttt gtc ttg aat gca ttt att ctt cgc ttc ctg      151
Phe Arg Leu Ile Thr Phe Val Leu Asn Ala Phe Ile Leu Arg Phe Leu
      -5              1              5              10

tca aag gaa atc gtt ggc gta gta aat gta aga cta acg ctg ctt tac      199
Ser Lys Glu Ile Val Gly Val Val Asn Val Arg Leu Thr Leu Leu Tyr
      15              20              25

tca acc acc ctc ttc ctg gcc aga gag gcc ttc cgc aga gca tgt ctc      247

```

Ser	Thr	Thr	Leu	Phe	Leu	Ala	Arg	Glu	Ala	Phe	Arg	Arg	Ala	Cys	Leu	
		30					35					40				
agt	ggg	ggc	acc	cag	cga	gac	tgg	agc	cag	acc	ctc	aac	ctg	ctg	tgg	295
Ser	Gly	Gly	Thr	Gln	Arg	Asp	Trp	Ser	Gln	Thr	Leu	Asn	Leu	Leu	Trp	
	45					50					55					
cta	aca	gtc	ccc	ctg	ggg	gtg	ttt	tgg	tcc	tta	ttc	ctg	ggc	tgg	atc	343
Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp	Ser	Leu	Phe	Leu	Gly	Trp	Ile	
60					65				70					75		
tgg	ttg	cag	ctg	ctt	gaa	gtg	cct	gat	cct	aat	gtt	gtc	cct	cac	tat	391
Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp	Pro	Asn	Val	Val	Pro	His	Tyr	
				80					85					90		
gca	act	gga	gtg	gtg	ctg	ttt	ggg	ctc	tcg	gca	gtg	gtg	gag	ctt	cta	439
Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu	Ser	Ala	Val	Val	Glu	Leu	Leu	
		95					100						105			
gga	gag	ccc	ttt	tgg	gtc	ttg	gca	caa	gca	cat	atg	ttt	gtg	aag	ctc	487
Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln	Ala	His	Met	Phe	Val	Lys	Leu	
	110						115					120				
aag	gtg	att	gca	gag	agc	ctg	tcg	gta	att	ctt	aag	agc	gtt	ctg	aca	535
Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val	Ile	Leu	Lys	Ser	Val	Leu	Thr	
	125					130					135					
gct	ttt	ctc	gtg	ctg	tgg	ttg	cct	cac	tgg	gga	ttg	tac	att	ttc	tct	583
Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His	Trp	Gly	Leu	Tyr	Ile	Phe	Ser	
140					145				150					155		
ttg	gcc	cag	ctt	ttc	tat	acc	aca	gtt	ctg	gtg	ctc	tgc	tat	gtt	att	631
Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val	Leu	Val	Leu	Cys	Tyr	Val	Ile	
			160						165					170		
tat	ttc	aca	aag	tta	ctg	ggg	tcc	cca	gaa	tca	acc	aag	ctt	caa	act	679
Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro	Glu	Ser	Thr	Lys	Leu	Gln	Thr	
		175					180						185			
ctt	cct	gtc	tcc	aga	ata	aca	gat	ctg	tta	ccc	aat	att	aca	aga	aat	727
Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	Leu	Pro	Asn	Ile	Thr	Arg	Asn	
	190						195					200				
gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	aaa	ctg	act	tgg	agt	ttt	ttc	775
Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	Lys	Leu	Thr	Trp	Ser	Phe	Phe	
	205					210					215					
aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	aca	gaa	ggc	gag	cga	tat	gtg	823
Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	Thr	Glu	Gly	Glu	Arg	Tyr	Val	
220					225				230					235		
atg	aca	ttt	ttg	aat	gta	ttg	aac	ttt	ggg	gat	cag	ggg	gtg	tat	gat	871
Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	Gly	Asp	Gln	Gly	Val	Tyr	Asp	
			240						245					250		
ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	gcc	aga	tta	att	ttc	cag	cca	919
Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val	Ala	Arg	Leu	Ile	Phe	Gln	Pro	
		255					260						265			
ata	gag	gaa	agt	ttt	tat	ata	ttt	ttt	gct	aag	gtg	ctg	gag	agg	gga	967
Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	Ala	Lys	Val	Leu	Glu	Arg	Gly	
	270						275					280				
aag	gat	gcc	aca	ctt	cag	aag	cag	gag	gac	gtt	gct	gtg	gct	gct	gca	1015
Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	Asp	Val	Ala	Val	Ala	Ala	Ala	
	285					290					295					
gtc	ttg	gag	tcc	ctg	ctc	aag	ctg	gcc	ctg	ctg	gcc	ggc	ctg	acc	atc	1063
Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	Leu	Leu	Ala	Gly	Leu	Thr	Ile	
300					305				310					315		
act	gtt	ttt	ggc	ttt	gcc	tat	tct	cag	ctg	gct	ctg	gat	atc	tac	gga	1111

Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	Leu	Ala	Leu	Asp	Ile	Tyr	Gly		
				320					325					330			
ggg	acc	atg	ctt	agc	tca	gga	tcc	ggg	cct	gtt	ttg	ctg	cgt	tcc	tac	1159	
Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	Pro	Val	Leu	Leu	Arg	Ser	Tyr		
			335					340					345				
tgt	ctc	tat	gtt	ctc	ctg	ctt	gcc	atc	aat	gga	gtg	aca	gag	tgt	tta	1207	
Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	Asn	Gly	Val	Thr	Glu	Cys	Leu		
		350					355					360					
aca	ttt	gct	gcc	atg	agc	aaa	gag	gag	gtc	gac	agg	tac	aat	ttt	gtg	1255	
Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu	Val	Asp	Arg	Tyr	Asn	Phe	Val		
	365					370				375							
atg	ctg	gcc	ctg	tcc	tcc	tca	ttc	ctg	gtg	tta	tcc	tat	ctc	ttg	acc	1303	
Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu	Val	Leu	Ser	Tyr	Leu	Leu	Thr		
380					385				390					395			
cgt	tgg	tgt	ggc	agc	gtg	ggc	ttc	atc	ttg	gcc	aac	tgc	ttt	aac	atg	1351	
Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile	Leu	Ala	Asn	Cys	Phe	Asn	Met		
			400					405					410				
ggc	att	cgg	atc	acg	cag	agc	ctt	tgc	ttc	atc	cac	cgc	tac	tac	cga	1399	
Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	Phe	Ile	His	Arg	Tyr	Tyr	Arg		
		415					420				425						
agg	agc	ccc	cac	agg	ccc	ctg	gct	ggc	ctg	cac	cta	tcg	cca	gtc	ctg	1447	
Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	Leu	His	Leu	Ser	Pro	Val	Leu		
		430				435				440							
ctc	ggg	aca	ttt	gcc	ctc	agt	ggg	ggg	gtt	act	gct	gtt	tcg	gag	gta	1495	
Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly	Val	Thr	Ala	Val	Ser	Glu	Val		
	445				450				455								
ttc	ctc	tgc	tgt	gat	cag	ggc	tgg	cca	gcc	aga	ctg	gca	cac	att	gct	1543	
Phe	Leu	Cys	Cys	Asp	Gln	Gly	Trp	Pro	Ala	Arg	Leu	Ala	His	Ile	Ala		
460				465				470					475				
gtg	ggg	gcc	ttc	tgt	ctg	gga	gca	act	ctc	ggg	aca	gca	ttc	ctc	aca	1591	
Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr	Leu	Gly	Thr	Ala	Phe	Leu	Thr		
		480				485				490							
gag	acc	aag	ctg	atc	cat	ttc	ctc	agg	act	cag	tta	ggg	gtg	ccc	aga	1639	
Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg	Thr	Gln	Leu	Gly	Val	Pro	Arg		
		495				500				505							
cgc	act	gac	aaa	atg	aca	tgacttcagg	gaagcctgga	cacccgagggc								1687	
Arg	Thr	Asp	Lys	Met	Thr												
		510															
acctggacca	gctatgggta	gttctgtggg	tggaaacacat	tctgtgtaag	agccccactg											1747	
agggctctgc	agcggagtga	cagcaacccc	agagatgagg	caccagagag	tgccactgca											1807	
tgagacacct	gtgaccattc	gaagtctgaa	atgcgggggg	ggagtttcat	ttttaagtga											1867	
agaccaaaag	ccctttaaaa	ataatagttt	tttatcattt	tatagtaatc	agcattttct											1927	
cttttactaa	tatactcatt	ccttttgaaa	aaaaaaaaaa	aa												1969	

<210> 60
 <211> 1132
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..937

<220>

<221> sig_peptide
 <222> 77..127
 <223> Von Heijne matrix
 score 3.74817238048175
 seq RIVSAALLAFVQT/HL

```

<400> 60
gttgggtgggg ctgggggatg agagctgcac cgcgcgggac aagtcgcccg cgccccgacg      60
gagcagaaga gagagc atg gag ctg gag agg atc gtc agt gca gcc ctc ctt      112
                Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu
                -15                                -10

gcc ttt gtc cag aca cac ctc ccg gag gcc gac ctc agt ggc ttg gat      160
Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp
-5                                1                                5                                10
gag gtc atc ttc tcc tat gtg ctt ggg gtc ctg gag gac ctg ggc ccc      208
Glu Val Ile Phe Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro
                15                                20                                25

tcg ggc cca tca gag gag aac ttc gat atg gag gct ttc act gag atg      256
Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met
                30                                35                                40

atg gag gcc tat gtg cct ggc ttc gcc cac atc ccc agg ggc aca ata      304
Met Glu Ala Tyr Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile
                45                                50                                55

ggg gac atg atg cag aag ctc tca ggg cag ctg agc gat gcc agg aac      352
Gly Asp Met Met Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn
60                                65                                70                                75
aaa gag aac ctg caa ccg cag agc tct ggt gtc caa ggt cag gtg ccc      400
Lys Glu Asn Leu Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro
                80                                85                                90

atc tcc cca gag ccc ctg cag cgg ccc gaa atg ctc aaa gaa gag act      448
Ile Ser Pro Glu Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr
                95                                100                                105

agg tct tcg gct gct gct gct gca gac acc caa gat gag gca act ggc      496
Arg Ser Ser Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly
                110                                115                                120

gct gag gag gag ctt ctg cca ggg gtg gat gta ctc ctg gag gtg ttc      544
Ala Glu Glu Glu Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe
                125                                130                                135

cct acc tgt tcg gtg gag cag gcc cag tgg gtg ctg gcc aaa gct cgg      592
Pro Thr Cys Ser Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg
140                                145                                150                                155
ggg gac ttg gaa gaa gct gtg cag atg ctg gta gag gga aag gaa gag      640
Gly Asp Leu Glu Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu
                160                                165                                170

ggg cct gca gcc tgg gag ggc ccc aac cag gac ctg ccc aga cgc ctc      688
Gly Pro Ala Ala Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu
                175                                180                                185

aga ggc ccc caa aag gat gag ctg aag tcc ttc atc ctg cag aag tac      736
Arg Gly Pro Gln Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr
                190                                195                                200

atg atg gtg gat agc gca gag gat cag aag att cac cgg ccc atg gct      784
Met Met Val Asp Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala
                205                                210                                215

ccc aag gag gcc ccc aag aag ctg atc cga tac atc gac aac cag gta      832

```

[illegible]

```
<210> 61
<211> 631
<212> DNA
<213> Homo sapiens
```

<220>
<221> CDS
<222> 9..503

```
<220>
<221> sig_peptide
<222> 9..113
<223> Von Heijne matrix
      score 10.2506494380376
      seq LLPLVLLPPLAAA/AA
```

<400>	61																
tgccaggg	atg	atg	cgc	tgc	tgc	cgc	cgc	cgc	tgc	tgc	tgc	cgg	caa	cca		50	
	Met	Met	Arg	Cys	Cys	Arg	Arg	Arg	Cys	Cys	Cys	Arg	Gln	Pro			
	-35					-30						-25					
ccc	cat	gcc	ctg	agg	ccg	ttg	ctg	ttg	ctg	ccc	ctc	gtc	ctt	tta	cct	98	
Pro	His	Ala	Leu	Arg	Pro	Leu	Leu	Leu	Leu	Pro	Leu	Val	Leu	Leu	Pro		
	-20					-15						-10					
ccc	ctg	gca	gca	gct	gca	gcg	ggc	cca	aac	cga	tgt	gac	acc	ata	tac	146	
Pro	Leu	Ala	Ala	Ala	Ala	Ala	Gly	Pro	Asn	Arg	Cys	Asp	Thr	Ile	Tyr		
	-5				1				5					10			
cag	ggc	ttc	gcc	gag	tgt	ctc	atc	cgc	ttg	ggg	gac	agc	atg	ggc	cgc	194	
Gln	Gly	Phe	Ala	Glu	Cys	Leu	Ile	Arg	Leu	Gly	Asp	Ser	Met	Gly	Arg		
			15					20					25				
gga	ggc	gag	ctg	gag	acc	atc	tgc	agg	tct	tgg	aat	tac	ttc	cat	gcc	242	
Gly	Gly	Glu	Leu	Glu	Thr	Ile	Cys	Arg	Ser	Trp	Asn	Tyr	Phe	His	Ala		
		30					35					40					
tgt	gcc	tct	cag	gtc	ctg	tca	ggc	tgt	ccg	gag	gag	gca	gct	gca	gtg	290	
Cys	Ala	Ser	Gln	Val	Leu	Ser	Gly	Cys	Pro	Glu	Glu	Ala	Ala	Ala	Val		
	45					50					55						
tgg	gaa	tca	cta	cag	caa	gaa	gct	cgc	cag	gcc	ccc	cgt	ccg	aat	aac	338	
Trp	Glu	Ser	Leu	Gln	Gln	Glu	Ala	Arg	Gln	Ala	Pro	Arg	Pro	Asn	Asn		
	60				65					70				75			
ttg	cac	act	ctg	tgc	qqt	qcc	ccg	qtg	cat	qtt	cqq	qaq	cqc	qgc	aca	386	

Leu	His	Thr	Leu	Cys	Gly	Ala	Pro	Val	His	Val	Arg	Glu	Arg	Gly	Thr		
				80					85					90			
ggc	tcc	gaa	acc	aac	cag	gag	acg	ctg	cgg	gct	aca	gcg	cct	gca	ctc		434
Gly	Ser	Glu	Thr	Asn	Gln	Glu	Thr	Leu	Arg	Ala	Thr	Ala	Pro	Ala	Leu		
			95					100					105				
ccc	atg	gcc	cct	gcg	ccc	cca	ctg	ctg	gcg	gct	gct	ctg	gct	ctg	gcc		482
Pro	Met	Ala	Pro	Ala	Pro	Pro	Leu	Leu	Ala	Ala	Ala	Leu	Ala	Leu	Ala		
		110					115					120					
tac	ctc	ctg	agg	cct	ctg	gcc	tagcttggtg	ggttgggtag	cagcgcccgt								533
Tyr	Leu	Leu	Arg	Pro	Leu	Ala											
		125				130											
acctccagcc	ctgctctggc	ggtgggtgtc	caggctctgc	agagcgcagc	agggcttttc												593
attaaaggta	tttatatttg	caaaaaaaaa	aaaaaaaa														631

<210> 62
 <211> 722
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21..464

<220>
 <221> sig_peptide
 <222> 21..95
 <223> Von Heijne matrix
 score 5.38058532480537
 seq AVTSLLSPTPATA/LA

<400> 62																	
ggaagtgagt	gatcgaaagc	atg	gcg	tcg	gtg	gtg	ttg	gcg	ctg	agg	acc	cgg					53
		Met	Ala	Ser	Val	Val	Leu	Ala	Leu	Arg	Thr	Arg					
		-25					-20					-15					
aca	gcc	gtt	aca	tcc	ttg	cta	agc	ccc	act	ccg	gct	aca	gct	ctt	gct		101
Thr	Ala	Val	Thr	Ser	Leu	Leu	Ser	Pro	Thr	Pro	Ala	Thr	Ala	Leu	Ala		
			-10				-5					1					
gtc	aga	tac	gca	tcc	aag	aag	tcg	ggt	ggt	agc	tcc	aaa	aac	ctc	ggt		149
Val	Arg	Tyr	Ala	Ser	Lys	Lys	Ser	Gly	Gly	Ser	Ser	Lys	Asn	Leu	Gly		
		5				10					15						
gga	aag	tca	tca	ggc	aga	cgc	caa	ggc	att	aag	aaa	atg	gaa	ggt	cac		197
Gly	Lys	Ser	Ser	Gly	Arg	Arg	Gln	Gly	Ile	Lys	Lys	Met	Glu	Gly	His		
	20				25				30								
tat	gtt	cat	gct	ggg	aac	atc	att	gca	aca	cag	cgc	cat	ttc	cgc	tgg		245
Tyr	Val	His	Ala	Gly	Asn	Ile	Ile	Ala	Thr	Gln	Arg	His	Phe	Arg	Trp		
	35			40				45					50				
cac	cca	ggt	gcc	cat	gtg	ggt	gtt	ggg	aag	aat	aaa	tgt	ctg	tat	gcc		293
His	Pro	Gly	Ala	His	Val	Gly	Val	Gly	Lys	Asn	Lys	Cys	Leu	Tyr	Ala		
			55					60				65					
ctg	gaa	gag	ggg	ata	gtc	cgc	tac	act	aag	gag	gtc	tac	gtg	cct	cat		341
Leu	Glu	Glu	Gly	Ile	Val	Arg	Tyr	Thr	Lys	Glu	Val	Tyr	Val	Pro	His		
		70					75					80					
ccc	aga	aac	acg	gag	gct	gtg	gat	ctg	atc	acc	agg	ctg	ccc	aag	ggt		389
Pro	Arg	Asn	Thr	Glu	Ala	Val	Asp	Leu	Ile	Thr	Arg	Leu	Pro	Lys	Gly		

85	90	95	
gct gtg ctc tac aag act ttt gtc cac gtg gtt cct gcc aag cct gag			437
Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro Ala Lys Pro Glu			
100	105	110	
ggc acc ttc aaa ctg gta gct atg ctt tgatgtcctg ttgaggccat			484
Gly Thr Phe Lys Leu Val Ala Met Leu			
115	120		
cggacagaga ctggagccca ggtgacagga gatggtgata ccagaagtca aggggttgggg			544
tggcgacacg gcctcccagag gaagaggtct gcttgatggt gactctgcag gagactctga			604
agtgactgct gggaaaccct ttgggagacc tgacctgggg ccaaaaaataa agtgagccag			664
cgtcatgaac gcatgctatt tagggacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa			722

<210> 63
 <211> 1442
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 178..1050

<220>
 <221> sig_peptide
 <222> 178..279
 <223> Von Heijne matrix
 score 10.0571391689271
 seq FLCLLSALLLTEG/KK

<400> 63	
agtgcatcgc tggagcgagg agaagctcac gaatcagctg caggtctctg ttttgaaaaa	60
gcagagatac agaggcagag gaaaagggca ctcctatgtg acctgttctt agagcaagac	120
aatcaccatc tgaattccag aagccctgtt catggttggg gatattttct cgactgc	177
atg gaa tca gaa aga agc aaa agg atg gga aat gcc tgc att ccc ctg	225
Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu	
-30 -25 -20	
aaa aga att gct tat ttc cta tgt ctc tta tct gcg ctt ttg ctg act	273
Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Leu Thr	
-15 -10 -5	
gag ggg aag aaa cca gcg aag cca aaa tgc cct gcc gtg tgt act tgt	321
Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys	
1 5 10	
acc aaa gat aat gct tta tgt gag aat gcc aga tcc att cca cgc acc	369
Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr	
15 20 25 30	
gtt cct cct gat gtt atc tca tta tcc ttt gtg aga tct ggt ttt act	417
Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr	
35 40 45	
gaa atc tca gaa ggg agt ttt tta ttc acg cca tcg ctg cag ctc ttg	465
Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu	
50 55 60	
tta ttc aca tcg aac tcc ttt gat gtg atc agt gat gat gct ttt att	513
Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile	
65 70 75	
ggg ctt cca cat cta gag tat tta ttc ata gaa aac aac aac atc aag	561

Gly	Leu	Pro	His	Leu	Glu	Tyr	Leu	Phe	Ile	Glu	Asn	Asn	Asn	Ile	Lys	
80						85				90						
tca	att	tca	aga	cat	act	ttc	cgg	gga	cta	aag	tca	tta	att	cac	ttg	609
Ser	Ile	Ser	Arg	His	Thr	Phe	Arg	Gly	Leu	Lys	Ser	Leu	Ile	His	Leu	
95					100					105					110	
agc	ctt	gca	aac	aac	aat	ctc	cag	aca	ctc	cca	aaa	gat	att	ttc	aaa	657
Ser	Leu	Ala	Asn	Asn	Asn	Leu	Gln	Thr	Leu	Pro	Lys	Asp	Ile	Phe	Lys	
				115					120						125	
ggc	ctg	gat	tct	tta	aca	aat	gtg	gac	ctg	agg	ggg	aat	tca	ttt	aat	705
Gly	Leu	Asp	Ser	Leu	Thr	Asn	Val	Asp	Leu	Arg	Gly	Asn	Ser	Phe	Asn	
			130					135					140			
tgt	gac	tgt	aaa	ctg	aaa	tgg	cta	gtg	gaa	tgg	ctt	ggc	cac	acc	aat	753
Cys	Asp	Cys	Lys	Leu	Lys	Trp	Leu	Val	Glu	Trp	Leu	Gly	His	Thr	Asn	
		145					150					155				
gca	act	ggt	gaa	gac	atc	tac	tgc	gaa	ggc	ccc	cca	gaa	tac	aag	aag	801
Ala	Thr	Val	Glu	Asp	Ile	Tyr	Cys	Glu	Gly	Pro	Pro	Glu	Tyr	Lys	Lys	
	160					165				170						
cgc	aaa	atc	aat	agt	ctc	tcc	tcg	aag	gat	ttc	gat	tgc	atc	att	aca	849
Arg	Lys	Ile	Asn	Ser	Leu	Ser	Ser	Lys	Asp	Phe	Asp	Cys	Ile	Ile	Thr	
175					180					185					190	
gaa	ttt	gca	aag	tct	caa	gac	ctg	cct	tat	caa	tca	ttg	tcc	ata	gac	897
Glu	Phe	Ala	Lys	Ser	Gln	Asp	Leu	Pro	Tyr	Gln	Ser	Leu	Ser	Ile	Asp	
				195					200					205		
act	ttt	tct	tat	ttg	aat	gat	gag	tat	gta	gtc	atc	gct	cag	cct	ttt	945
Thr	Phe	Ser	Tyr	Leu	Asn	Asp	Glu	Tyr	Val	Val	Ile	Ala	Gln	Pro	Phe	
			210					215					220			
act	gga	aaa	tgc	att	ttc	ctt	gaa	tgg	gac	cat	gtg	gaa	aag	acc	ttc	993
Thr	Gly	Lys	Cys	Ile	Phe	Leu	Glu	Trp	Asp	His	Val	Glu	Lys	Thr	Phe	
		225					230					235				
cgg	aat	tat	gac	aac	att	aca	gtt	tta	agg	gaa	ata	cac	aga	ttt	aca	1041
Arg	Asn	Tyr	Asp	Asn	Ile	Thr	Val	Leu	Arg	Glu	Ile	His	Arg	Phe	Thr	
	240					245				250						
aac	atg	tca	tagttgactt	aagcgc	catga	gacaccaa	aat	tctgtg	ggctg							1090
Asn	Met	Ser														
255																
ccatcagaaa	ttttctacag	tacatgaccc	ggatgaactc	aatgcatgat	gactcttctt											1150
atcacacttg	caaatgaatg	cctttcaaac	attgagactg	ctagaaccaa	gcactaccag											1210
tatctccatc	cttaactgtc	cagtcacgtg	atgtgggaag	ttacctttta	taagacaaaa											1270
tttaattgtg	taactgttct	ttgcagtga	gatgtgtaaa	taagcgttta	atggatatctg											1330
ttactccaaa	aagaaatatt	aatatgtact	tttccattta	tttattcatg	tgtacagaaa											1390
caactgc	ccaa	ataaaa	atggtt	tacattttct	ttcagaaaaa	aaaaaaaaaa	aa									1442

<210> 64
 <211> 795
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 32..274

<220>
 <221> sig_peptide
 <222> 32..178

<223> Von Heijne matrix
 score 4.30837886795471
 seq LMVELLKVFVVEA/AV

<400> 64
 gttccggtgg gcgcgcgttg aggctgcggt c atg gag gga gca gga gct gga 52
 Met Glu Gly Ala Gly Ala Gly
 -45
 tcc ggc ttc cgg aag gag ctg gtg agc agg ctg ctg cac ctg cac ttc 100
 Ser Gly Phe Arg Lys Glu Leu Val Ser Arg Leu Leu His Leu His Phe
 -40 -35 -30
 aag gat gac aag acc aaa gtg agc ggg gac gcg ctg cag ctc atg gtg 148
 Lys Asp Asp Lys Thr Lys Val Ser Gly Asp Ala Leu Gln Leu Met Val
 -25 -20 -15
 gag ttg ctg aag gtc ttc gtt gtg gaa gca gca gtc cgc ggc gtg cgg 196
 Glu Leu Leu Lys Val Phe Val Val Glu Ala Ala Val Arg Gly Val Arg
 -10 -5 1 5
 cag gcc cag gca gaa gac gcg ctc cgt gtg gac gtg gac cag ctg gag 244
 Gln Ala Gln Ala Glu Asp Ala Leu Arg Val Asp Val Asp Gln Leu Glu
 10 15 20
 aag gtg ctt ccg cag ctg ctc ctg gac ttc tagggatctc agccgtggct 294
 Lys Val Leu Pro Gln Leu Leu Leu Asp Phe
 25 30
 gagggcacc ccagaggagc ccctggtcca cagaagcagg ccttgtgttt ccagcggcct 354
 ctgataagag gcaggaagg acctgaagga tttggagttg attcaaaca gatctctggg 414
 agtctccagc ctgtgcagaa ggggcaggac tgcagtgcac tgcgggcctt ggagtgtcca 474
 gtggggacac tgggtgtggga aggggcagca cctggggagt ccctgcctct cctccctggg 534
 acaatagtgt gcatgccacc cggggtccta caggcagggt ctgggaaagg cctggccagc 594
 aggtagcctg tgtgtttgac aaacagcagc tggcagcgt gcctcctgcc cacattcctg 654
 ccaccgcaca tcaaagctgg cgtgtgacct ttccagccat gcgatattcc ccttggaaga 714
 tgcttcccca ggctataaat ttgtttctcac aaagcaacat caataaatca aaactgtctc 774
 tctcaaaaaa aaaaaaaaaa a 795

<210> 65
 <211> 1236
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 222..920

<220>
 <221> sig_peptide
 <222> 222..311
 <223> Von Heijne matrix
 score 4.35083245061594
 seq VAHALSLPAESYG/ND

<400> 65
 accgaaaatt actgacgagt caatcacctc agatctctca agcagtcag cctacgcaac 60
 agtactccac ctctgcgcct gtgcggggag ggtaaggcgg ggccagcaac ttctcagct 120
 ggagggagag cgcacggtgg agccgccagt tgagaaggac tctgatccgg ctcagctttc 180
 caatcagctg cggaaggagc cagcgtttcg ggggttgcaa g atg gcg gcc acc agt 236

<211> 881
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 101..355

<220>
 <221> sig_peptide
 <222> 101..160
 <223> Von Heijne matrix
 score 9.32665652007071
 seq LFLCYLLLF TCSG/VE

<400> 66
 ttactcgctg ctgtgcccac ctatcagcag gctccgggct gaagattgct tctcttctct 60
 cctccaaggt ctagtgcagg agcccgcgcg cggcgccacc atg cgg cag aag gcg 115
 Met Arg Gln Lys Ala
 -20
 gta tcg ctt ttc ttg tgc tac ctg ctg ctc ttc act tgc agt ggg gtg 163
 Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly Val
 -15 -10 -5 1
 gag gca ggt aag aaa aag tgc tcg gag agc tcg gac agc ggc tcc ggg 211
 Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser Gly
 5 10 15
 ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca gtc 259
 Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala Val
 20 25 30
 gcc ggg ctg ccc gcg ctg ggc ttc acc ggc gcc ggc atc gcg gcc aac 307
 Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala Asn
 35 40 45
 tcg gtg gct gcc tcg ctg atg agc tgg tct gcg atc ctg aat ggg ggc 355
 Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly Gly
 50 55 60 65
 tagtggccac gctgcagagc ctcgggggctg gtggcagcag cgtcgtcata ggtaatatg 415
 gtgccctgat gggctacgcc acccacaagt atctcgatag tgaggaggat gaggagtagc 475
 cagcagctcc cagaacctct tcttccttct tggcctaact cttccagtta ggatctagaa 535
 ctttgccctt tttttttttt tttttttttt ttgagatggg ttctcactat attgtccagg 595
 ctagagtga gkggctattc acagatgcga acatagtaca ctgcagcctc caactcctag 655
 cctcaagtga tcctcctgtc tcaacctccc aagtaggatt acaagcatgc gccgacgatg 715
 cccaraatcc araactttgt ctatcactct ccccaacaac ctatagtgtga aaacagaata 775
 aacttcaccc agaaaaaaaa aaammacaar aaaaaaaaaa aaaaaaaaaa aaaaaaaaaam 835
 aaaaaaaaaa rrraaaaaaaa aaaaaaaaga aaaaaaaaaa aaaaaa 881

<210> 67
 <211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 173..487

<220>
 <221> sig_peptide
 <222> 173..301
 <223> Von Heijne matrix
 score 4.27484469223909
 seq AGSLVATLQSVGA/AG

<400> 67
 agggcagagt aggcgcgtcc ctactggatg gagggggaag taacacccca agaacgctgt 60
 catttcctgg gccaaagtgg gacccggacg gcctcaccat gatgaaacgg gcagctgctg 120
 ctgcagtggg aggagccctg gcagtggggg ctgtgccgtg gtgctcagtg cc atg ggc 178
 Met Gly
 ttc act ggg gca gga atc gcc gcg tcc tcc ata gca gcc aag atg atg 226
 Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met
 -40 -35 -30
 tcc gca gca gcc att gcc aac ggg ggt ggt gtt tct gcg ggg agc ctg 274
 Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu
 -25 -20 -15 -10
 gtg gct act ctg cag tcc gtg ggg gca gct gga ctc tcc aca tca tcc 322
 Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser
 -5 1 5
 aac atc ctc ctg gcc tct gtt ggg tca gtg ttg ggg gcc tgc ttg ggg 370
 Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly
 10 15 20
 aat tca cct tct tct tct ctc cca gct gaa ccc gag gct aaa gaa gat 418
 Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp
 25 30 35
 gag gca aga gaa aat gta ccc caa ggt gaa cct cca aaa ccc cca ctc 466
 Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu
 40 45 50 55
 aag tca gag aaa cat gag gaa taaaggtcac atgcagatgc aaaaaaaaaa 517
 Lys Ser Glu Lys His Glu Glu
 60
 aaaaaaa 524

<210> 68
 <211> 1472
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 210..1082

<220>
 <221> sig_peptide
 <222> 210..311
 <223> Von Heijne matrix
 score 10.0571391689271
 seq FLCLLSALLLTEG/KK

<400> 68
 acagtacctc acaggtctct tccccgagc agtgcattgc tggagcgagg agaagctcac 60
 gaatcagctg caggtctctg ttttgaaaaa gcagagatac agaggcagag gaaaagggtg 120

gactcctatg tgacctgttc ttagagcaag acaatcacca tctgaattcc agaagccctg	180
ttcatgggtg gggatatattt ctcgactgc atg gaa tca gaa aga agc aaa agg	233
Met Glu Ser Glu Arg Ser Lys Arg	
-30	
atg gga aat gcc tgc att ccc ctg aaa aga att gct tat ttc cta tgt	281
Met Gly Asn Ala Cys Ile Pro Leu Lys Arg Ile Ala Tyr Phe Leu Cys	
-25 -20 -15	
ctc tta tct gcg ctt ttg ctg act gag ggg aag aaa cca gcg aag cca	329
Leu Leu Ser Ala Leu Leu Leu Thr Glu Gly Lys Lys Pro Ala Lys Pro	
-10 -5 1 5	
aaa tgc cct gcc gtg tgt act tgt acc aaa gat aat gct tta tgt gag	377
Lys Cys Pro Ala Val Cys Thr Cys Thr Lys Asp Asn Ala Leu Cys Glu	
10 15 20	
aat gcc aga tcc att cca cgc acc gtt cct cct gat gtt atc tca tta	425
Asn Ala Arg Ser Ile Pro Arg Thr Val Pro Pro Asp Val Ile Ser Leu	
25 30 35	
tcc ttt gtg aga tct gtt ttt act gaa atc tca gaa ggg agt ttt tta	473
Ser Phe Val Arg Ser Val Phe Thr Glu Ile Ser Glu Gly Ser Phe Leu	
40 45 50	
ttc acg cca tcg ctg cag ctc ttg tta ttc aca tcg aac tcc ttt gat	521
Phe Thr Pro Ser Leu Gln Leu Leu Leu Phe Thr Ser Asn Ser Phe Asp	
55 60 65 70	
gtg atc agt gat gat gct ttt att ggt ctt cca cat cta gag tat tta	569
Val Ile Ser Asp Asp Ala Phe Ile Gly Leu Pro His Leu Glu Tyr Leu	
75 80 85	
ttc ata gaa aac aac aac atc aag tca att tca aga cat act ttc cgg	617
Phe Ile Glu Asn Asn Asn Ile Lys Ser Ile Ser Arg His Thr Phe Arg	
90 95 100	
gga cta aag tca tta att cac ttg agc ctt gca aac aac aat ctc cag	665
Gly Leu Lys Ser Leu Ile His Leu Ser Leu Ala Asn Asn Asn Leu Gln	
105 110 115	
aca ctc cca aaa gat att ttc aaa ggc ctg gat tct tta aca aat gtg	713
Thr Leu Pro Lys Asp Ile Phe Lys Gly Leu Asp Ser Leu Thr Asn Val	
120 125 130	
gac ctg agg ggt aat tca ttt aat tgt gac tgt aaa ctg aaa tgg cta	761
Asp Leu Arg Gly Asn Ser Phe Asn Cys Asp Cys Lys Leu Lys Trp Leu	
135 140 145 150	
gtg gaa tgg ctt ggc cac acc aat gca act gtt gaa gac atc tac tgc	809
Val Glu Trp Leu Gly His Thr Asn Ala Thr Val Glu Asp Ile Tyr Cys	
155 160 165	
gaa ggc ccc cca gaa tac aag aag cgc aaa atc aat agt ctc tcc tcg	857
Glu Gly Pro Pro Glu Tyr Lys Lys Arg Lys Ile Asn Ser Leu Ser Ser	
170 175 180	
aag gat ttc gat tgc atc att aca gaa ttt gca aag tct caa gac ctg	905
Lys Asp Phe Asp Cys Ile Ile Thr Glu Phe Ala Lys Ser Gln Asp Leu	
185 190 195	
cct tat caa tca ttg tcc ata gac act ttt tct tat ttg aat gat gag	953
Pro Tyr Gln Ser Leu Ser Ile Asp Thr Phe Ser Tyr Leu Asn Asp Glu	
200 205 210	
tat gta gtc atc gct cag cct ttt act gga aaa tgc att ttc ctt gaa	1001
Tyr Val Val Ile Ala Gln Pro Phe Thr Gly Lys Cys Ile Phe Leu Glu	
215 220 225 230	
tgg gac cat gtg gaa aag acc ttc cgg aat tat gac aac att aca gtt	1049
Trp Asp His Val Glu Lys Thr Phe Arg Asn Tyr Asp Asn Ile Thr Val	

	235	240	245	
tta agg gaa ata cac aga ttt aca aac atg tca tagttgactt aagcgcatga				1102
Leu Arg Glu Ile His Arg Phe Thr Asn Met Ser				
	250	255		
gacaccaaatt tctgtggctg ccatcagaaa ttttctacag tacatgaccc ggatgaactc				1162
aatgcatgat gactcttctt atcacacttg caaatgaatg cctttcaaac attgagactg				1222
ctagaaccaa gcactaccag tatctccatc cttaactgtc cagtccagtg atgtgggaag				1282
ttacctttta taagacaaaa tttaattgtg taactgttct ttgcagtga gatgtgtaaa				1342
taagcgttta atggtatctg ttactccaaa aagaaatatt aatatgtact tttccattta				1402
tttattcatg tgtacagaaa caactgccaa ataaaatggt tacattttct tacaacaaaa				1462
aaaaaaaaa				1472
<210>	69			
<211>	1737			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	172..1449			
<220>				
<221>	sig_peptide			
<222>	172..255			
<223>	Von Heijne matrix			
	score 5.94825670923113			
	seq XVLLEPFVHQVGG/HS			
<400>	69			
aaacaatagg acggaacgc cgaggaaccc ggctgaggcg gcagagcatc ctggccagaa				60
caagccaagg agccaagacg agagggacac acggacaaac aacagacaga agacgtactg				120
gccgctggac tccgtgcct ccccatctc cccgccatct gcgcccggag g atg agc				177
			Met Ser	
cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt				225
Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu				
-25 -20 -15				
ctg gag ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc				273
Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg				
-10 -5 1 5				
ttc aat gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag				321
Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln				
10 15 20				
ttc tac gag acc ctc cct gct gag atg cgc aaa ttc act ccc cag tac				369
Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr				
25 30 35				
aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat gaa gac agg aac ttg				417
Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu				
40 45 50				
tgt cta ata gca tat cca ttg aaa ggg gac cat gga att gtg gac att				465
Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile				
55 60 65 70				
gta gat aat tca gac tgt gaa cca aaa agt aag ctc cta agg tgg aca				513
Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg Trp Thr				
75 80 85				

aca aac aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac	561
Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp	
90 95 100	
tgg gtg cgt cag cac cgt aaa gag gag aaa atg aag agc cat aag tta	609
Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu	
105 110 115	
gaa gaa gaa ttt gag tgg cta aag aaa tct gaa gtc ttg tac tac act	657
Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr	
120 125 130	
gta gag aag aag ggg aat ata agt tcc cag ctt aaa cac tat aac cct	705
Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr Asn Pro	
135 140 145 150	
tgg agc atg aaa tgt cac cag caa cag tta cag aga atg aag gag aat	753
Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys Glu Asn	
155 160 165	
gca aag cat cgg aac cag tac aaa ttt atc tta ctg gaa aac ctg act	801
Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn Leu Thr	
170 175 180	
tcc cgc tat gag gtg cct tgt gtc ctt gac ctc aag atg ggc aca cga	849
Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg	
185 190 195	
caa cat ggt gat gat gct tca gag gag aag gca gcc aac cag atc cga	897
Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln Ile Arg	
200 205 210	
aaa tgt cag cag agc aca tct gca gtc att ggt gtg cgt gtg tgt ggc	945
Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val Cys Gly	
215 220 225 230	
atg cag gtg tac caa gca ggc agt ggg cag ctc atg ttc atg aac aag	993
Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met Asn Lys	
235 240 245	
tac cat gga cgg aag cta tcg atg cag ggc ttc aag gag gca ctt ttc	1041
Tyr His Gly Arg Lys Leu Ser Met Gln Gly Phe Lys Glu Ala Leu Phe	
250 255 260	
cag ttc ttc cac aat ggg cgg tac ctg cgc cgt gaa ctc ctg ggc cct	1089
Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu Gly Pro	
265 270 275	
gtg ctc aag aag ctg act gag ctc aag gca gtg ttg gag cga cag gag	1137
Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg Gln Glu	
280 285 290	
tcc tac cgc ttc tac tca agc tcc ctg ctg gtc att tat gat ggc aag	1185
Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp Gly Lys	
295 300 305 310	
gag cgg ccc gaa gtg gtc ctg gac tca gat gct gag gat ttg gag gac	1233
Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu Glu Asp	
315 320 325	
ctg tca gag gaa tca gct gat gag tct gct ggt gcc tat gcc tac aaa	1281
Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala Tyr Lys	
330 335 340	
ccc atc ggc gcc agc tct gta gat gtg cgc atg atc gac ttt gca cac	1329
Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe Ala His	
345 350 355	
acc acc tgc agg ctg tat ggc gag gac acc gtg gtg cat gag ggc cag	1377
Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu Gly Gln	
360 365 370	

gat gct ggc tat atc ttc ggg ctc cag agc ctg ata gac att gtc aca	1425
Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile Val Thr	
375 380 385 390	
gag ata agt gag gag agt ggg gag tgagcttgct agctgctcca gtacttgaga	1479
Glu Ile Ser Glu Glu Ser Gly Glu	
395	
gcgactctgt gtcccaggca cagctgtgct gcgtcagggg ggaagccagt atggccaggt	1539
ggtggctcct gcagcctgga gctgatgtgc agtggcctct gtgagcccca gcctgagcca	1599
gtcccagctg tgcttgaggc ctttatttat tttaactatt tcttcaacat tccacatttg	1659
atgatgatac ctctttcttc cctgagtgta tatgtttctaa tacaaatctt tttgtttatt	1719
gaaaaaaaaa aaaaaaaaaa	1737

Leu	Leu	Glu	Val	Gly	Ser	Arg	Pro	Gly	Pro	Ala	Ser	Gln	Leu	Pro	Arg	
105					110					115					120	
ttt	gtg	cgt	gtg	aac	act	ctc	aag	acc	tgc	tcc	gat	gat	gta	gtt	gat	485
Phe	Val	Arg	Val	Asn	Thr	Leu	Lys	Thr	Cys	Ser	Asp	Asp	Val	Val	Asp	
				125					130						135	
tat	ttc	aag	aga	caa	ggg	ttc	tcc	tat	cag	ggg	cgg	gct	tcc	agc	ctc	533
Tyr	Phe	Lys	Arg	Gln	Gly	Phe	Ser	Tyr	Gln	Gly	Arg	Ala	Ser	Ser	Leu	
			140					145					150			
gat	gac	tta	cga	gcc	ctc	aag	ggg	aag	cat	ttt	ctc	ctg	gac	ccc	ttg	581
Asp	Asp	Leu	Arg	Ala	Leu	Lys	Gly	Lys	His	Phe	Leu	Leu	Asp	Pro	Leu	
		155					160					165				
atg	ccg	gag	ctg	ctg	gtg	ttt	ccc	gcc	cag	aca	gat	ctg	cat	gaa	cac	629
Met	Pro	Glu	Leu	Leu	Val	Phe	Pro	Ala	Gln	Thr	Asp	Leu	His	Glu	His	
		170				175					180					
cca	ctg	tac	cgg	gcc	gga	cac	ctc	att	ctg	cag	gac	agg	gcc	agc	tgt	677
Pro	Leu	Tyr	Arg	Ala	Gly	His	Leu	Ile	Leu	Gln	Asp	Arg	Ala	Ser	Cys	
185					190					195					200	
ctc	cca	gcc	atg	ctg	ctg	gac	ccc	ccg	cca	ggc	tcc	cat	gtc	atc	gat	725
Leu	Pro	Ala	Met	Leu	Leu	Asp	Pro	Pro	Pro	Gly	Ser	His	Val	Ile	Asp	
				205					210					215		
gcc	tgt	gcc	gcc	cca	ggc	aat	aag	acc	agt	cac	ttg	gct	gct	ctt	ctg	773
Ala	Cys	Ala	Ala	Pro	Gly	Asn	Lys	Thr	Ser	His	Leu	Ala	Ala	Leu	Leu	
			220				225						230			
aag	aac	caa	ggg	aag	atc	ttt	gcc	ttt	gac	ctg	gat	gcc	aag	cgg	ctg	821
Lys	Asn	Gln	Gly	Lys	Ile	Phe	Ala	Phe	Asp	Leu	Asp	Ala	Lys	Arg	Leu	
		235				240						245				
gca	tcc	atg	gcc	acg	ctg	ctg	gcc	cgg	gct	ggc	gtc	tct	tgc	tgt	gaa	869
Ala	Ser	Met	Ala	Thr	Leu	Leu	Ala	Arg	Ala	Gly	Val	Ser	Cys	Cys	Glu	
		250				255					260					
ctg	gct	gag	gag	gac	ttc	ctg	gcg	gtc	tcc	ccc	tcg	gat	cca	cgc	tac	917
Leu	Ala	Glu	Glu	Asp	Phe	Leu	Ala	Val	Ser	Pro	Ser	Asp	Pro	Arg	Tyr	
265					270					275					280	
cat	gag	gtc	cac	tac	atc	ctg	ctg	gat	cct	tcc	tgc	agt	ggc	tcg	ggg	965
His	Glu	Val	His	Tyr	Ile	Leu	Leu	Asp	Pro	Ser	Cys	Ser	Gly	Ser	Gly	
				285					290					295		
atg	ccg	agc	aga	cag	ctg	gag	gag	ccc	ggg	gca	ggc	aca	cct	agc	ccg	1013
Met	Pro	Ser	Arg	Gln	Leu	Glu	Glu	Pro	Gly	Ala	Gly	Thr	Pro	Ser	Pro	
			300					305					310			
gtg	cgt	ctg	cat	gcc	ctg	gca	ggc	ttc	cag	cag	cga	gcc	ctg	tgc	cac	1061
Val	Arg	Leu	His	Ala	Leu	Ala	Gly	Phe	Gln	Gln	Arg	Ala	Leu	Cys	His	
			315				320					325				
gcg	ctc	act	ttc	cct	tcc	ctg	cag	cgg	ctc	gtc	tac	tcc	acg	tgc	tcc	1109
Ala	Leu	Thr	Phe	Pro	Ser	Leu	Gln	Arg	Leu	Val	Tyr	Ser	Thr	Cys	Ser	
		330				335					340					
ctc	tgc	cag	gag	gag	aat	gaa	gac	gtg	gtg	cga	gat	gcg	ctg	cag	cag	1157
Leu	Cys	Gln	Glu	Glu	Asn	Glu	Asp	Val	Val	Arg	Asp	Ala	Leu	Gln	Gln	
345					350					355					360	
aac	ccg	ggc	gcc	ttc	agg	cta	gct	ccc	gcc	ctg	cct	gcc	tgg	ccc	cac	1205
Asn	Pro	Gly	Ala	Phe	Arg	Leu	Ala	Pro	Ala	Leu	Pro	Ala	Trp	Pro	His	
				365				370						375		
cga	ggc	ctg	agc	acg	ttc	ccg	ggg	gcc	gag	cac	tgc	ctc	cgg	gcc	tcc	1253
Arg	Gly	Leu	Ser	Thr	Phe	Pro	Gly	Ala	Glu	His	Cys	Leu	Arg	Ala	Ser	
			380					385					390			
cct	gag	acc	aca	ctc	agc	agt	ggc	ttc	ttc	gtt	gct	gta	att	gaa	cgg	1301

Pro	Glu	Thr	Thr	Leu	Ser	Ser	Gly	Phe	Phe	Val	Ala	Val	Ile	Glu	Arg	
		395					400					405				
gtc	gag	gtg	cca	agc	tca	gcc	tca	cag	gcc	aaa	gca	tca	gca	cca	gaa	1349
Val	Glu	Val	Pro	Ser	Ser	Ala	Ser	Gln	Ala	Lys	Ala	Ser	Ala	Pro	Glu	
		410					415					420				
cgc	aca	ccc	agc	cca	gcc	cca	aag	aga	aag	aag	aga	cag	caa	aga	gcc	1397
Arg	Thr	Pro	Ser	Pro	Ala	Pro	Lys	Arg	Lys	Lys	Arg	Gln	Gln	Arg	Ala	
		425					430				435				440	
gca	gcc	ggg	gct	tgc	aca	ccg	cct	tgc	aca	tagcagaggc	tccgggctga					1447
Ala	Ala	Gly	Ala	Cys	Thr	Pro	Pro	Cys	Thr							
					445				450							
ctccttctctg	gtgggaaagg	aagatgcctg	tcctctccgt	ggaggaccct	gggccctcac											1507
cgcaggaagc	agtttgggtt	ttgaaagggtt	attgggtccc	ttccttgggc	tgtgttcttg											1567
ctggtgagca	aagtgttacc	tgcaaaaata	aaatgcagaa	cgtactctac	gacaaaaaaa											1627
aaaaaaaaaa																1637

<210> 71
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..1175

<220>
 <221> sig_peptide
 <222> 30..77
 <223> Von Heijne matrix
 score 3.71064775937629
 seq YAAAAGVLAGVES/RQ

<400> 71																
cta	atc	gaaa	agtaa	aggcg	cg	cg	ggaac	atg	ggg	ctg	tat	gct	gca	gct	gca	53
								Met	Gly	Leu	Tyr	Ala	Ala	Ala	Ala	
								-15							-10	
ggc	gtg	ttg	gcc	ggc	gtg	gag	agc	cgc	cag	ggc	tct	atc	aag	ggg	ttg	101
Gly	Val	Leu	Ala	Gly	Val	Glu	Ser	Arg	Gln	Gly	Ser	Ile	Lys	Gly	Leu	
			-5					1				5				
gtg	tac	tcc	agc	aac	ttc	cag	aac	gtg	aag	cag	ctg	tac	gcg	ctg	gtg	149
Val	Tyr	Ser	Ser	Asn	Phe	Gln	Asn	Val	Lys	Gln	Leu	Tyr	Ala	Leu	Val	
		10				15					20					
tgc	gaa	acg	cag	cgc	tac	tcc	gcc	gtg	ctg	gat	gct	gtg	atc	gcc	agc	197
Cys	Glu	Thr	Gln	Arg	Tyr	Ser	Ala	Val	Leu	Asp	Ala	Val	Ile	Ala	Ser	
					30					35					40	
gcc	ggc	ctc	ctc	cgt	gcg	gag	aag	aag	ctg	cgg	ccg	cac	ctg	gcc	aag	245
Ala	Gly	Leu	Leu	Arg	Ala	Glu	Lys	Lys	Leu	Arg	Pro	His	Leu	Ala	Lys	
					45				50						55	
gtg	cta	gtg	tat	gag	ttg	ttg	ttg	gga	aag	ggc	ttt	cga	ggg	ggg	ggg	293
Val	Leu	Val	Tyr	Glu	Leu	Leu	Leu	Gly	Lys	Gly	Phe	Arg	Gly	Gly	Gly	
			60					65					70			
ggc	cga	tgg	aag	gct	ctg	ttg	ggc	cgg	cac	cag	gcg	agg	ctc	aag	gct	341
Gly	Arg	Trp	Lys	Ala	Leu	Leu	Gly	Arg	His	Gln	Ala	Arg	Leu	Lys	Ala	
		75						80								
													85			

gag ttg gct cgg ctc aag gtt cat cgg ggt gtg agc cgg aat gag gac	389
Glu Leu Ala Arg Leu Lys Val His Arg Gly Val Ser Arg Asn Glu Asp	
90 95 100	
ctg ttg gaa gtg gga tcc agg cct ggt cca gcc tcc cag ctg cct cga	437
Leu Leu Glu Val Gly Ser Arg Pro Gly Pro Ala Ser Gln Leu Pro Arg	
105 110 115 120	
ttt gtg cgt gtg aac act ctc aag acc tgc tcc gat gat gta gtt gat	485
Phe Val Arg Val Asn Thr Leu Lys Thr Cys Ser Asp Asp Val Val Asp	
125 130 135	
tat ttc aag aga caa ggt ttc tcc tat cag ggt cgg gct tcc agc ctc	533
Tyr Phe Lys Arg Gln Gly Phe Ser Tyr Gln Gly Arg Ala Ser Ser Leu	
140 145 150	
gat gac tta cga gcc ctc aag ggg aag cat ttt ctc ctg gac ccc ttg	581
Asp Asp Leu Arg Ala Leu Lys Gly Lys His Phe Leu Leu Asp Pro Leu	
155 160 165	
atg ccg gag ctg ctg gtg ttt ccc gcc cag aca gat ctg cat gaa cac	629
Met Pro Glu Leu Leu Val Phe Pro Ala Gln Thr Asp Leu His Glu His	
170 175 180	
cca ctg tac cgg gcc gga cac ctc att ctg cag gac agg gcc agc tgt	677
Pro Leu Tyr Arg Ala Gly His Leu Ile Leu Gln Asp Arg Ala Ser Cys	
185 190 195 200	
ctc cca gcc atg ctg ctg gac ccc ccg cca ggc tcc cat gtc atc gat	725
Leu Pro Ala Met Leu Leu Asp Pro Pro Pro Gly Ser His Val Ile Asp	
205 210 215	
gcc tgt gcc gcc cca ggc aat aag acc agt cac ttg gct gct ctt ctg	773
Ala Cys Ala Ala Pro Gly Asn Lys Thr Ser His Leu Ala Ala Leu Leu	
220 225 230	
aag aac caa ggg aag atc ttt gcc ttt gac ctg gat gcc aag cgg ctg	821
Lys Asn Gln Gly Lys Ile Phe Ala Phe Asp Leu Asp Ala Lys Arg Leu	
235 240 245	
gca tcc atg gcc acg ctg ctg gcc cgg gct ggc gtc tct tgc tgt gaa	869
Ala Ser Met Ala Thr Leu Leu Ala Arg Ala Gly Val Ser Cys Cys Glu	
250 255 260	
ctg gct gag gag gac ttc ctg gcg gtc tcc ccc tcg gat cca cgc tac	917
Leu Ala Glu Glu Asp Phe Leu Ala Val Ser Pro Ser Asp Pro Arg Tyr	
265 270 275 280	
cat gag gtc cac tac atc ctg ctg gat cct tcc tgc agt ggc tcg ggt	965
His Glu Val His Tyr Ile Leu Leu Asp Pro Ser Cys Ser Gly Ser Gly	
285 290 295	
atg ccg agc aga cag ctg gag gag ccc ggg gca ggc aca cct agc ccg	1013
Met Pro Ser Arg Gln Leu Glu Glu Pro Gly Ala Gly Thr Pro Ser Pro	
300 305 310	
gtg cgt ctg cat gcc ctg gca gct tcc agc agc gag ccc tgt gcc acg	1061
Val Arg Leu His Ala Leu Ala Ala Ser Ser Ser Glu Pro Cys Ala Thr	
315 320 325	
cgc tca ctt tcc ctt ccc tgc agc ggc tcg tct act cca cgt gct ccc	1109
Arg Ser Leu Ser Leu Pro Cys Ser Gly Ser Ser Thr Pro Arg Ala Pro	
330 335 340	
tct gcc agg agg aga atg aag acg tgg tgc gag atg cgc tgc agc aga	1157
Ser Ala Arg Arg Arg Met Lys Thr Trp Cys Glu Met Arg Cys Ser Arg	
345 350 355 360	
acc cgg gcg cct tca ggc tagctccgc cctgctgccc tggccccacc	1205
Thr Arg Ala Pro Ser Gly	
365	

gaggcctgag	cacgttcccg	ggtgccgagc	actgcctccg	ggcctcccct	gagaccacac	1265
tcagcagtgg	cttcttcggt	gctgtaattg	aacgggtcga	ggtgccaaagc	tcagcctcac	1325
aggccaaagc	atcagcacca	gaacgcacac	ccagcccagc	cccaaagaga	aagaagagac	1385
agcaaagagc	cgcagccggt	gcttgccacac	cgccttgcac	atagcagagg	ctccgggctg	1445
actccttcct	ggtgggaaag	gaagatgcct	gtcctctccg	tggaggacc	tgggccctca	1505
ccgcaggaag	cagtttgggt	tttgaaaggt	tattgggtcc	cttccttggg	ctgtgttctt	1565
gctggtgagc	aaagtgttac	ctgcaaaaat	aaaatgcaga	acgtactcta	cgacaaaaaa	1625
aaaaaaaaaa	a					1636

```
<220>  
<221> CDS  
<222> 66..839
```

<400>	72																		
agaggaggtg	gcgg	tgg	tgg	ccctgc	cctg	tggcccccg	t	gctg	cttgca	ctcgaactcg									60
tcgcc	atg	gag	gag	ctc	cag	gag	cct	ctg	aga	gga	gag	ctc	cgg	ctc	tgc				110
	Met	Glu	Glu	Leu	Gln	Glu	Pro	Leu	Arg	Gly	Glu	Leu	Arg	Leu	Cys				
	-35						-30					-25							
ttc	acg	caa	gct	gcc	cgg	act	agc	ctc	tta	ctg	ctc	agg	ctc	aac	gac				158
Phe	Thr	Gln	Ala	Ala	Arg	Thr	Ser	Leu	Leu	Leu	Leu	Arg	Leu	Asn	Asp				
	-20						-15					-10							
gct	gcc	ctg	cgg	gcg	ctg	caa	gag	tgt	cag	cgg	caa	cag	gta	cgg	ccg				206
Ala	Ala	Leu	Arg	Ala	Leu	Gln	Glu	Cys	Gln	Arg	Gln	Gln	Val	Arg	Pro				
-5					1			5					10						
gtg	att	gct	ttc	caa	ggc	cac	cga	ggg	tat	ctg	aga	ctc	cca	ggc	cct				254
Val	Ile	Ala	Phe	Gln	Gly	His	Arg	Gly	Tyr	Leu	Arg	Leu	Pro	Gly	Pro				
			15				20					25							
ggt	tgg	tcc	tgc	ctc	ttc	tcc	ttc	ata	gtg	tcc	cag	tgt	tgt	cag	gag				302
Gly	Trp	Ser	Cys	Leu	Phe	Ser	Phe	Ile	Val	Ser	Gln	Cys	Cys	Gln	Glu				
			30				35				40								
ggc	gct	ggt	ggt	agc	ttg	gac	ctt	gtg	tgc	caa	cgc	ttc	ctc	agg	tct				350
Gly	Ala	Gly	Gly	Ser	Leu	Asp	Leu	Val	Cys	Gln	Arg	Phe	Leu	Arg	Ser				
	45						50				55								
ggg	cct	aac	agc	ctc	cac	tgc	ctg	ggc	tca	ctc	agg	gag	cgc	ctc	att				398
Gly	Pro	Asn	Ser	Leu	His	Cys	Leu	Gly	Ser	Leu	Arg	Glu	Arg	Leu	Ile				
60					65				70					75					
att	tgg	gca	gcc	atg	gat	tct	atc	cca	gcc	cca	tca	tca	gtt	cag	gga				446
Ile	Trp	Ala	Ala	Met	Asp	Ser	Ile	Pro	Ala	Pro	Ser	Ser	Val	Gln	Gly				
				80				85					90						
cac	aac	ctg	act	gaa	gat	gcc	aga	cat	cct	gag	agt	tgg	cag	aac	aca				494
His	Asn	Leu	Thr	Glu	Asp	Ala	Arg	His	Pro	Glu	Ser	Trp	Gln	Asn	Thr				
			95				100						105						

gga ggc tat tct gaa gga gat gca gta tca cag cca cag atg gca cta	542
Gly Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu	
110 115 120	
gag gag gtg tca gtg tca gat cca ctg gca agc aac caa gga cag tca	590
Glu Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser	
125 130 135	
ctc cca gga tcc tca agg gag cac atg gca cag tgg gaa gtg aga agc	638
Leu Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser	
140 145 150 155	
cag acc cat gtt cca aac aga gaa cct gtt cag gca ctg cct tcc tct	686
Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser	
160 165 170	
gcc agc cgg aaa cgt ctg gac aag aaa cgt tca gtg cct gta gcc act	734
Ala Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr	
175 180 185	
gta gaa ctg gaa gaa aag agg ttc aga act ctg cct tta gtg ccc ccc	782
Val Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Pro	
190 195 200	
cct aca agg cct gac caa tca gga ttt aca aga ggg aga aga ttg gga	830
Pro Thr Arg Pro Asp Gln Ser Gly Phe Thr Arg Gly Arg Arg Leu Gly	
205 210 215	
gca aga aga tgaggacatg gaccccagat tagaacacaa ttcctcagtt	879
Ala Arg Arg	
220	
caagaagatt ctgaatcccc aagtcctgaa gatataccag actacctcct gcaatacagg	939
gccatccaca gtgcagaaca gcaacatgcc tatgagcagg actttgagac agattatgct	999
gaataccgca tcctgcatgc ccgtgttggg actgcaagcc aaaggttcat agagctggga	1059
gcagagatta aaagagttcg gcgaggaact ccagaataca aggtcctgga agacaagata	1119
atccaggaat ataaaaagtt caggaagcag taccacagtt acagagaaga aaagcgtcgc	1179
tgtgagtacc ttcaccagaa attgtcccac attaaaggctc tcatcctgga gtttgaggaa	1239
aagaacaggg gcagctgaag ttatcaaggg aattttttgag cctctgctta gtgaaacaca	1299
aaggaacaaa gcagctataa actaaataga atgcaactat ctgcttttct tatgctgacc	1359
actggagtc atggtggcaa gtagagagct gctctaggtt cttgagggtt gggtttcatt	1419
attaattttt aggggtatggg cactgtgcaa agactccata gctgtgccta ggagtcctag	1479
aaaagtgaca gaggttggc ttttttacct ttagttcagc caagtcattt tcaagtcctg	1539
agaaatgaca tcatcttcag gataaaataa tgaggacatt agacaaacca aactaagtga	1599
attttagcct ggtagcctct ctaaggaaac agtaataata acttctgata agagttaaaa	1659
gaacttgtag catacctgga tataacggga aagggcctgg gtgttaccca tgtactgaaa	1719
atgaactttt accaacatgg ccaaaaaaaaa aaaaaaaaaa	1758

<210> 73

<211> 1647

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 64..903

<220>

<221> sig_peptide

<222> 64..162

<223> Von Heijne matrix

score 10.6748773272319

seq LLLLPFLPLLLLA/AP

<400> 73

agctcaaggg gcctcgagga ctctctgcgt ctctggagac aagggcacta cacgcacttc	60
aga atg aag agt tgc ggg agc atg ctg ggg ctc tgg ggg cag cgg ctc	108
Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu	
-30 -25 -20	
ccc gcg gcg tgg gtc ctg ctt ctg ttg cct ttc ctg ccg ctg ctg ctg	156
Pro Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu	
-15 -10 -5	
ctt gca gcc ccc gcg ccc cac cgc gcg tcc tac aag ccg gtc atc gtg	204
Leu Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val	
1 5 10	
gtg cat ggg ctc ttc gac agc tgc tac agc ttc cgc cac ctg ctg gaa	252
Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu	
15 20 25 30	
tac atc aat gag aca cac ccc ggg act gtg gtg aca gtg ctc gat ctc	300
Tyr Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu	
35 40 45	
ttc gat ggg aga gag agc ttg cga ccc ctg tgg gaa cag gtg caa ggg	348
Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly	
50 55 60	
ttc cga gag gct gtg gtc ccc atc atg gca aag gcc cct caa ggg gtg	396
Phe Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val	
65 70 75	
cat ctc atc tgc tac tgc cag ggg ggc ctt gtg tgc cgg gct ctg ctt	444
His Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu	
80 85 90	
tct gtc atg gat gat cac aac gtg gat tct ttc atc tcc ctc tcc tct	492
Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser	
95 100 105 110	
cca cag atg gga cag tat gga gac acg gac tac ttg aag tgg ctg ttc	540
Pro Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe	
115 120 125	
ccc acc tcc atg cgg tct aac ctc tat cgg atc tgc tat agc ccc ctg	588
Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro Leu	
130 135 140	
atc aat ggg gaa aga gac cat ccc aat gcc aca gta tgg cgg aag aac	636
Ile Asn Gly Glu Arg Asp His Pro Asn Ala Thr Val Trp Arg Lys Asn	
145 150 155	
ttt ctg cgt gtg ggc cac ctg gtg ctg att ggg ggc cct gat gat ggt	684
Phe Leu Arg Val Gly His Leu Val Leu Ile Gly Gly Pro Asp Asp Gly	
160 165 170	
gtt att act ccc tgg cag tcc agc ttc ttt ggt ttc tat gat gca aat	732
Val Ile Thr Pro Trp Gln Ser Ser Phe Phe Gly Phe Tyr Asp Ala Asn	
175 180 185 190	
gag acc gtc ctg gag atg gag gag caa ctg gtt tat ctg cgg gat tct	780
Glu Thr Val Leu Glu Met Glu Glu Gln Leu Val Tyr Leu Arg Asp Ser	
195 200 205	
ttt ggg ttg aag act cta ttg gcc cgg ggg gcc ata gtg agg tgt cca	828
Phe Gly Leu Lys Thr Leu Leu Ala Arg Gly Ala Ile Val Arg Cys Pro	
210 215 220	
atg gcc ggt atc tcc cac aca gcc tgg cac tcc aac cgt acc ctt tat	876
Met Ala Gly Ile Ser His Thr Ala Trp His Ser Asn Arg Thr Leu Tyr	

225	230	235	
gag acc tgc att gaa cct tgg ctc tcc tgaggatata ttcaggggtc			923
Glu Thr Cys Ile Glu Pro Trp Leu Ser			
240	245		
cccaggaact	cctcgggtcca	gagaccaagt	983
ggtgtgcctg	tgaccacctc	attgctccca	1043
ttttagtaga	gacttggcct	cccagaaccc	1103
ccaggcctcc	cctacctcat	gtcctctcat	1163
ctcaaggccg	aagttcggaa	gtgagaaacc	1223
tgctgctcct	ccgtatctgg	ctgtatgggt	1283
tctccttcca	ggccactcag	gacattttta	1343
tctaaagtcc	cctgacatca	gccctcccaa	1403
ggttctgaggc	tcccctatgg	ggacagttcc	1463
tgtggcctat	gaggcccatc	tcaggtttgg	1523
agtaccccc	tgggagagcc	tagtttcttt	1583
gaataggtgt	tatccctgta	tttatggaaa	1643
aaaa			1647

<210> 74
 <211> 1646
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 64..585

<220>
 <221> sig_peptide
 <222> 64..162
 <223> Von Heijne matrix
 score 10.6748773272319
 seq LLLLPFLPLLLA/AP

<400> 74	
agctcaaggg gcctcgagga ctctctgcgt ctctggagac aagggcacta cacgcacttc	60
aga atg aag agt tgc ggg agc atg ctg ggg ctc tgg ggg cag cgg ctc	108
Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu	
-30 -25 -20	
ccc gcg gcg tgg gtc ctg ctt ctg ttg cct ttc ctg ccg ctg ctg ctg	156
Pro Ala Ala Trp Val Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu	
-15 -10 -5	
ctt gca gcc ccc gcg ccc cac cgc gcg tcc tac aag ccg gtc atc gtg	204
Leu Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val	
1 5 10	
gtg cat ggg ctc ttc gac agc tgc tac agc ttc cgc cac ctg ctg gaa	252
Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu	
15 20 25 30	
tac atc aat gag aca cac ccc ggg act gtg gtg aca gtg ctc gat ctc	300
Tyr Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu	
35 40 45	
ttc gat ggg aga gag agc ttg cga ccc ctg tgg gaa cag gtg caa ggg	348
Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly	
50 55 60	

ttc cga gag gct gtg gtc ccc atc atg gca aag gcc cct caa ggg gtg	396
Phe Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val	
65 70 75	
cat ctc atc tgc tac tcg cag ggg ggc ctt gtg tgc cgg gct ctg ctt	444
His Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu	
80 85 90	
tct gtc atg gat gat cac aac gtg gat tct ttc atc tcc ctc tcc tct	492
Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser	
95 100 105 110	
cca cag atg gga cag tat gga gac acg gac tac ttg aag tgg ctg ttc	540
Pro Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe	
115 120 125	
ccc acc tcc atg cgg tct aac ctc tat cgg atc tgc tat agc ccc	585
Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro	
130 135 140	
tgatcaatgg ggaaagagac catcccaatg ccacagtatg gcggaagaac tttctgctgtg	645
tgggccacct ggtgctgatt gggggccctg atgatggtgt tattactccc tggcagtcca	705
gcttcttttg tttctatgat gcaaatgaga ccgtcctgga gatggaggag caactggttt	765
atctgcggga ttcttttggg ttgaagactc tattggcccg gggggccata gtgaggtgtc	825
caatggccgg tatctccac acagcctggc actccaaccg taccctttat gagacctgca	885
ttgaaccttg gctctcctga ggatatattc aggggtcccc aggaactcct cggtcagag	945
accaagtggg ggccttgaa agcagatgtc aggccttgggt gtgcctgtga ccacctcatt	1005
gctcccatat tatcccccat ttttagtaga gacggggttt tagtagagac ttggcctccc	1065
agaacccccct tcctctgctc ctccatgaat gacaattcca ggccctccct acctcatgtc	1125
ctctcatttg ggggattgct ccgtgctgtc cctttctctc aaggccgaag ttcggaagtg	1185
agaaaccatg tttttaactt gtggctgctc ttgctgctgc tgctcctccg tatctggctg	1245
tatgggtgga gaaccaccc actgcccacc acaggggtct ccttcaggc cactcaggac	1305
atttttagct tctctcctcc ccatgttccc ttttttctct aaagtcccct gacatcagcc	1365
ctcccaactc ctaagaggga ctacctatga gagtgggggt ctgaggctcc cctatgggga	1425
cagttccgtt cttgaagtgt cagtgttggg gaatatctgt ggcctatgag gcccatctca	1485
ggtttgggga tccccagtc cctatgatca gtgttggagt acccccctgg gagagcctag	1545
tttctttgag gccccaggcc ctcttttaac tacctttgaa taggtgttat ccctgtattt	1605
atggaaataa agttccattt cctcaaaaaa aaaaaaaaaa a	1646

<210> 75
 <211> 1963
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 274..753

<220>
 <221> sig_peptide
 <222> 274..324
 <223> Von Heijne matrix
 score 4.4969823290892
 seq FAAFCYMLSLVLC/AA

<400> 75	
cttcttcgat ttgcggacgg ttccctccag cgactctcga cacacgtttt cctgtcttcg	60
ccggagggcc ggggtctgggg tcgccggagc ctgcgggaat ccagcgctta ttcgctaacc	120
ctcgagtcgc ttcgctagct gtgcgccctc ctgggcacta gcctggagag gagcgtgcag	180

acgcggtctcc ttggagggag tgcggtcctc tagggaggca tcgggctcct aggggcttct 240
 tggcgtgtgt ggtgggattg ggggtccgccg gcc atg gcc ttc act ttc gct gcg 294
 Met Ala Phe Thr Phe Ala Ala
 -15
 ttc tgc tac atg ctg tct ctg gtg ctg tgc gct gcg ctc atc ttc ttc 342
 Phe Cys Tyr Met Leu Ser Leu Val Leu Cys Ala Ala Leu Ile Phe Phe
 -10 -5 1 5
 gcc atc tgg cac ata att gcc ttt gat gag tta agg aca gat ttt aag 390
 Ala Ile Trp His Ile Ile Ala Phe Asp Glu Leu Arg Thr Asp Phe Lys
 10 15 20
 agc ccc ata gac cag tgc aat cct gtt cat gcg agg gaa cgg ttg agg 438
 Ser Pro Ile Asp Gln Cys Asn Pro Val His Ala Arg Glu Arg Leu Arg
 25 30 35
 aac atc gag cgc atc tgc ttc ctt ctg cga aag ctg gtg ctg cca gaa 486
 Asn Ile Glu Arg Ile Cys Phe Leu Leu Arg Lys Leu Val Leu Pro Glu
 40 45 50
 tac tcc atc cat agc ctc ttc tgc att atg ttc ctg tgt gcg caa gag 534
 Tyr Ser Ile His Ser Leu Phe Cys Ile Met Phe Leu Cys Ala Gln Glu
 55 60 65 70
 tgg ctc acg ctg ggg ctg aat gtc cct cta ctt ttc tat cac ttc tgg 582
 Trp Leu Thr Leu Gly Leu Asn Val Pro Leu Leu Phe Tyr His Phe Trp
 75 80 85
 agg tat ttc cac tgt cca gca gat agc tca gaa cta gcc tac gac cca 630
 Arg Tyr Phe His Cys Pro Ala Asp Ser Ser Glu Leu Ala Tyr Asp Pro
 90 95 100
 ccg gtg gtc atg aat ccc gac act ttg agt tac tgt cag aag gag gcc 678
 Pro Val Val Met Asn Pro Asp Thr Leu Ser Tyr Cys Gln Lys Glu Ala
 105 110 115
 tgg tgt aag ctg gcc ttc tat ctc ctc tcc ttc ttc tac tac ctt tac 726
 Trp Cys Lys Leu Ala Phe Tyr Leu Leu Ser Phe Phe Tyr Tyr Leu Tyr
 120 125 130
 tgc atg atc tac act tta gtg agc tct taacgcaaag accatgcaca 773
 Cys Met Ile Tyr Thr Leu Val Ser Ser
 135 140
 tcatcagaga ctgagatggg agaggcctga gacggagagg tgcatttctg ctggtgactg 833
 gaggagggac cagaatgagg atacgtgaga aatagacccg gcaggcagtc agactgaatg 893
 ggagctggaa tcacgcagca gttgggagcc gagttaaccc tgcgtgtctg tgtcacccctg 953
 tttgtcaatc tttggcattc gaattccaca cacgggggtcc tagagccctt ctgagcatca 1013
 gtggtgtggg ggagtaggtg acgaaacact agacctctcc tgagagagaa ttgctgcttc 1073
 ctgaatccac ttcattgaac agcaccttgc aagttcaaat gagttcctgg gagcggaggc 1133
 tggaaggcca caaggtgctt gctaaggaac agaagaccc agagtcaagg ccaagtctgc 1193
 agggacctgt tgaaagcctc gagaatgtct tggctgcccc agactcttgt tgcctttctt 1253
 ccaagccatg gccatgccct ttttctcaaa tgggaggggc tggaggggtgt gtgggatttg 1313
 tcttcagctg caaccagcct tgagcctgct gggctathtt cagctgagga ggggtaatat 1373
 aggaaaaatg catttttgaa acgtttgcaa catgatcaag gtgttagttc tccaccacac 1433
 aagttgtatt cttcttttgc cacctcaaac catcacagag tcttttaaat caaatcaatt 1493
 ggtcaatgct agtcaaagct atgttcttac aaaaacccca gacagctcag agctcagaaa 1553
 atcctgtgga gtggctgctc tgtaccgtgg gcatccggca gccaggaagt gagacaacat 1613
 aattataact ttgttttatg atgctgcac atttgtactg tttaggtcga cgtgaggaca 1673
 tcatcttatt tagaattttc cgtttggcat tctcttttgg gtgggagtta tgctgggggt 1733
 tgtaataaat gacaaggctg agatttttat gatgtttaaa ttgggcacaa tgattttgac 1793
 cttattcccc aaacttcttt tcttttctac tgtttaacat acacaggcta tttatacacg 1853
 tccccagctc ccatctgaaa cctgtgactc aggtttatga atggtgtttg tgtagcaaca 1913
 cattgtgtgc tatgtttatt aaaatgcagc gacaaaaaaa aaaaaaaaaa 1963

<210> 76
 <211> 1757
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 191..1468

<220>
 <221> sig_peptide
 <222> 191..274
 <223> Von Heijne matrix
 score 4.02941490119842
 seq GXLLEPFVHQVGG/HS

<400> 76
 catttttggtg cgagagaaac aataggacgg aaacgccgag gaacccggct gaggcggcag 60
 cagagcatcc tggccagaac aagccaagga gccaaagacga gagggacaca ctgacaaaca 120
 acagacagaa gacgtactgg ccgctggact ccgctgcctc ccccatctcc ccgccatctg 180
 cgcccgagg atg agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc 229
 Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg
 -25 -20
 gcc aaa ggc gtc ctt ctg gag ccc ttt gtc cac cag gtc ggg ggg cac 277
 Ala Lys Gly Val Leu Glu Pro Phe Val His Gln Val Gly Gly His
 -15 -10 -5 1
 tca tgc gtg ctc cgc ttc aat gag aca acc ctg tgc aag ccc ctg gtc 325
 Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val
 5 10 15
 cca agg gaa cat cag ttc tac gag acc ctc cct tct gag atg cgc aaa 373
 Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys
 20 25 30
 ttc act ccc cag tac aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat 421
 Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp
 35 40 45
 gaa gac agg aac ttg tgt cta ata gca tat cca ttg aaa ggg gac cat 469
 Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His
 50 55 60 65
 gga att gtg gac att gta gat aat tca gac tgt gaa cca aaa agt aag 517
 Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys
 70 75 80
 ctc cta agg tgg aca aca aac aaa aaa cat cat gtc tta gaa aca gaa 565
 Leu Leu Arg Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu
 85 90 95
 aag acc cct aag gac tgg gtg cgt cag cac cgt aaa gag gag aaa atg 613
 Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met
 100 105 110
 aag agc cat aag tta gaa gaa gaa ttt gag tgg cta aag aaa tct gaa 661
 Lys Ser His Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu
 115 120 125
 gtc ttg tac tac act gta gag aag aag ggg aat ata agt tcc cag ctt 709
 Val Leu Tyr Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu
 130 135 140 145

aaa cac tat aac cct tgg agc atg aaa tgt cac cag caa cag tta cag	757
Lys His Tyr Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln	
150 155 160	
aga atg aag gag aat gca aag cat cgg aac cag tac aaa ttt atc tta	805
Arg Met Lys Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu	
165 170 175	
ctg gaa aac ctg act tcc cgc tat gag gtg cct tgt gtc ctt gac ctc	853
Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu	
180 185 190	
aag atg ggc aca cga caa cat ggt gat gat gct tca gag gag aag gca	901
Lys Met Gly Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala	
195 200 205	
gcc aac cag atc cga aaa tgt cag cag agc aca tct gca gtc att ggt	949
Ala Asn Gln Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly	
210 215 220 225	
gtg cgt gtg tgt ggc atg cag gtg tac caa gca ggc agt ggg cag ctc	997
Val Arg Val Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu	
230 235 240	
atg ttc atg aac aag tac cat gga cgg aag cta tcg gtg cag ggc ttc	1045
Met Phe Met Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe	
245 250 255	
aag gag gca ctt ttc cag ttc ttc cac aat ggg cgg tac ctg cgc cgt	1093
Lys Glu Ala Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg	
260 265 270	
gaa ctc ctg ggc cct gtg ctc aag aag ctg act gag ctc aag gca gtg	1141
Glu Leu Leu Gly Pro Val Lys Lys Leu Thr Glu Leu Lys Ala Val	
275 280 285	
ttg gag cga cag gag tcc tac cgc ttc tac tca agc tcc ctg ctg gtc	1189
Leu Glu Arg Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val	
290 295 300 305	
att tat gat ggc aag gag cgg ccc gaa gtg gtc ctg gac tca gat gct	1237
Ile Tyr Asp Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala	
310 315 320	
gag gat ttg gag gac ctg tca gag gaa tca gct gat gag tct gct ggt	1285
Glu Asp Leu Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly	
325 330 335	
gcc tat gcc tac aaa ccc atc ggc gcc agc tct gta gat gtg cgc atg	1333
Ala Tyr Ala Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met	
340 345 350	
atc gac ttt gca cac acc acc tgc agg ctg tat ggc gag gac acc gtg	1381
Ile Asp Phe Ala His Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val	
355 360 365	
gtg cat gag ggc cag gat gct ggc tat atc ttc ggg ctc cag agc ctg	1429
Val His Glu Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu	
370 375 380 385	
ata gac att gtc aca gag ata agt gag gag agt ggg gag tgagcttgct	1478
Ile Asp Ile Val Thr Glu Ile Ser Glu Glu Ser Gly Glu	
390 395	
agctgctcca gtacttgaga gcgactctgt gtcccaggca cagctgtgct gcgtcagggg	1538
ggaagccagt atggccagggt ggtggctcct gcagcctgga gctgatgtgc agtggcctct	1598
gtgagcccca gcctgagcca gtcccagctg tgcttgaggat ctttatttat tttaactatt	1658
tcttcaacat tccacatttg atgatgatac ctctttcttc cctgagtgta tatgttctaa	1718
tacaaatctt tttgtttatt gtaaaaaaaaa aaaaaaaaaa	1757

<210> 77
 <211> 2027
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 48..950

<220>
 <221> sig_peptide
 <222> 48..107
 <223> Von Heijne matrix
 score 6.64507667657896
 seq LLPLLSLLVGAWL/KL

<400> 77
 atg cgc cag cg ggg ccg tggg tgt acg cggc gcag cgc ggc agt cctg atg gcc cgg 56
 Met Ala Arg
 -20
 cat ggg tta ccg ctg ctg ccc ctg ctg tcg ctc ctg gtc ggc gcg tgg 104
 His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val Gly Ala Trp
 -15 -10 -5
 ctc aag cta gga aat gga cag gct act agc atg gtc caa ctg cag ggt 152
 Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln Leu Gln Gly
 1 5 10 15
 ggg aga ttc ctg atg gga aca aat tct cca gac agc aga gat ggt gaa 200
 Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg Asp Gly Glu
 20 25 30
 ggg cct gtg cgg gag gcg aca gtg aaa ccc ttt gcc atc gac ata ttt 248
 Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile Asp Ile Phe
 35 40 45
 cct gtc acc aac aaa gat ttc agg gat ttt gtc agg gag aaa aag tat 296
 Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu Lys Lys Tyr
 50 55 60
 cgg aca gaa gct gag atg ttt gga ttg agc ttt gtc ttt gag gac ttt 344
 Arg Thr Glu Ala Glu Met Phe Gly Leu Ser Phe Val Phe Glu Asp Phe
 65 70 75
 gtc tct gat gag ctg aga aac aaa gcc acc cag cca atg aag tct gta 392
 Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met Lys Ser Val
 80 85 90 95
 ctc tgg tgg ctt cca gtg gaa aag gca ttt tgg agg cag cct gca ggt 440
 Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln Pro Ala Gly
 100 105 110
 cct ggc tct ggc atc cga gag aga ctg gag cac cca gtg tta cac gtg 488
 Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val Leu His Val
 115 120 125
 agc tgg aat gac gcc cgt gcc tac tgt gct tgg cgg gga aaa cga ctg 536
 Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly Lys Arg Leu
 130 135 140
 ccc acg gag gaa gag tgg gag ttt gcc gcc cga ggg ggc ttg aag ggt 584
 Pro Thr Glu Glu Glu Trp Glu Phe Ala Ala Arg Gly Gly Leu Lys Gly
 145 150 155
 caa gtt tac cca tgg ggg aac tgg ttc cag cca aac cgc acc aac ctg 632

Gln Val Tyr Pro Trp Gly Asn Trp Phe Gln Pro Asn Arg Thr Asn Leu	
160 165 170 175	
tgg cag gga aag ttc ccc aag gga gac aaa gct gag gat ggc ttc cat	680
Trp Gln Gly Lys Phe Pro Lys Gly Asp Lys Ala Glu Asp Gly Phe His	
180 185 190	
gga gtc tcc cca gtg aat gct ttc ccc gcc cag aac aac tac ggg ctc	728
Gly Val Ser Pro Val Asn Ala Phe Pro Ala Gln Asn Asn Tyr Gly Leu	
195 200 205	
tat gac ctc ctg ggg aac gtg tgg gag tgg aca gca tca ccg tac cag	776
Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser Pro Tyr Gln	
210 215 220	
gct gct gag cag gac atg cgc gtc ctc cgg ggg gca tcc tgg atc gac	824
Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly Ala Ser Trp Ile Asp	
225 230 235	
aca gct gat ggc tct gcc aat cac cgg gcc cgg gtc acc acc agg atg	872
Thr Ala Asp Gly Ser Ala Asn His Arg Ala Arg Val Thr Thr Arg Met	
240 245 250 255	
ggc aac act cca gat tca gcc tca gac aac ctc ggt ttc cgc tgt gct	920
Gly Asn Thr Pro Asp Ser Ala Ser Asp Asn Leu Gly Phe Arg Cys Ala	
260 265 270	
gca gac gca ggc cgg ccg cca ggg gag ctg taagcagccg ggtggtgaca	970
Ala Asp Ala Gly Arg Pro Pro Gly Glu Leu	
275 280	
aggagaaaag ccttctaggg tcaactgtcat tccctggcca tgttgcaaac agcgcaattc	1030
caagctcgag agcttcagcc tcaggaaaga acttcccctt cctgtctctc catccctctg	1090
tggcaggcgc ctctcaccag ggcaggagag gactcagcct cctgtgtttt ggagaagggg	1150
cccaatgtgt gttgacgatg gctggggggc aggtgtttct gttagaggcc aagtattatt	1210
gacacaggat tgcaaacaca caaacaattg gaacagagca ctctgaaagg ccatttttta	1270
agcattttta aatctattct ctcccccttt ctccctggat gattcaggaa gctgacattg	1330
tttcctcaag gcagaatttt cctgggttctg ttttctcagc cagttgctgt ggaaggagaa	1390
tgttttcttt gtggcctcat ctgtgggtttc gtgtccctct gaaggaaact agtttccact	1450
gtgtaacagg cagacatgta actattttaa gcacagttca gtcctaaaag ggtctgggag	1510
aaccagatga tgtactaggt gaagcattgc attgtgggaa tcacaaagca aatagtactc	1570
cagaaagaca aatatcagaa gcttcctatt cttttttttt tttttttttt tttggagaca	1630
gggtctttct ctgttgccca ggctagagtg cactgggtgat cacggctcac tctagccttg	1690
aattcctggg cccaagcaat tctcccacct cagcctcctg agtagctggg actacaagtg	1750
tgcaccacca tgcctggcta attttttgaa tttttgtagt gatgggatct cgctctgttg	1810
cccagggttg tctcgaaact ctggcctcaa gcgatcctcc cacctcgacc tcccaaagtg	1870
ctgggattac aggtgtgagc cacctcgctt gggccccctt ctccatattg ctccaaaaac	1930
atgtccctgg agagtagcct gctcccacac tgtcactgga tgtcatgggg ccaataaaat	1990
ctcctgcaat tgtgtatctc aaaaaaaaaa aaaaaaa	2027

<210> 78
 <211> 1880
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 156..512

<220>
 <221> sig_peptide
 <222> 156..206

<223> Von Heijne matrix
 score 3.55618791452243
 seq WLTAVASLLPSPG/NS

<400> 78

atatacaggt ggcagctctc gtcccttgag agcgggcgaa ggccagggtc ccacactcgc	60
agcgctgcga cggcgctcgg gacctccctc gtccactgct tgagttccag aggtgggtgc	120
ttccctgtcc tgaacttcag agtgcgagat cataa atg ggt tcc ggc tgg ctt	173
Met Gly Ser Gly Trp Leu	
-15	
act gca gta gcc tcg ctc ctc ccc agc ccc ggt aac tcc gag cta ccc	221
Thr Ala Val Ala Ser Leu Leu Pro Ser Pro Gly Asn Ser Glu Leu Pro	
-10 -5 1 5	
gtc cag gcc ctc ggg cgt cgc ggg ggc agg gac tgg gcg cgg aac gag	269
Val Gln Ala Leu Gly Arg Arg Gly Gly Arg Asp Trp Ala Arg Asn Glu	
10 15 20	
gca ggg agg gac ctg gaa aaa cca ccc aga ttg cat tgc agt ggg cga	317
Ala Gly Arg Asp Leu Glu Lys Pro Pro Arg Leu His Cys Ser Gly Arg	
25 30 35	
ggc cgc ctg gag gag ccg gtt ccc cct aac cac ctc ccc gtg ggg ctc	365
Gly Arg Leu Glu Glu Pro Val Pro Pro Asn His Leu Pro Val Gly Leu	
40 45 50	
tcg gtg cgc ggt tcc cag gtg ctc agc tct gct ggg ccc agg agg tgc	413
Ser Val Arg Gly Ser Gln Val Leu Ser Ser Ala Gly Pro Arg Arg Cys	
55 60 65	
cgc ctc aca ggg acg cgg aac ccc gtg cgt ggc ccc cgc cgg gtg gaa	461
Arg Leu Thr Gly Thr Arg Asn Pro Val Arg Gly Pro Arg Arg Val Glu	
70 75 80 85	
cag ata gcg cgg ggc ggt ccg gag gct cgt cgc caa gca ggt gac tct	509
Gln Ile Ala Arg Gly Gly Pro Glu Ala Arg Arg Gln Ala Gly Asp Ser	
90 95 100	
tgc tgaaaaagtg gttggaacac ttaaggaaac ccggccccgc ctgttctttc	562
Cys	
taggtctttg gagtttggat taatcatttg tgtagcccgt ttggataaac cgaagacttt	622
attaaatcag cgcgtttaac aggaattccg cagtagtatc cacattagaa tcttgagtct	682
tggagttgaa catattcaca cagacttgcc ttcttcctgt ttagtttatg ccttggtgtc	742
cgttattgga acgctaagct tgtgggagtt gtttacatcc tactgctcaa ggtcatcgct	802
aagggtgat ttttcacaaa aagaatttgc aacctccggc atgaatgact taagggaagt	862
ctaatacccg tttctgattt tttttttttt ttaatttaaa agttaatctt tctgggccgg	922
gcgcggtggc tcacgcctgt aatcccagca ctttgggagg ccgaggcgga tcacgaggtc	982
aggagttcga gaccagcctg accaactatg tgaaaccccg tctctactaa aaacacaaaa	1042
attagccggg cggggtggcg cgcacctgta atcccagctg ctcgggaggc tgaggcagga	1102
gaatcgcttg aacctgggag gcgggggggt gcagtgagcc gagatctggc cattgcactc	1162
cagcgtgggc aacagagtga gactccatct caaaaaaaaaa ggttaatctt tccaactaga	1222
ttttcaagga tgaggatttt gttgttgttg ttgttgttgt tctcaaagt attcccaggg	1282
cttggaacag agcctgacat atactaggca ctcaacaaat atttgttgaa tgattgtaat	1342
gagtaacacc catttttgca gatctttgtc ttctgagcct agggcatagg tcatcactgc	1402
aggggtgaga ttgtcaaaat gggagtctac aggttaattta agacttaaat gtttaaagag	1462
tatgtgctca ttcttcaaca aacttacttt tgttaaatta aaatggtaaa atgtgggtgga	1522
gggggttgaa tatatgtaat tcaagacagt tctgaataca aaaatgtttt actgtctatc	1582
accaccatct ataaatctaa ttcactaagg ataactctgt taagggtggc ggaaagaacc	1642
ttgaggagag aggcattatt aagtattggc tcaggaccac acctaaaatt ctcaaaacgt	1702
tgagattctg ttgttttgtt ttttaagcgc agagacccaa gttgaggaac agcctataaa	1762
ataactggcc tgtactctta catacatgaa agccatcaaa gacaaagact gaagaagaac	1822

ttttgcagat taaaggactt taagagacat gatcctgaac caaaaaaaaa aaaaaaaa 1880

<210> 79
<211> 584
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 67..351

<220>
<221> sig_peptide
<222> 67..183
<223> Von Heijne matrix
score 10.6473524146908
seq FLCALCSFCPISA/AS

<400> 79
ctgattcttc gaaatgatat aagtcctgag ggcttcagtc ccattcgcg c actcatactt 60
gcaatc atg gac tac agc cgt gtc ttt cag ggt gtg ttc ttc acc ttc 108
Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe
-35 -30
aag cat gct ttt gct gat ggt gct tgg gat ctt tca ttt ctc tgt gct 156
Lys His Ala Phe Ala Asp Gly Ala Trp Asp Leu Ser Phe Leu Cys Ala
-25 -20 -15 -10
ctt tgc agt ttc tgc cca atc tca gct gcc tct ggc aga cct tac agg 204
Leu Cys Ser Phe Cys Pro Ile Ser Ala Ala Ser Gly Arg Pro Tyr Arg
-5 1 5
tac ttg gaa ttc tgg aga tta tac ctg tct cct agt tcc atg gaa aat 252
Tyr Leu Glu Phe Trp Arg Leu Tyr Leu Ser Pro Ser Ser Met Glu Asn
10 15 20
gga gtt caa aaa ttc cac gaa act ttt ttc att gtc ttt ttg ctt ttg 300
Gly Val Gln Lys Phe His Glu Thr Phe Phe Ile Val Phe Leu Leu Leu
25 30 35
ttt gat atc gag agg aaa gga aaa agt tct gtt tgt cca ttt tgt tac 348
Phe Asp Ile Glu Arg Lys Gly Lys Ser Ser Val Cys Pro Phe Cys Tyr
40 45 50 55
aga taaggaaagt ggtttcacia aggttaagca acttggttcag tgttaccag 401
Arg
caaagagcag aatgattttc aacatttcagt ttaaaagtcg gcgggggggca gtgggtcaca 461
cctgtaatat cagcaacttg ggaggccaag gtggtacggt cgcttgaagc caaggagttc 521
aagaccagcc tgggtcaacat agcaaaacct tgtctttaca aaaagtaaaa aaaaaaaaaa 581
aaa 584

<210> 80
<211> 1351
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 259..831

<220>
 <221> sig_peptide
 <222> 259..375
 <223> Von Heijne matrix
 score 5.809301698725
 seq FCVCVIAIGVVQA/LI

<400> 80
 aagctcccgg ccgggctgac tcaagcggag gcgcgcggaa cagtcgccga ggcgattccc 60
 gcccagcagt tcgacagaag tgtacagagg cttctggcaa cacggattgc cgtctacctg 120
 atgacctttc tcatcgtgac agtggcctgg gcagcacaca caaggttggtt ccaagttggt 180
 gggaaaacag acgacacact tgccctgctc aacctggccg catcatggct gtgatgcctt 240
 ccctccctcc aggcctgc atg atg acc atc acc ttc ctg cct tac acg ttt 291
 Met Met Thr Ile Thr Phe Leu Pro Tyr Thr Phe
 -35 -30
 tcg tta atg gtg acc ttc cct gat gtg cct ctg ggc atc ttc ttg ttc 339
 Ser Leu Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe Leu Phe
 -25 -20 -15
 tgt gtg tgt gtg atc gcc atc ggg gtc gtg cag gca ctg att gtg ggg 387
 Cys Val Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile Val Gly
 -10 -5 1
 tac gca ttc cac ttc ccg cac ctg ctg agc ccg cag atc cag cgc tct 435
 Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln Arg Ser
 5 10 15 20
 gcc cac agg gct ctg tac cga cga cac gtc ctg ggc atc gtc ctc caa 483
 Ala His Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln
 25 30 35
 ggc ccg gcc ctg tgc ttt gca gcg gcc atc ttc tct ctc ttc ttt gtc 531
 Gly Pro Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val
 40 45 50
 ccc ttg tct tac ctg ctg atg gtg act gtc atc ctc ctc ccc tat gtc 579
 Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val
 55 60 65
 agc aag gtc acc ggc tgg tgc aga gac agg ctc ctg ggc cac agg gag 627
 Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu
 70 75 80
 ccc tcg gct cac cca gtg gaa gtc ttc tcg ttt gac ctc cac gag cca 675
 Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro
 85 90 95 100
 ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac gcc atc 723
 Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile
 105 110 115
 gtg gcc acg ctt ctc atc ctg gac atc tgc ccc tcc tgc tcc ctt tgg 771
 Val Ala Thr Leu Leu Ile Leu Asp Ile Cys Pro Ser Cys Ser Leu Trp
 120 125 130
 ctg gct gtt gct tcc ttc cag cgt ctg ctc ctc cgc ggc ctc atc tgc 819
 Leu Ala Val Ala Ser Phe Gln Arg Leu Leu Leu Arg Gly Leu Ile Cys
 135 140 145
 ctc ttc gtc tgt tagagcgcgc gtctcgtctc agtcgtcacg tttttggttt 871
 Leu Phe Val Cys
 150
 ttgtgggggtt tttttttttt tttttttttg agacagtcct gctgtgtcgc ccaggctgga 931
 gtatagtggc tcaagctcag ctcaactgcaa cctccgcctc ccaggttcaa gcaattctcc 991
 tgcctcagcc tcccaagtag ttgggattac aagcaccac caccatgccc agctaacttt 1051

```

ttgcattttt aatagagatg aggtttcacc aagtggcca ggctggtctt gaactcctga 1111
cctcaggtga tctgcccacc tcggcctccc aaagtgctgg gattacaggt gtaagccacc 1171
gtgcccggcc atcgtaatgt ttgaatttgc ttttttacat cttccatcct tttggagtgt 1231
cttgttccct cgtcatagtt cagcactgtg accaccttgg ggtagacac tatggtttta 1291
tatcctgtac ttgatattct cgagtccaag tctcctgatg ctctcaaaaa aaaaaaaaaa 1351

```

```

<210> 81
<211> 720
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 111..377

```

```

<220>
<221> sig_peptide
<222> 111..233
<223> Von Heijne matrix
      score 5.26415334394122
      seq LWFLAQIPSRVAG/SL

```

```

<400> 81
aaaccgaaac cagcgctcca aacaattggg acccgggatc ttatgccagt gaggtgtgac 60
tgcggctgag cgggcctccc atccctctta aaagagttag gcatttagcc atg cct 116
                                     Met Pro
                                     -40
ccc acc cgg gac cct ttc cag cag cct aca tta gat aac gat gat tcc 164
Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp Asp Ser
          -35          -30          -25
tac tta gga gaa ctg cgg gct tcc aag gta ctg tgg ttt ctt gcg cag 212
Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu Ala Gln
          -20          -15          -10
att ccc agt agg gtc gcc ggt agt ctt ctt tct gtc tgt gtg atg agc 260
Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val Met Ser
          -5          1          5
aga gat ggt aac ata aag gac tct ggt gaa gac act cag tcg ggt acc 308
Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser Gly Thr
10          15          20          25
agg gaa gtc tgt ttt ctg cct gcc tcc cta tct cca tat tca agt cgg 356
Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser Ser Arg
          30          35          40
cta acg ttt cag agg cgt ttt tgagcagagg aaagtagagt tctagtctag 407
Leu Thr Phe Gln Arg Arg Phe
          45
aggaacaagg ggctctggca gctcaaatac attaaccaag atccaattcc ctggagaatt 467
tttaaccctt cccactccac ccatcacttg cctggctaac atcagacact ggatcaacct 527
taaaaaggag tccatccaca gcatccaagg atccatagtg tcccctcaca ctgcagccac 587
caatggaggc tactcccgaa agaaagatgg tggcttcttc tccacctagt gttgacagat 647
ccctgaacta attatagtga aacatactgc ggcccacttc cattaaatag atttgtgcaa 707
aaaaaaaaaa aaa 720

```

```

<210> 82
<211> 1029

```

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 223..432

<220>
<221> sig_peptide
<222> 223..336
<223> Von Heijne matrix
score 4.17665217008018
seq LVNVLFFFTPLMT/LV

<400> 82
gttttttgtat tggaagcagt tgtttggcct tgctgagcaa acgtctatgc cttctccatt 60
acatccaaag gagaatagcc ccatgtgaag aatggaatca gtagatgttt ggctcgtgta 120
ccatatccac tcctaggata caacaagagc aagcccaatt ctcttggtgg tgtgggcagt 180
cggcttgcac cacgtaccta tctcagctct ttttggaagc tt atg tcc tcc cca 234
Met Ser Ser Pro
-35
caa ctt cca gct ttc tta tgg gac aag ggt aca ctc acc act gcc ata 282
Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu Thr Thr Ala Ile
-30 -25 -20
tct aat cct gct tgc ctg gta aat gtt ctc ttc ttc ttt aca ccc ctg 330
Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe Phe Thr Pro Leu
-15 -10 -5
atg act ctg gtc act cta ctc atc ctg gtc tgg aaa gta acc aaa gac 378
Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys Val Thr Lys Asp
1 5 10
aaa agc aac aag aac aga gag aca cac cca aga aag gag gca aca tgg 426
Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys Glu Ala Thr Trp
15 20 25 30
ctg cca taaagatctg gatctcttgg tggggactcc actgaggtga agacctgatt 482
Leu Pro
gtacaagaga ggcacggcca ctggagctgt ctcagagccc agagccaggg gagccagagc 542
tgcttttagcc accctgttcc tccattgcca gatgtccccc caggcctcat ttccttcctc 602
tgccaccatc cctcttataa tgcactcctc ctgcggttct ttggcttgtc ccagcttctg 662
agtttgaatg tctttttttt tttttttttt tttttgkga tcttcaagac tgaaatagta 722
aatggctctt gatttctgca ctaacagagg aaagaaacaa gtacatggaa aagtaaaaat 782
tgattacaaa gcctaaattt tcctctataa attgggcatg tgctgactgt gggatattga 842
aattattggg agctcacagc atctcaagtt atataatgaa gctattctgg aagctcattt 902
ccagaagatc cttaaaatga aatggctcac tctctgctga attaatgttg agcaagttaa 962
ctcctttttc aaatgaaatc caaattaaag aggcagtttt ttttgaaaaa ccaaaaaaaa 1022
aaaaaaa 1029

<210> 83
<211> 1788
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 769..1272

<220>
 <221> sig_peptide
 <222> 769..843
 <223> Von Heijne matrix
 score 5.65786415517206
 seq AAHLLVVILPANA/AL

<400> 83
 ttgggcagaa aaattcaagc aggagattgt atttcttttg gagttgtacg atttccttta 60
 ttattttgaac tgcagtaaag aaagctggga tgggctcctc tagggatact tccagatccc 120
 tgggcgggtg tagccctggc tcctcttttaa atggatttgg tttcaaagac gatcatctcc 180
 gtcttctcgg atgtcatagt gccactgac atctccagct cctggccacc ctgggctttc 240
 tccacttttg cctctatgtt ttgcttctcc accgtcttag ccacgatac tacctctctg 300
 tcatgtgatg tgacccttgt ttttgaacca ggagtggccc tgaggctcct taaaaaagag 360
 ctgatcttac tggcttttct ttgtaaagct cctgtgctag atgcagattg gttcttcccc 420
 agttcctgag ttgttctcga ctcttttttg gtggagctgt ggggtggagct cttgcgagag 480
 gagccatgtc gcttgccctc tacgttgctg tacccttttt cttttttgtc atctctcgtg 540
 tttttatggc cagatgcgga ccggtgggaa gacgctttct gattcttgtc ccccgctctc 600
 ctgcggtgac tttcacctgc cttgcggtga tgagaacttt tcctactggg atgtctgtcc 660
 ttcttttctc ttcttttctt gttttcattc cagacttcag cactgggctg ggaaactttc 720
 tggtttccat ctggttcact catgtagcct tcgctttgca aggtggag atg agg ggt 777
 Met Arg Gly
 -25
 ccc act gct ggt cct tca gtt ctt tct gct gca cac ttg ctg gtc gta 825
 Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu Leu Val Val
 -20 -15 -10
 ata ctg cct gca aac gcc gca ctg aag ctg ctg tct tgg gag aga ctg 873
 Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp Glu Arg Leu
 -5 1 5 10
 gcg gcc ccc gcc atc gag gtg gaa gta cct tcc aag gag gtg ctt gca 921
 Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu Val Leu Ala
 15 20 25
 gca ccc acc aag gcc aag cta ata ccc tct gag gat atg ttg gca gca 969
 Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met Leu Ala Ala
 30 35 40
 cct gcc atg gac ttg ctg gat tca ttt tct cct gga ttt ttg ata gct 1017
 Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe Leu Ile Ala
 45 50 55
 gct ccc gcc agc gct gtg atc act tgg cct ggg cct gca gat ttg gtt 1065
 Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala Asp Leu Val
 60 65 70
 gtt gct atg ctg ata gca cct gtt gca gga ctg att gct gcc cct gct 1113
 Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala Ala Pro Ala
 75 80 85 90
 att gcc aca tct gtt cta ggt cct gtt gct gtt cct gcc act gcc atg 1161
 Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala Thr Ala Met
 95 100 105
 cca cct gct gtc ctt gct gct cct cct tca gca gcc cct gga gtg ctg 1209
 Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro Gly Val Leu
 110 115 120
 gtg gat gga gaa gcc gca cta gcc gtt ccg tgg gag gca tgt tgg att 1257
 Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala Cys Trp Ile
 125 130 135

ccc tct ccc cca gca taagcagaag aggtggctgc agatacatca caaggcttgt 1312
Pro Ser Pro Pro Ala

140
agagcccagt ctactctga tccccttctc tgtggagctc tgcagcctat accaagggga 1372
agagaaacag atgagattga gatgactgaa agggagatca gaactttcta ctctctctt 1432
atcctggagt taattcaagg gcttataatt agaagaacct gggtcgggtg tggaggctca 1492
cgctgtaat cccaacactt tgggaggcca aggagggcag atcgcttgag gccaggagtt 1552
caagaccagc cttgccaaca tagcaaaacc ccgactctac taaaaataca aaaaattagc 1612
tggacaggat ggcgcagcc tgtaatcca gctactcagt aggctgaggt aggagtatcg 1672
cttgaactcg gatggcggag gctgcagtga gccaaagactg cgccactcca ctgcactcca 1732
gcctgggcaa cagagtgaga cactgtttaa aaaaaagaaa gaaaaaaaaa aaaaaa 1788

<210> 84
<211> 805
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..527

<220>
<221> sig_peptide
<222> 30..74
<223> Von Heijne matrix
score 8.68924532952647
seq PLLIICLLPAIEG/KN

<400> 84
actggggcac agtaggagga acccagaag atg ctg cct ctc ctg atc atc tgt 53
Met Leu Pro Leu Leu Ile Ile Cys
-15 -10
ctc ctg cct gcc att gaa ggg aag aac tgc ctc cgc tgc tgg cca gaa 101
Leu Leu Pro Ala Ile Glu Gly Lys Asn Cys Leu Arg Cys Trp Pro Glu
-5 1 5
ctg tct gcc ttg ata gac tat gac ctg cag atc ctc tgg gtg acc cca 149
Leu Ser Ala Leu Ile Asp Tyr Asp Leu Gln Ile Leu Trp Val Thr Pro
10 15 20 25
ggg cca ccc aca gaa ctt tct caa aat cgt gac cat ttg gaa gaa gaa 197
Gly Pro Pro Thr Glu Leu Ser Gln Asn Arg Asp His Leu Glu Glu Glu
30 35 40
aca gcc aaa ttc ttc act caa gta cac caa gcc att aaa acg tta cga 245
Thr Ala Lys Phe Phe Thr Gln Val His Gln Ala Ile Lys Thr Leu Arg
45 50 55
gat gat aaa aca gta ctt ctg gaa gag atc tac acg cac aag aat ctc 293
Asp Asp Lys Thr Val Leu Leu Glu Glu Ile Tyr Thr His Lys Asn Leu
60 65 70
ttt act gag agg ctg aat aag ata tct gat ggg ctg aag gag aag gac 341
Phe Thr Glu Arg Leu Asn Lys Ile Ser Asp Gly Leu Lys Glu Lys Asp
75 80 85
ata cag tcc aca ctg aag gtc acc agc tgt gct gac tgc agg act cac 389
Ile Gln Ser Thr Leu Lys Val Thr Ser Cys Ala Asp Cys Arg Thr His
90 95 100 105
ttc ctc tcc tgc aat gac ccc act ttc tgc cca gcc agg aac cgg cgg 437

Phe	Leu	Ser	Cys	Asn	Asp	Pro	Thr	Phe	Cys	Pro	Ala	Arg	Asn	Arg	Arg		
				110					115				120				
acc	tcc	ctg	tgg	gct	gtg	agt	ctc	agc	agt	gct	cta	ctc	ctg	gcc	ata	485	
Thr	Ser	Leu	Trp	Ala	Val	Ser	Leu	Ser	Ser	Ala	Leu	Leu	Leu	Ala	Ile		
			125					130					135				
gct	gga	gat	gtt	tct	ttt	act	ggc	aaa	gga	aga	agg	agg	cag			527	
Ala	Gly	Asp	Val	Ser	Phe	Thr	Gly	Lys	Gly	Arg	Arg	Arg	Gln				
			140					145					150				
taa	agc	agga	acag	ggc	cagc	ccg	cat	gtct	tcc	aga	agt	aac	agagg	gcc	gcag	ctacca	587
ccg	tcac	aaaa	gttc	act	cat	ctct	gggt	ccc	cggt	gacccc	atcccc	cccat	acc	ctcc	atc		647
ctg	gggt	cctg	ggg	cccc	aaaa	gct	ctg	aggc	ctagg	agact	gcg	ctgt	ctc	gtg	gttt	gcc	707
tact	cctaca	ccttt	gtaaa	gagt	ctctt	c	att	aaaa	cccc	ctctt	cataa	aaaaaaaa					767
aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aata	aaaa	aaaa	aaaa								805

<210> 85
 <211> 814
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 39..506

<220>
 <221> sig_peptide
 <222> 39..83
 <223> Von Heijne matrix
 score 5.91494342964539
 seq ILMLTFIICGLLT/RV

<400> 85																	
att	cct	cagg	acac	agag	ct	tcct	ctct	ctcc	cagg	agcc	atg	aat	atc	ctg	atg	ctg	56
											Met	Asn	Ile	Leu	Met	Leu	
											-15					-10	
acc	ttc	att	atc	tgt	ggg	ttg	cta	act	cgg	gtg	acc	aaa	ggg	agc	ttt		104
Thr	Phe	Ile	Ile	Cys	Gly	Leu	Leu	Thr	Arg	Val	Thr	Lys	Gly	Ser	Phe		
				-5				1				5					
gaa	ccc	caa	aaa	tgt	tgg	aag	aat	aat	gta	gga	cat	tgc	aga	aga	cga		152
Glu	Pro	Gln	Lys	Cys	Trp	Lys	Asn	Asn	Val	Gly	His	Cys	Arg	Arg	Arg		
		10				15					20						
tgt	tta	gat	act	gaa	agg	tac	ata	ctt	ctt	tgt	agg	aac	aag	cta	tca		200
Cys	Leu	Asp	Thr	Glu	Arg	Tyr	Ile	Leu	Leu	Cys	Arg	Asn	Lys	Leu	Ser		
	25			30				35									
tgc	tgc	att	tct	ata	ata	tca	cat	gaa	tat	act	cga	cga	cca	gca	ttt		248
Cys	Cys	Ile	Ser	Ile	Ile	Ser	His	Glu	Tyr	Thr	Arg	Arg	Pro	Ala	Phe		
	40			45				50							55		
cct	gtg	att	cac	cta	gag	gat	ata	aca	ttg	gat	tat	agt	gat	gtg	gac		296
Pro	Val	Ile	His	Leu	Glu	Asp	Ile	Thr	Leu	Asp	Tyr	Ser	Asp	Val	Asp		
			60					65							70		
tct	ttt	act	ggg	tcc	cca	gta	tct	atg	ttg	aat	gat	ctg	ata	aca	ttt		344
Ser	Phe	Thr	Gly	Ser	Pro	Val	Ser	Met	Leu	Asn	Asp	Leu	Ile	Thr	Phe		
			75					80							85		
gac	aca	act	aaa	ttt	gga	gaa	acc	atg	aca	cct	gag	acc	aat	act	cct		392
Asp	Thr	Thr	Lys	Phe	Gly	Glu	Thr	Met	Thr	Pro	Glu	Thr	Asn	Thr	Pro		


```

          90          95          100
gag act act atg cca cca tcc gag gcc act act ccc gag act act atg      440
Glu Thr Thr Met Pro Pro Ser Glu Ala Thr Thr Pro Glu Thr Thr Met
      105          110          115
cca cca tct gag act gct act tcc gag act atg cca cca cct tct cag      488
Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr Met Pro Pro Pro Ser Gln
120          125          130          135
aca gct ctt act cat aat taattaacat ttacttctgg tatggaacaa      536
Thr Ala Leu Thr His Asn
      140
ctagaaatac tgctggaaat aatatccaaa gagctgattc taccaatcca atttcaccag      596
gaaaattcca tcagggattg gatgaccatg gggatggaca taattgctac taccaacaca      656
acagccaaga gagttgcctt acaattagaa atgtgtagac agaaatgtat agaagatata      716
aggattctct taattggact taaattcttt atctgtcttc ctccgatgta ctcaaatata      776
tgagctaatt tttgtcttaa gtgaaaaaaaa aaaaaaaaa      814

<210> 86
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..429

<220>
<221> sig_peptide
<222> 115..210
<223> Von Heijne matrix
      score 8.2583062681354
      seq LVAAMVLLSVVFC/LY

<400> 86
attctaccag ctctggctga gcctgagctt ccaaaagtga gctgagctgt tcaaccttgg      60
atcttaatta ctctagcag ggataattag gtccctcttt ctcagattac aggc atg      117
                                     Met
gca aag atg ttt gat ctc agg acg aag atc atg atc ggc atc gaa agc      165
Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu Ser
      -30          -25          -20
agc tta ctg gtt gcc gcg atg gtg ctc cta agt gtt gtg ttc tgt ctt      213
Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys Leu
      -15          -10          -5          1
tac ttc aaa gta gct aag gca cta aaa gct gca aag gac cct gat gct      261
Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp Ala
      5          10          15
gtg gct gta aaa aat cac aac cca gac aag gtg tgt tgg gcc acg aac      309
Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr Asn
      20          25          30
agc cag gcc aaa gcc acc acc atg gag tct tgt cca tct ctc cag tgc      357
Ser Gln Ala Lys Ala Thr Thr Met Glu Ser Cys Pro Ser Leu Gln Cys
      35          40          45
tgt gaa ggt tgt aga atg cat gcc agt tct gat tcc ctg cca cct tgc      405
Cys Glu Gly Cys Arg Met His Ala Ser Ser Asp Ser Leu Pro Pro Cys
50          55          60          65

```

tgt tgt gac ata aat gag ggc ctc tgacttggga aagctgggca caaaaatctt 459
Cys Cys Asp Ile Asn Glu Gly Leu

70

catgagcaat atttctttct taatagaatg ttttattatt caagtcaagt tctagagtgt 519
ttacatacta ttatataatg tacagtgtta ttttctgtac ttctgaataa atgtgcaata 579
ttgcaaaaaa aaaaaaaaaa 598

<210> 87

<211> 699

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 332..574

<220>

<221> sig_peptide

<222> 332..412

<223> Von Heijne matrix
score 7.96491294552426
seq ILGLFCCLPLAIP/AV

<400> 87

aatccccctgt ggttggtgat caaggaagag catagtgcc aacctaggtg ccttcctggg 60
aatgttccag gagggcagga gtaggaggag gagggttaga gtagagggga aatgatgaga 120
gcagaaagga gaggctcgct ctgtcaccga ggctggagtg cagtggcagg atcttggctc 180
acttcaacct ccacctcccg agttctgcct cagcctccca agtagctggg attacaggctc 240
cagtcactcc acgcttgcag agtccaatta acaagagcaa gttctggtag aaagaagggtg 300
actttattcc agagctcagg tgtttgaact g atg tct gat gag gat gaa tcc 352
Met Ser Asp Glu Asp Glu Ser
-25

agc gac tac ctc tgc ctg tcc atc ctg ggc ctc ttc tgt tgc ctt ccc 400
Ser Asp Tyr Leu Cys Leu Ser Ile Leu Gly Leu Phe Cys Cys Leu Pro
-20 -15 -10 -5

cta gcc atc cca gcc gtg atc ttt tct tgc ctg aca aag aac tac aat 448
Leu Ala Ile Pro Ala Val Ile Phe Ser Cys Leu Thr Lys Asn Tyr Asn
1 5 10

aaa tcc agt gac tat gag ctg gca gcc aag acc tcc aaa caa gcc tac 496
Lys Ser Ser Asp Tyr Glu Leu Ala Ala Lys Thr Ser Lys Gln Ala Tyr
15 20 25

tac tgg gcc atc gcg agc atc act gtg gga atc tta ggt acc atc ttg 544
Tyr Trp Ala Ile Ala Ser Ile Thr Val Gly Ile Leu Gly Thr Ile Leu
30 35 40

tac acc tac ctg ata tac tta ctt aga ttg taaactgctt cccagctctt 594
Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg Leu
45 50

gaacaaacca ccaaatatac accacagtgc aattttaaaaa aaaaaaaaaa aaaaaaaaaa 654
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gaaaaaaaaa aaaaaa 699

<210> 88

<211> 905

<212> DNA

<213> Homo sapiens

<220>
 <221> CDS
 <222> 133..417

<220>
 <221> sig_peptide
 <222> 133..213
 <223> Von Heijne matrix
 score 11.106948594338
 seq LTSLILVTLISA/FV

<400> 88
 atttccaggg agctgaggag ctgagggcag agctagcttt tggttatttg ggatgttatt 60
 gccagtttcc tcccagggcc attgttacca cctgatcatt tgagtttttag tttctctagc 120
 agatgctgac ta atg act gac cag gat cga atc atc aat tta gtt gtt ggc 171
 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly
 -25 -20 -15
 agc tta aca tcc tta ttg att cta gta acg ctg ata agt gct ttt gtt 219
 Ser Leu Thr Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val
 -10 -5 1
 ttc cct caa cta cct cca aaa ccg ttg aat ata ttc ttt gct gtc tgc 267
 Phe Pro Gln Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys
 5 10 15
 atc tct ttg agt agt att act gcc tgc ata atc tac tgg tat cga caa 315
 Ile Ser Leu Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln
 20 25 30
 gga gac tta gaa ccg aaa ttt aga aag cta att tac tat atc ata ttt 363
 Gly Asp Leu Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe
 35 40 45 50
 tct atc atc atg ttg tgt ata tgt gca aac ctg tac ttc cat gat gtg 411
 Ser Ile Ile Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val
 55 60 65
 gga agg tgaggctgcc aaggagaagt acttaccagg actcttcaaa atgatacatt 467
 Gly Arg
 aggacagtga gtaatttttg gataaggtat gctgaagaat ctctctgcaga agtctgatac 527
 atgattttca tgtaattgt aaatgttaat tccctcttgc aaggagagaca tatcctagat 587
 cactttgctt tttctttaag gagctgatgt tgcacctaaa cattccaacc cttaaagcta 647
 aaacagcaca aaaaaatttc acttttgaaa tgaaattttt ataattgtat ggcaaaaggc 707
 tatgtaaaaa caaatcttgc atcttaagac aaatattctt ttatttctgt taaactgaat 767
 atacaattgt tccctaggca accaactttt gcttataact acaatttaat ttcacgttga 827
 caaaacacag tgaaaagaca actttgtgaa gatctaatta caataataaa taaaataatt 887
 tacaaaaaaa aaaaaaaa 905

<210> 89
 <211> 514
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 113..364

<220>

```

<221> sig_peptide
<222> 113..172
<223> Von Heijne matrix
      score 4.37180298395146
      seq SLLLSLPPHQGLT/FS

<400> 89
ttttttacat ggtgttccca cagctgggag gacaccaca tggtcggcgt gcaggatatt      60
tcgctggacc ctagaaaagc caccacgacc tgtgggccat gatgctaccc ca atg gct      118
                                         Met Ala
                                         -20
gct gct gct gtt cct tct ctt ctt ctt tct ctt cct cct cac cag ggg      166
Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His Gln Gly
      -15                                -10                                -5
ctc act ttc tcc aac aaa ata caa cct ttt gga gct caa gga gtc ttg      214
Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly Val Leu
      1                                5                                10
cat ccg gaa cca gga ctg cga gac tgg ctg ctg cca acg tgc tcc aga      262
His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys Ser Arg
      15                                20                                25                                30
caa ttg cga gtc gca ctg ccg gag aag ggg tcc gag ggc agt ctg tgt      310
Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser Leu Cys
      35                                40                                45
caa acg cag ctg cca gct act cca tgc ttc ctg cct tcg aat acg gtg      358
Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn Thr Val
      50                                55                                60
aga acg tgaagtcatg agctgctgct aaggcatgtg gcaaccttga agagaaggtc      414
Arg Thr
aagagctacc agccaccaaaa agaatgccag cacttctctgt gtcttttgctt tggattcatg      474
agaaatatac gttcctatatt gcttcaaaaa aaaaaaaaaa      514

<210> 90
<211> 518
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 9..380

<220>
<221> sig_peptide
<222> 9..104
<223> Von Heijne matrix
      score 4.73369226787171
      seq AVFAVLFFVFLFA/ML

<400> 90
acatccta atg gtg gtg gtt gaa cca gga gcc agt tta ttc cca aat ggt      50
      Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly
      -30                                -25                                -20
gtt cct tgg ctc tat gct gtg ttt gct gtg ctt ttt gta ttt ttt ctt      98
Val Pro Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu
      -15                                -10                                -5

```

ttt gcc atg tta tct ccc ttt tta ctt gag ata gac cag cac ata aag	146
Phe Ala Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys	
1 5 10	
aaa ttc ttg atc aga tgc agg tat tct ctg cat aac act gtg cat aag	194
Lys Phe Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys	
15 20 25 30	
gac aaa aaa aac agt gag ata aag atg gac cat cta gaa agg cca ggc	242
Asp Lys Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly	
35 40 45	
tgt cca ctg gag tca cca agg aga gga gtt ctg gga ggg aag aaa aat	290
Cys Pro Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn	
50 55 60	
ggg atg gga aac gac cca tta cta ttt gtg aaa gtg aca aaa gaa ccc	338
Gly Met Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro	
65 70 75	
agg gat tct gag gct gaa atc tat acc cct ggg cct tca gtt	380
Arg Asp Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val	
80 85 90	
tgagagtcatt ttagcctata tggaattacc tgtgacatta cattccagag agatgagaaa	440
ttctgagacc cttattatcg atgtttatat tgaaaaaatg gtaataaata ttttgagact	500
ccccaaaaaa aaaaaaaa	518

<210> 91
 <211> 808
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 155..340

<220>
 <221> sig_peptide
 <222> 155..292
 <223> Von Heijne matrix
 score 8.64329745298384
 seq AVLLLILFAIVFG/LL

<400> 91	
cttttcctct caacagttgc ttctttgagt caggggtgcag ctctgggtcac ctggcggcct	60
cttcagctca gccctccaca aagtgtgagc ctgaaggacc accctgaatt gcccttgtag	120
gaccagaac agctaccagc agaatcagat tctc atg gac caa ctg gta ttc aaa	175
Met Asp Gln Leu Val Phe Lys	
-45 -40	
gag aca atc tgg aat gat gcg ttc tgg cag aac ccc tgg gac cag ggg	223
Glu Thr Ile Trp Asn Asp Ala Phe Trp Gln Asn Pro Trp Asp Gln Gly	
-35 -30 -25	
ggc ctg gca gtg att atc tta ttc atc acc gct gtc ctg ctt ctc atc	271
Gly Leu Ala Val Ile Ile Leu Phe Ile Thr Ala Val Leu Leu Leu Ile	
-20 -15 -10	
tta ttt gcc atc gtg ttt ggt tta ctc act tcc aca gaa aac act cag	319
Leu Phe Ala Ile Val Phe Gly Leu Leu Thr Ser Thr Glu Asn Thr Gln	
-5 1 5	
tgt gaa gcg ggt gaa gag gag tgacctgact tgctggggac tgagatggca	370

Cys Glu Ala Gly Glu Glu Glu

```

10                               15
gcaggggagg cgagctgacc tgccccatt ccagtggtag gccccttcgc ggttcctct 430
ggctcagggg ccaagccctg gtgtcttctt ttcccaccag gaaaaagtct agtaaaatac 490
tgtatctggc ttaggggttg tcagactagt aagatgggga ggctgggtctg agaccaattc 550
tggctccttg accctattgt ttttaggggt ccccgaccag aaccctaaaa gcacatggag 610
aggatggctc cactgcctca ggtggaagga gctatggcta acaagggttct ctaacaggct 670
cacaggcca gccagcaatt tcacaaatcc ttgacagaga aagacacaac caaatgaaat 730
aaaaattcct tttcaaatct gctaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 790
aaaaaaaaa aaaaaaaaaa

```

<210> 92
 <211> 737
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 185..634

<220>
 <221> sig_peptide
 <222> 185..253
 <223> Von Heijne matrix
 score 9.49395175807817
 seq SLLFICFFGESFC/IC

```

<400> 92
atattttgct gactggcaag gttatatgaa gtgcttttat tgaagcacca ttttaactaa 60
tagctcctgg tattttctgc ttcccttcgt aggggaattta gttattttat tttattattt 120
agctaattta gctattttta aatagctaaa ttttagctac ttttttttca attgacaaag 180
aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229
    Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile
          -20          -15          -10
tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca 277
Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr
          -5          1          5
aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa ggt 325
Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly
          10          15          20
tgt tta tat ctc att tat aat tta tta caa gct gtc ttc ttc gtc tta 373
Cys Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu
          25          30          35          40
ttt gtt ttg tct gtg cat tac ctg tgg aag aaa tgg aag aaa cac caa 421
Phe Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln
          45          50          55
aaa aag ctg aaa aag caa gcc tcc tta gaa aaa cct ggt aat gat cta 469
Lys Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu
          60          65          70
gaa agc cca ttg atc aac aac att gac caa aca ctc cac aga gtg gca 517
Glu Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala
          75          80          85
acc aca gca tca gtg ata tac aag atc tgg gag cac agg tct cac cat 565
Thr Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His

```

90	95	100	
cct tcc tct aag aaa att aag cac tgc aaa tta aag aag aag agt aaa			613
Pro Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys			
105	110	115	120
gaa gaa gga gcc aga aga tac taaataaatg catatgcaaa tgtagcttag			664
Glu Glu Gly Ala Arg Arg Tyr			
	125		
tcaattatag atatcacaaa agaaatctat catctaagga ttaaaaattg ttctttggaa			724
aaaaaaaaaa aaa			737

<210> 93
 <211> 728
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 53..646

<220>
 <221> sig_peptide
 <222> 53..91
 <223> Von Heijne matrix
 score 4.95353272042967
 seq MLLGRLTSQLLRA/VP

<400> 93	
aatttgagcc gcgtcgagct cccctgggac ctgtggccgc cgcccacaga cc atg ctc	58
	Met Leu
ctg ggg cgc ctg act tcc cag ctg ttg agg gcc gtt cct tgg gca ggc	106
Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp Ala Gly	
-10 -5 1 5	
ggc cgc ccg cct tgg ccc gtc tct gga gtg ctg ggc agc cgg gtc tgc	154
Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg Val Cys	
10 15 20	
ggg ccc ctt tac agc aca tcg ccg gcc ggc cca ggt agg gcg gcc tct	202
Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala Ala Ser	
25 30 35	
ctc cct cgc aag ggg gcc cag ctg gag ctg gag gag atg gtc ccc agg	250
Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Met Val Pro Arg	
40 45 50	
aag atg tcc gtc agc ccc ctg gag agc tgg ctc acg gcc cgc tgc ttc	298
Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg Cys Phe	
55 60 65	
ctg ccc aga ctg gat acc ggg acc gca ggg act gtg gct cca ccg caa	346
Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro Pro Gln	
70 75 80 85	
tcc tac cag tgt ccg ccc agc cag ata ggg gaa ggg gcc gag cag ggg	394
Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu Gln Gly	
90 95 100	
gat gaa ggc gtc gcg gat gcg cct caa att cag tgc aaa aac gtg ctg	442
Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn Val Leu	
105 110 115	
aag atc cgc cgg cgg aag atg aac cac cac aag tac cgg aag ctg gtg	490

Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys Leu Val	
120 125 130	
aag aag acg cgg ttc ctg cgg agg aag gtc cag gag gga cgc ctg aga	538
Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg Leu Arg	
135 140 145	
cgc aag cag atc aag ttc gag aaa gac ctg agg cgc atc tgg ctg aag	586
Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp Leu Lys	
150 155 160 165	
gcg ggg cta aag gaa gcc ccc gaa ggc tgg cag acc ccc aag atc tac	634
Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys Ile Tyr	
170 175 180	
ctg cgg ggc aaa tgagtctggc gccgcccttc ccgcccggtt ctgctgtgat	686
Leu Arg Gly Lys	
185	
ccgtagtaat aaattctcag aggacccaaa aaaaaaaaaa aa	728

<210> 94
 <211> 582
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 247..510

<220>
 <221> sig_peptide
 <222> 247..318
 <223> Von Heijne matrix
 score 5.20026065148038
 seq FCALEVVLPS CDC/RS

<400> 94	
atcataactca ccatggctca caaactgcct gtttgaaact cccttcagtt ctgagaggat	60
gggaacattc tttaagcggg tctgtcttggc acgagacata aggcagttca acatcaagcc	120
cttgccctga acagttccaa atgccaagaa ctggcgaatt actacttttg tttcaatggg	180
tggtccaaaa ggatcatcaa gcttcaggag ctttctgacc ttgaagaaag ggaaaatgaa	240
gatagc atg gtg cca ctt ccg aag caa agc ctg aag ttc ttc tgt gct	288
Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala	
-20 -15	
tta gaa gtg gtg ttg cca tcc tgt gat tgc agg agt cct ggc att ggc	336
Leu Glu Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly	
-10 -5 1 5	
ttg gtg gag gag cct atg gat aag gtg gag gaa gga cca tta tca ttc	384
Leu Val Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe	
10 15 20	
ctt atg aaa agg aag aca gcc cag aag ctt gct att cag aag gct ttg	432
Leu Met Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu	
25 30 35	
tca gat gca ttc cag aaa ctg ttg att gtt gtt cta ggt aag act gtc	480
Ser Asp Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val	
40 45 50	
ttg atc atc ctt gaa gta ctt cag ttt cag taagcaaata aactcatttt	530
Leu Ile Ile Leu Glu Val Leu Gln Phe Gln	


```

55                               60
gaaaagttaa ttgaataaaa atattgatat ctaaagcaaa aaaaaaaaaa aa      582

<210> 95
<211> 1913
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 143..592

<220>
<221> sig_peptide
<222> 143..277
<223> Von Heijne matrix
      score 5.94057630118762
      seq VLVDLAILGQAYA/FA

<400> 95
atttttttgt gcctaagatg cccagtgcgt tgctggggtt ttctgctgtc ctcgggctct      60
ggacatgagg ccagacctg tgacctgtt ggcagtgggc agtggcttga tgtgaggtcc      120
cagagacggc aggttcatca ag atg gtg ctc atg tgg acc agt ggt gac gcc      172
              Met Val Leu Met Trp Thr Ser Gly Asp Ala
              -45                               -40

ttc aag acg gcc tac ttc ctg ctg aag ggt gcc cct ctg cag ttc tcc      220
Phe Lys Thr Ala Tyr Phe Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser
-35                               -30                               -25                               -20
gtg tgc ggc ctg ctg cag gtg ctg gtg gac ctg gcc atc ctg ggg cag      268
Val Cys Gly Leu Leu Gln Val Leu Val Asp Leu Ala Ile Leu Gly Gln
              -15                               -10                               -5

gcc tac gcc ttc gcc cca ccc cca gaa gcc ggc gcc cca cgc cgt gca      316
Ala Tyr Ala Phe Ala Pro Pro Pro Glu Ala Gly Ala Pro Arg Arg Ala
              1                               5                               10

ccc cac tgg cac caa ggc cct ctg aca gtg ggg agg acg agg atg tgg      364
Pro His Trp His Gln Gly Pro Leu Thr Val Gly Arg Thr Arg Met Trp
              15                               20                               25

gac cgc cag ccg cgg gca ctg gtg ggc cct gac ctc ccc gcg ggg agg      412
Asp Arg Gln Pro Arg Ala Leu Val Gly Pro Asp Leu Pro Ala Gly Arg
              30                               35                               40                               45

gtg ggt gcc gtg gcc cct gca ggt gtg gca gag atg ggg cac ggg cat      460
Val Gly Ala Val Ala Pro Ala Gly Val Ala Glu Met Gly His Gly His
              50                               55                               60

tgg ggt ctc cat cag cct ctg tgg ggt gtc tca ggg tgg gca gtg ggg      508
Trp Gly Leu His Gln Pro Leu Trp Gly Val Ser Gly Trp Ala Val Gly
              65                               70                               75

gtg ggg ctg gga cgc tgt ttg tgc tca gcg ggg aca gcc agg gtt gat      556
Val Gly Leu Gly Arg Cys Leu Cys Ser Ala Gly Thr Ala Arg Val Asp
              80                               85                               90

ctg gcc ccg agg gtt ttg gat gtt ttt agg atg aca taaaaagcaa      602
Leu Ala Pro Arg Val Leu Asp Val Phe Arg Met Thr
              95                               100                               105

gtgttttccc catttctct tatgaaacac cgtctgagcc caaggtacac attgggcggc      662
ctgcaggaac ctgctccagg tggacacacg ggccagcagc cgcgaaacctt gaagctgggg      722

```

tgaccgcagg	agaccctgta	aggcctgtga	gcggagccct	cgaccccgctg	acaccctggc	782
cagacaccct	gcttggactg	gggtggcctc	tgctaccag	gggtctggca	cgggggaggg	842
ctggggcttt	ctctgcctgg	tacacacgga	aaggcggtg	tgcgacgca	gggtcaccgt	902
gctccgggtt	ttctgacagt	cggtgtttcc	tgggcctttg	gagtggctgc	gaggcctgaa	962
cgccttgttg	atccgctgtg	tccagcccgg	ctgagcatcg	ccagggctag	ctcatgctgc	1022
tcttgtcagc	ctctggttct	cctcgagtc	ttggggacgt	ggcagatgcc	agcgaccatc	1082
agacaacgtg	gaggccctca	tgggcaatgg	ctgagggggc	cgggctgagg	ctgtgcacat	1142
gcagtctgca	cgccactctt	gggctctgct	ggcggagatc	cccttccttc	tgggtgcaga	1202
ctgcacctcc	ggatgcagtt	ttgatgtcca	tcttcagga	gagagacggt	ctcgggtcca	1262
gggagtggag	ggggctgccc	ctgccgtgca	ggcctggcc	gatggcgcc	tacctgctg	1322
ccctgggctt	ttggcctgaa	gcaaattcct	gagtgggggg	tactggggcc	tgccgcatcc	1382
tgtcctgtcc	actgcccacc	cccgtgtgct	ggctccctca	cttctggctg	cagtggggagc	1442
cgccagtctg	acccttgtca	ccgcacgctc	tgccccacc	ccgttgcaag	aggtcacacc	1502
atgtcagcag	ccttgcactg	accgcagccg	gccccaggc	ctcagagttc	tggatgcttc	1562
cgtgcggctc	caacaggcat	cgtcttcctt	tccgcagggtg	gaggggcccgc	ttcccgcagg	1622
catctgagct	ctgtgccggg	gccgtggcca	tgggaagatg	ttccacgctg	cctcctcctc	1682
gagttttcct	cggaacact	cttgaatgtc	tgagtgaggg	tctgtcttag	ctctttggcc	1742
tgtgagatgc	tttgaatatt	tttatttttt	taagatgaag	caagatgtct	gtagcggtaa	1802
ttgcctcaca	ttaactgtc	gccgactgca	ggcgcagtga	ctgctgaatg	taccctgtgt	1862
ggcgacttgg	aatcaataaa	ccatttgtgg	atcctaaaaa	aaaaaaaaaa	a	1913

<210> 96
 <211> 670
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 33..458

<220>
 <221> sig_peptide
 <222> 33..89
 <223> Von Heijne matrix
 score 6.45239823575329
 seq SVFLLMVNGQVES/AQ

<400> 96																						
agg	tgg	gtc	ccc	ggc	cacc	ccc	agac	cctg	cc	atg	gcg	acc	gcg	agt	cct	agc	53					
										Met	Ala	Thr	Ala	Ser	Pro	Ser						
																	-15					
gtc	ttt	cta	ctc	atg	gtc	aac	ggg	cag	gtg	gag	agc	gcc	cag	ttt	cca		101					
Val	Phe	Leu	Leu	Met	Val	Asn	Gly	Gln	Val	Glu	Ser	Ala	Gln	Phe	Pro							
										-10												
										-5												
										1												
gag	tat	gat	gac	ttc	tac	tgc	aag	tac	tgc	ttt	gtg	tac	ggc	cag	gac		149					
Glu	Tyr	Asp	Asp	Phe	Tyr	Cys	Lys	Tyr	Cys	Phe	Val	Tyr	Gly	Gln	Asp							
5						10						15						20				
tgg	gcc	ccc	aca	gcg	ggg	ctg	gag	gag	ggg	atc	tca	cag	atc	aca	tcc		197					
Trp	Ala	Pro	Thr	Ala	Gly	Leu	Glu	Glu	Gly	Ile	Ser	Gln	Ile	Thr	Ser							
										25						30						35
aag	agc	caa	gat	gtg	cgg	caa	gca	ctg	gtg	tgg	aac	ttc	ccc	att	gat		245					
Lys	Ser	Gln	Asp	Val	Arg	Gln	Ala	Leu	Val	Trp	Asn	Phe	Pro	Ile	Asp							
										40						45						50
gtc	acc	ttt	aaa	agc	acc	aac	ccc	tac	ggc	tgg	cca	cag	atc	gtg	ctc		293					

Val	Thr	Phe	Lys	Ser	Thr	Asn	Pro	Tyr	Gly	Trp	Pro	Gln	Ile	Val	Leu	
	55						60				65					
agc	gtg	tat	gga	cca	gat	gtg	ttc	ggg	aac	gat	gtg	ggt	cga	ggc	tat	341
Ser	Val	Tyr	Gly	Pro	Asp	Val	Phe	Gly	Asn	Asp	Val	Val	Arg	Gly	Tyr	
	70					75					80					
ggg	gcc	gtg	cac	gtg	ccc	ttc	tca	cct	ggc	cgg	cac	aaa	agg	acc	atc	389
Gly	Ala	Val	His	Val	Pro	Phe	Ser	Pro	Gly	Arg	His	Lys	Arg	Thr	Ile	
85					90				95						100	
ccc	atg	ttt	gtc	cca	gaa	tct	acg	tct	aaa	ctg	cag	aag	ttt	aca	aga	437
Pro	Met	Phe	Val	Pro	Glu	Ser	Thr	Ser	Lys	Leu	Gln	Lys	Phe	Thr	Arg	
				105					110					115		
tct	gca	agc	tgc	tcc	acc	cac	tgaggacaaa	tagaaacagg	tcccctggga							488
Ser	Ala	Ser	Cys	Ser	Thr	His										
	120															
gtgctgagtc	acggggctcc	cttcagccct	gttccagcag	cagaaggccg	ggcgatttta											548
ccctgtgccc	tgtgaaaaat	ctttgtgtct	gagggggcag	aggaaaaact	cttgtcagat											608
gggaaaaatg	ctcatgacat	aatgtgacat	taaaaggtgg	gaaacaaaaa	aaaaaaaaaa											668
aa																670

<210> 97
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..336

<220>
 <221> sig_peptide
 <222> 1..81
 <223> Von Heijne matrix
 score 3.68137078794859
 seq AHLCSDSLPEQQ/QD

<400> 97																
act	tcc	gaa	gag	aga	acc	gcc	atg	aag	aga	gaa	ggg	ggt	gcc	gcc	cac	48
Thr	Ser	Glu	Glu	Arg	Thr	Ala	Met	Lys	Arg	Glu	Gly	Gly	Ala	Ala	His	
	-25					-20					-15					
ctc	tgc	tcc	gac	agc	ctc	ccg	gag	tcc	cag	cag	caa	gac	ggc	aac	cac	96
Leu	Cys	Ser	Asp	Ser	Leu	Pro	Glu	Ser	Gln	Gln	Gln	Asp	Gly	Asn	His	
	-10				-5				1				5			
gca	ccc	aac	ttc	tcc	agc	cac	ggc	tca	tgc	cgc	cgt	cgc	cag	cgg	scc	144
Ala	Pro	Asn	Phe	Ser	Ser	His	Gly	Ser	Cys	Arg	Arg	Arg	Gln	Arg	Xaa	
			10					15					20			
gac	atg	aca	agg	cgc	tgc	atg	ccc	gct	agg	cca	ggt	ttc	ccc	tca	tcc	192
Asp	Met	Thr	Arg	Arg	Cys	Met	Pro	Ala	Arg	Pro	Gly	Phe	Pro	Ser	Ser	
		25					30				35					
cca	gcc	ccg	ggg	tgc	tgc	ccc	ccg	cgc	tgc	cat	ctg	aga	ccc	ggt	agt	240
Pro	Ala	Pro	Gly	Ser	Ser	Pro	Pro	Arg	Cys	His	Leu	Arg	Pro	Gly	Ser	
	40					45					50					
acc	gcc	cat	gct	gca	gcg	gga	aag	aga	aca	gag	agt	cct	ggg	gac	agg	288
Thr	Ala	His	Ala	Ala	Ala	Gly	Lys	Arg	Thr	Glu	Ser	Pro	Gly	Asp	Arg	
	55					60					65					

tac cgt gca gag ggc ttg aga agg ggc cgg gtc	gcg ggg gca agg gta	336
Tyr Arg Ala Glu Gly Leu Arg Arg Gly Arg Val	Ala Gly Ala Arg Val	
70	75 80 85	
tgaggggagg gctgcagacc gccgctcttc cagttcccgc	catcctccgc gagctcaggc	396
gttggcattt cggggcctgg caaatccccg cccgcctcc	gcgcaggggc tactgggagt	456
tggagtttgc ttctctgtag ttgggcagct gctcttggtc	tagtgaccac cagcctggac	516
agctacggag aaccgcctt aggtagaaag aaagtgattt	ttttcctttg caagagtttg	576
acccgggacc ctaactgctt aatgcatatt tagatcgttt	tctgtacgtt gtcagttcta	636
ctgacctag tggtttagta atataaacct tttctatggt	gtgggtgaaa ttatgtaacc	696
tgtgatgagg gaatccctt cacgaattac tttgtagtc	agcgtgcacg ctagtgcata	756
cttaaaagaa cttgcagatt tggaatgtga cgtgttttct	ctttcagtaa cttcacgcct	816
ctccaagagg ctaatttttt tgtaaagatt ttgtgggagc	tatgtaatga gatggggagt	876
ttcatctaata gacatcctct gacaataaaa aatgttttaa	ttccccaaaa aaaaaaaaaa	936
aaa		939

<210> 98
 <211> 661
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 174..443

<220>
 <221> sig_peptide
 <222> 174..269
 <223> Von Heijne matrix
 score 4.13107367257584
 seq SSLAFCQVGFLTA/QP

<400> 98	
aaaaaggaac tttcagtgat aatgaacaaa actcaggagc	tatgtggatg acaggagcac
ctagatgacc gactttaccc acttcaaata ctaccttgac	cctagcactc tctccaccct
gcacctcac ctcagaccat cagttgggta ggccaacagc	tcaccatcaa ttc atg
	Met
ccc tgc cta gac caa cag ctc act gtt cat gcc	cta ccc tgc cct gcc
Pro Cys Leu Asp Gln Gln Thr Val His Ala	Leu Pro Cys Pro Ala
-30 -25 -20	
cag ccc tcc tct ctg gcc ttc tgc caa gtg ggg	ttc tta aca gca cag
Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly	Phe Leu Thr Ala Gln
-15 -10 -5 1	
cct tca cct ccg aga agg cgc aat ggg aaa gac	aga tac acg ttg gtt
Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp	Arg Tyr Thr Leu Val
5 10 15	
ctg caa cac cag gaa tgc cag gat gat tta gcc	acc tcc tca ctt gtc
Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala	Thr Ser Ser Leu Val
20 25 30	
tac ctt tcc ctc ccc tgc ttc aaa gac ttg ggt	cga tcg aag cac caa
Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly	Arg Ser Lys His Gln
35 40 45	
agc atc act gtt gct gac act aac aag tagtgccaag	ggattgcctt
Ser Ile Thr Val Ala Asp Thr Asn Lys	
50 55	

taaggaagat caggagcgga acatctggtg gcaaagaaaa tctttctaag agccccattc	523
tagtgaccac cttcaacctc ctcatagcag gagagtttgg gagtagggga cttaggatgt	583
tttgttcttt taatcaattc agaaaatatg tatgtttgaa ataaaaataa aaatacttga	643
gccaaaaaaaa aaaaaaaaa	661

<210> 99
 <211> 647
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 282..521

<220>
 <221> sig_peptide
 <222> 282..386
 <223> Von Heijne matrix
 score 3.64439944832387
 seq LEPGLSSSAACNG/KE

<400> 99	
acttgctgtg caccgttacc gtagcgactg ggcttctgga ctgtatatcc tagctgcctt	60
gtcaacatct tcgagcatcg gcagctccgg aggccggggg aactggcagg taggaaacta	120
tgtgaaagaa tctcctgatg tcataatttc cgggtgtcac cggaacattt gatcatcatt	180
cctttggcaa ttccagcctt ctgtggaaag gccagtagaa agcattgatt tattcacctc	240
tacaggaatc agactcagcc tcttttgggt ttcagtgaag t atg cct ttt caa ttt	296
	Met Pro Phe Gln Phe
	-35
gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca att	344
Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser Ile	
-30 -25 -20 -15	
gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag gag	392
Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys Glu	
-10 -5 1	
atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc ctg	440
Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys Leu	
5 10 15	
aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag cca	488
Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys Pro	
20 25 30	
cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt aagtcttttg	541
Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys	
35 40 45	
tcaaggtctg actaggtcaa gggtaatgga ccagtatcat ctggtgatct ggtaaacaaa	601
taaaagtggg ggcaccttta gatgatgaca aaaaaaaaaa aaaaaa	647

<210> 100
 <211> 1006
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 251..643

<220>

<221> sig_peptide

<222> 251..295

<223> Von Heijne matrix
score 3.74215118492367
seq LLMFTQLLLCGFL/YV

<400> 100

```
aggaagccag agggctggaa atacagcagc ctttgaagta cctctgttta atttggatgg      60
atctcagtgt gccccgttcg agacctctcc accaacacct tctgatcttg cgatttgctc    120
ttcttgactt taattagtat ctaggaaagt ctaaactttg gacctacctc tttttttgat    180
actcattttt gtacttttgc tctctgggat tggttttctta aagaatctgg atccttttta    240
atatgtcaaa atg agt ctg ctg atg ttt aca caa cta ctg ctc tgt gga      289
      Met Ser Leu Leu Met Phe Thr Gln Leu Leu Leu Cys Gly
      -15                -10                -5

ttt tta tat gtt cgg gtt gat gga tgc cgt ctt cgc cag gag gac ttt      337
Phe Leu Tyr Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe
      1                5                10

ccc ccg cgg att gtg gag cat cct tcc gat gtc atc gtc tct aag ggc      385
Pro Pro Arg Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly
      15                20                25                30

gag ccc acg act ctg aac tgc aag gcg gag ggc cgg cca acg ccc acc      433
Glu Pro Thr Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr
      35                40                45

att gag tgg tac aaa gat ggg gag cga gtg gag act gac aag gac gat      481
Ile Glu Trp Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp
      50                55                60

ccc cgg tcc cac agg atg ctt ctg ccc agc gga tcc tta ttc ttc ttg      529
Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu
      65                70                75

cgc atc gtg cac ggg cgc agg agt aaa cct gat gaa gga agc tac gtt      577
Arg Ile Val His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val
      80                85                90

tgt gtt gcg agg aac tat ctt ggt gaa gca gtg agt cga aat gcg tct      625
Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser
      95                100                105                110

ctg gaa gtg gca tgt aag tgaacataat gaacctcatg tgcacattta      673
Leu Glu Val Ala Cys Lys
      115

cttttatttta tttcaagtaa gttttgatgt gttcccatag acgctgaaac ctaaagaatc    733
aatcaacaca ctgcataatt ttacttggtc ttcttcagag aagtctggtc aagatagtat    793
caagccaggg tgttgtagta agttttgttta tatgaaatca agatgaccaa tatgttatta    853
taagaaagca ggccggggcgc ggtggctcac gcctgtaatc ccagcacttt gggaggcgga    913
ggcggggcgga tcacgaggtc aggagatcga gaccatcctg ggtagcacgg tggggccccc    973
tctctacaaa aaatacaaaa aaaaaaaaaa aaa                                1006
```

<210> 101

<211> 1059

<212> DNA

<213> Homo sapiens

<220>

```

<221> CDS
<222> 179..475

<220>
<221> sig_peptide
<222> 179..295
<223> Von Heijne matrix
      score 4.14109371250204
      seq PSLIAGLFGCLA/GY

<400> 101
gtttttccag gagggagcgg cctttgctca gcgcgagacg gctggggcgcc gagtgggaca      60
gcgctggtgc ggagactgct tccggactcc aggtaccgcg cttggcgcca gctggcccca      120
gacttctgtc ttttcagctg cagtgaaggc tcggggctgc agaattgcaa ccttgcca      178
atg gac ctg atc ggt ttt ggt tat gca gcc ctc gtg aca ttt gga agc      226
Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
                        -35                        -30                        -25
att ttt gga tat aag cgg aga ggt ggt gtt ccg tct ttg att gct ggt      274
Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
                        -20                        -15                        -10
ctt ttt gtt gga tgt ttg gcc ggc tat gga gct tac cgt gtc tcc aat      322
Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
                        -5                        1                        5
gac aaa cga gat gta aaa gtg tca ctg ttt aca gct ttc ttc ctg gct      370
Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
10                        15                        20                        25
acc ata atg ggt gtg aga ttt aag agg tcc aag aaa ata atg cct gct      418
Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
                        30                        35                        40
ggt ttg gtt gca ggt tta agc ctc atg atg atc ctg aga ctt gtc ttg      466
Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
                        45                        50                        55
ttg ctg ctc tgagcatctg gaggaacaga aaactaagtt catgtcatcc      515
Leu Leu Leu
60
tgctgtaatg ggcagagcat attttttttg tattttaaag ataaacttca atatggaatg      575
ctagaaacac aaatagcact gtcacctcta atatgaacat tagtttgagg tagttttttt      635
ctaaagcaaa aattttaact gtttttcta atgtcaagcac tatttttcatt aaaagtgtct      695
aatgaatcat gatatactct tccatttgtt gtgtctatatt tttatatatt tggatttttt      755
tgaaaattcc aaatactcat gtctcaagta agcttaaaact acaacttgtc acataaagga      815
agtcttaagt ggagttcaca gaatgataat gtatctatatt gtcatttggt ttatatattga      875
aattattaga aattatgctt tttccatttt aattgtattg ctgccagtgc tatttttttc      935
tttaaaaaat tttattctta gcacactggt atgtcctaac tgaatgtatt cagtattcaa      995
ataaaagaca ttttgggtcca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      1055
aaaaa
1059

<210> 102
<211> 514
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 34..327

```

```

<220>
<221> sig_peptide
<222> 34..162
<223> Von Heijne matrix
      score 5.69273078757386
      seq LGDALLFLRPAGS/CA

<400> 102
agagacctat ggggttcgcc tgaagccccc gga atg tgt gag aca ctt ctt act      54
                               Met Cys Glu Thr Leu Leu Thr
                               -40
agt aaa tgg gct tca gta tcc ccc atc cct gca ctc ctg cag gaa ggt      102
Ser Lys Trp Ala Ser Val Ser Pro Ile Pro Ala Leu Leu Gln Glu Gly
-35                               -30                               -25
gag aat cgg gac agt cgc agg ctg gga gac gct ctg ctt ttc ctg cgt      150
Glu Asn Arg Asp Ser Arg Arg Leu Gly Asp Ala Leu Leu Phe Leu Arg
-20                               -15                               -10                               -5
cct gct ggg agc tgc gcg ctc cag gta tcc tgg cct gcc gcc cta gcc      198
Pro Ala Gly Ser Cys Ala Leu Gln Val Ser Trp Pro Ala Ala Leu Ala
                               1                               5                               10
ggc cca agg agc cac aca gga cag ttg acc caa cac ttc tgc cac ctg      246
Gly Pro Arg Ser His Thr Gly Gln Leu Thr Gln His Phe Cys His Leu
                               15                               20                               25
aag aac gac acc tgc att cct cca tct ctg gga cca cca agg aac tca      294
Lys Asn Asp Thr Cys Ile Pro Pro Ser Leu Gly Pro Pro Arg Asn Ser
                               30                               35                               40
ggg agc ttg gaa tct ctc aga tca aaa aga tac tgactcatcg gatagccatg      347
Gly Ser Leu Glu Ser Leu Arg Ser Lys Arg Tyr
45                               50                               55
gcacacctgaa aacggccttc cttgtgtgta cattatttgc aacaagcaac aagtttataa      407
gcacttttggg aaaattgcat gtgagggtta aaatattaaa gtcagtgcgt caacttgaaa      467
taaattgatga gttattgatt actgctaaag aaaaaaaaaa aaaaaaaa      514

<210> 103
<211> 1158
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 303..953

<220>
<221> sig_peptide
<222> 303..359
<223> Von Heijne matrix
      score 5.47911600153114
      seq LCCSGCVPSLCCS/SY

<400> 103
aaaaacttcc gccgccgct ccgccgcctc cggaactaaa cgggggtgagg tcacattcgg      60
ttatctctaa cggttgaaaa cgatggagct aacaccatt atggagatta accacttttc      120
atcagggtttt taacttaagt cgtgaggaat acaacggtga acacaagatt cattttattt      180

```



```

tcatcaccat gggacgtatc ctgttgttga gttctctggg tcagacctct gaagacttct 240
cagatggatc ctagtctctg ggcttgccct gaaattactc gctgctcagg gagagagttg 300
aa atg gtt ggc atc ctc cca ctc tgt tgc tcc ggc tgt gtc ccc tcg 347
    Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser
          -15          -10          -5
ctc tgt tgt tcc agc tat gtc ccc tct gtt gct cca act gca gct cat 395
Leu Cys Cys Ser Ser Tyr Val Pro Ser Val Ala Pro Thr Ala Ala His
          1          5          10
tct gtt aga gtt cct cat tca gct ggt cac tgt ggc cag agg gtg ttg 443
Ser Val Arg Val Pro His Ser Ala Gly His Cys Gly Gln Arg Val Leu
          15          20          25
gcc tgc tcc ctt cct caa gta ttc tta aag cca tgg att ttt gtg gag 491
Ala Cys Ser Leu Pro Gln Val Phe Leu Lys Pro Trp Ile Phe Val Glu
          30          35          40
cat ttt tct tcc tgg ctc tcc ctt gag tta ttt tcc ttt ctt cgc tat 539
His Phe Ser Ser Trp Leu Ser Leu Glu Leu Phe Ser Phe Leu Arg Tyr
          45          50          55          60
ctt ggg act ctt ctt tgt gct tgc gga cat cgg ttg aga gaa gga cga 587
Leu Gly Thr Leu Leu Cys Ala Cys Gly His Arg Leu Arg Glu Gly Arg
          65          70          75
ctt ctt cct tgt ctc ctt ggt gtt ggc tcg tgg ttg ctc ttc aac aac 635
Leu Leu Pro Cys Leu Leu Gly Val Gly Ser Trp Leu Leu Phe Asn Asn
          80          85          90
tgg act gga ggc tct tgg ttt tct ctt cat ctt caa caa gtc agt ctc 683
Trp Thr Gly Gly Ser Trp Phe Ser Leu His Leu Gln Gln Val Ser Leu
          95          100          105
tct caa ggg tct cac gtt gca gca ttc tta cca gag gcc att ggg cct 731
Ser Gln Gly Ser His Val Ala Ala Phe Leu Pro Glu Ala Ile Gly Pro
          110          115          120
gga gtt cca gtt cca gtg tct gga gag tcc acc tca gct cag caa tct 779
Gly Val Pro Val Pro Val Ser Gly Glu Ser Thr Ser Ala Gln Gln Ser
          125          130          135          140
cat gcc ggt tgg caa ttg tca gca gaa gcc gat gcc tgc cca tca gtt 827
His Ala Gly Trp Gln Leu Ser Ala Glu Ala Asp Ala Cys Pro Ser Val
          145          150          155
ctt tac tct gag gtg tta gag tgg aat aaa aat ata aat act tat act 875
Leu Tyr Ser Glu Val Leu Glu Trp Asn Lys Asn Ile Asn Thr Tyr Thr
          160          165          170
agt ttt cat gac ttc tgc tta ata ttg ggt att ttt ktt gtt ttg ttt 923
Ser Phe His Asp Phe Cys Leu Ile Leu Gly Ile Phe Xaa Val Leu Phe
          175          180          185
tgt ttt ggc ggt gat agg ctt acc tta cat taaaccaggc cttagccttt 973
Cys Phe Gly Gly Asp Arg Leu Thr Leu His
          190          195
ctgtggcttt gttatggcaa agcctcatat tactctctag tctgggttcag caggacagtc 1033
aggtccacac ctggggctgt ttgttttcta cgtttacctc aacataaggt accttatcat 1093
tgtcagcctt catctcctga tccaaaataa aataaaatgc cacaggtcaa aaaaaaaaaa 1153
aaaaa 1158

```

```

<210> 104
<211> 1563
<212> DNA
<213> Homo sapiens

```

<220>
 <221> CDS
 <222> 97..645

<220>
 <221> sig_peptide
 <222> 97..156
 <223> Von Heijne matrix
 score 8.42885652997473
 seq AVVGCLLVPPAEA/NK

<220>
 <221> misc_feature
 <222> 972
 <223> n=a, g, c or t

<400> 104
 aatagaagct aggagagggc ggggacaact gggctcttttg cggctgcagc gggctttag 60
 gtgtccggct ttgctggccc agcaagcctg ataagc atg aag ctc tta tct ttg 114
 Met Lys Leu Leu Ser Leu
 -20 -15
 gtg gct gtg gtc ggg tgt ttg ctg gtg ccc cca gct gaa gcc aac aag 162
 Val Ala Val Val Gly Cys Leu Leu Val Pro Ala Glu Ala Asn Lys
 -10 -5 1
 agt tct gaa gat atc cgg tgc aaa tgc atc tgt cca cct tat aga aac 210
 Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn
 5 10 15
 atc agt ggg cac att tac aac cag aat gta tcc cag aag gac tgc aac 258
 Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn
 20 25 30
 tgc ctg cac gtg gtg gag ccc atg cca gtg cct ggc cat gac gtg gag 306
 Cys Leu His Val Val Glu Pro Met Pro Val Pro Gly His Asp Val Glu
 35 40 45 50
 gcc tac tgc ctg ctg tgc gag tgc agg tac gag gag cgc agc acc acc 354
 Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr
 55 60 65
 acc atc aag gtc atc att gtc atc tac ctg tcc gtg gtg ggt gcc ctg 402
 Thr Ile Lys Val Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu
 70 75 80
 ttg ctc tac atg gcc ttc ctg atg ctg gtg gac cct ctg atc cga aag 450
 Leu Leu Tyr Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys
 85 90 95
 ccg gat gca tac act gag caa ctg cac aat gag gag gag aat gag gat 498
 Pro Asp Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp
 100 105 110
 gct cgc tct atg gca gca gct gct gca tcc ctc ggg gga ccc cga gca 546
 Ala Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
 115 120 125 130
 aac aca gtc ctg gag cgt gtg gaa ggt gcc cag cag cgg tgg aag ctg 594
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys Leu
 135 140 145
 cag gtg cag gag cag cgg aag aca gtc ttc gat cgg cac aag atg ctc 642
 Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys Met Leu
 150 155 160

```

agc tagatgggct ggtgtggttg ggtcaaggcc ccaacacccat ggctgccagc      695
Ser
ttccaggctg gacaaagcag ggggctactt ctcccttccc tcggttccag tcttcccttt      755
aaaagcctgt ggcatttttc ctcccttctcc ctaacttttag aaatgttgta cttggctatt      815
ttgattaggg aagaggggatg tgggtctctga tctctgttgt cttcttgggt ctttgggggt      875
gaagggaggg ggaaggcagg ccacasaagg aatggagaca ttcgaggcgg cctcaggagt      935
ggatgcatc ttgtctctcc tkggcctccc actcttngcc gccttccagc tctgagtctt      995
gggaatgttg ttacccttgg aagataaagy ctgggtcttc aggaactcag tgtctgggag     1055
gaaagcatgg ccagcattc agcatgtgtt cctttctgca gtggttctta tcaccacctc     1115
cctcccagcc ccagcgctc agccccagcc ccagctccag ccctgaggac agctctgatg     1175
ggagagctgg gccccctgag cccactgggt cttcagggtg cactggaagc tgggtgttcgc     1235
tgtcccctgt gcacttctcg cactggggca tggagtgcc atgcatactc tgctgccggt     1295
ccccctacct gcacttgagg ggtctgggca gtccctcctc tccccagtgt ccacagtcac     1355
tgagccagac ggtcggttg aacatgagac tcgaggctga gcgtggatct gaacaccaca     1415
gccctgtac ttgggttgcc tcttgtccct gaacttcgtt gtaccagtgc atggagagaa     1475
aattttgtcc tcttgtctta gagttgtgtg taaatcaagg aagccatcat taaattgttt     1535
tatttctctc taaaaaaaaa aaaaaaaaaa                                1563

```

```

<210> 105
<211> 1621
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 80..820

```

```

<220>
<221> sig_peptide
<222> 80..118
<223> Von Heijne matrix
      score 5.76690322882439
      seq MLVLRSAALTRALA/SR

```

```

<400> 105
acctttccac tcgggaaacc ttcagaggag tctcagaaag gacacggctg gctgcttttc      60
tcagcgccga agccgcgcc atg ctc gtc ctc aga agc gcc ctg act cgg gcg      112
                Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala
                        -10                                -5
ctg gcc tca cgg acg ctg gcg cct cag atg tgc tca tct ttt gct acg      160
Leu Ala Ser Arg Thr Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr
                1                                5                                10
gga ccc aga caa tac gat gga ata ttc tat gaa ttt cgt tct tat tac      208
Gly Pro Arg Gln Tyr Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr
15                20                25                30
ctt aag ccc tca aag atg aat gag ttc ctg gaa aat ttt gag aaa aac      256
Leu Lys Pro Ser Lys Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn
                35                40                45
gct cat ctt cgg aca gct cac tct gaa ttg gtt gga tac tgg agt gta      304
Ala His Leu Arg Thr Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val
                50                55                60
gaa ttt gga ggc aga atg aat aca gtg ttt cat att tgg aag tat gat      352
Glu Phe Gly Gly Arg Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp
        65                70                75

```

aat ttt gct cat cga act gaa gtt cag aaa gcc ttg gcc aaa gat aag	400
Asn Phe Ala His Arg Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys	
80 85 90	
gaa tgg caa gaa caa ttc ctc att cca aat ttg gct ctc att gat aaa	448
Glu Trp Gln Glu Gln Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys	
95 100 105 110	
caa gag agt gag att act tat ctg gta cca tgg tgc aaa tta gaa aaa	496
Gln Glu Ser Glu Ile Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys	
115 120 125	
cct cca aaa gaa gga gtc tat gaa ctg gcc act ttt cag atg aaa cct	544
Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro	
130 135 140	
ggg ggg cca gct ctg tgg ggt gat gca ttt aaa agg gca gtt cat gct	592
Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala	
145 150 155	
cat gtc aat cta ggc tac aca aaa cta gtt gga gtg ttc cac aca gag	640
His Val Asn Leu Gly Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu	
160 165 170	
tac gga gca ctc aac aga gtt cat gtt ctt tgg tgg aat gag agt gca	688
Tyr Gly Ala Leu Asn Arg Val His Val Leu Trp Trp Asn Glu Ser Ala	
175 180 185 190	
gat agt cgt gca gct ggg aga cat aag tcc cat gag gat ccc aga gtt	736
Asp Ser Arg Ala Ala Gly Arg His Lys Ser His Glu Asp Pro Arg Val	
195 200 205	
gtg gca gct gtt cgg gaa agt gtc aac tac cta gta tct cag cag aat	784
Val Ala Ala Val Arg Glu Ser Val Asn Tyr Leu Val Ser Gln Gln Asn	
210 215 220	
atg ctt ctg att cct aca tcg ttt tca cca ctg aaa tagttttcta	830
Met Leu Leu Ile Pro Thr Ser Phe Ser Pro Leu Lys	
225 230	
ctgaaataca aaacatttca ttaactgcta taggatctct ctgctaattgg tgcttaaatt	890
ctcccaagag gttctcactt ttatttgaag gaggtggtaa gttaatttgc tatgtttctt	950
gcattatgaa ggctacatct gtgctttgta agtaccactt caaaaaatag ttctgtttac	1010
tttctgcatg gtatttcagt gtctgtcata cattaaaaat acttgtcact gttttaagat	1070
cttgactctt catttgtttc agaatagctc ttctactgta ttctgacaac tctttgcttt	1130
atagcatttt gttgtattca aatgataatg gtagcatttc catgcttggtg acagcatttt	1190
taagttatta atatatttta tcaacctttc catcatgtct gttttcctgg ttttttttgg	1250
ttgttttttg accagtaaaa tttattttgt aataccaaat aggatttaag aaaattaacg	1310
tatttcttta ctatggaaaa ccacattgtc atttgtgaca tcatctatat taaatatggt	1370
tttcacatta gttatttgtc acttacttgg aaaatgatgc tgtttaggtcc tggattataa	1430
aatctagaaa agacttggtg gtttatgtgc tgaaatgtct ttatttataa ttaattttta	1490
ctactatttta ctttatttcg gatectgttt aacaaagata cttgagacat ccatttggtt	1550
taatgaaatc tgtatggata tggaaatgct tgccctaata aaagcctaca tatacaaaaa	1610
aaaaaaaaa a	1621

<210> 106

<211> 557

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 77..388

```

<220>
<221> sig_peptide
<222> 77..217
<223> Von Heijne matrix
      score 4.57105404339594
      seq FLYLTLNQSCIFA/NY

<400> 106
aacaccctcc ctggaccctc tgcctggagg acggggaatc acagcagctg gtttgggggtg      60
cctcccaaac caaaag atg ttc tct ccg cgc caa gct ttg acg ccc gac ccc      112
      Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro
      -45 -40
ctg cac tct ccc gcc tac tca ccg gtc cta ggg ggt tgg tcc cgc ttt      160
Leu His Ser Pro Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe
-35 -30 -25 -20
cgt agt gtg gat ttt cgt ttc ctc tac ttg act cta aat caa tcc tgt      208
Arg Ser Val Asp Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys
      -15 -10 -5
ata ttc gca aac tac aaa gag gcg cat gca aat aga tac tgt act gag      256
Ile Phe Ala Asn Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu
      1 5 10
ggc aga tac acg cgc gag atc cag agg ctt aca tcc cca gcc gct tgg      304
Gly Arg Tyr Thr Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp
      15 20 25
ccc acc aga gac aag aac agg atg ata agc aat gga atg gca ttg aac      352
Pro Thr Arg Asp Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn
      30 35 40 45
tct cct gct gaa gga ctt gca ttt caa tgt aga ttc tgaggctggg      398
Ser Pro Ala Glu Gly Leu Ala Phe Gln Cys Arg Phe
      50 55
tgaaaacttc tctgtcacct ttactacagc attctcaccc atttatatatt ctttcccctt      458
ctacatctct attactgttg cactatgtta tgcattacac catggcaaaa ttaatcaatt      518
aatacaataa aagcttaatt ttaaaaaaaaa aaaaaaaaaa      557

<210> 107
<211> 600
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 139..513

<220>
<221> sig_peptide
<222> 139..201
<223> Von Heijne matrix
      score 5.86857787719223
      seq IVMGVQVVGRAFA/RA

<400> 107
gaggcaatgc gcatgcccag cgccgtatcg cgcacgctct ctgcggcttt ccttgacctc      60
tgaccgcgcg accacgcttg atccccggcc gcggggccag gaagtcggag tttgagcccc      120
ggaggcagag cggctgcc atg gcc aag tac ctg gcc cag atc att gtg atg      171

```

	Met	Ala	Lys	Tyr	Leu	Ala	Gln	Ile	Ile	Val	Met	
	-20						-15					
ggc gtg cag gtg gtg ggc agg gcc ttt gca cgg gcc ttg cgg cag gag												219
Gly Val Gln Val Val Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu												
-10	-5						1			5		
ttt gca gcc agc cgg gcc gca gct gat gcc cga gga cgc gct gga cac												267
Phe Ala Ala Ser Arg Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His												
	10						15			20		
cgg tct gca gcc gct tcc aac ctc tcc ggc ctc agc ctc cag gag gca												315
Arg Ser Ala Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala												
	25						30			35		
cag cag att ctc aac gtg tcc aag ctg agc cct gag gag gtc cag aag												363
Gln Gln Ile Leu Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys												
	40						45			50		
aac tat gaa cac tta ttt aag gtg aat gat aaa tcc gtg ggt ggc tcc												411
Asn Tyr Glu His Leu Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser												
55							60			65		70
ttc tac ctg cag tca aag gtg gtc cgc gca aag gag cgc ctg gat gag												459
Phe Tyr Leu Gln Ser Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu												
	75						80			85		
gaa ctc aaa atc cag gcc cag gag gac aga gaa aaa ggg cag atg ccc												507
Glu Leu Lys Ile Gln Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro												
	90						95			100		
cat acg tgactgctcg gctcccccg cccaccccg cgcttctaatt ttatagcttg												563
His Thr												
gtaataaatt tcttttctac aaaaaaaaaa aaaaaaa												600

<210> 108
 <211> 1129
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 81..986

<220>
 <221> sig_peptide
 <222> 81..134
 <223> Von Heijne matrix
 score 5.03543461931947
 seq ITLLGLAVNVVTT/LV

<400> 108	
acagcgcggc gggcgtctcg ctgctcgagc cgccgctgca gctctactgg acctggctgc	60
tccagtggat cccgctctgg atg gcc ccc aac tcc atc acc ctg ctg ggg ctc	113
Met Ala Pro Asn Ser Ile Thr Leu Leu Gly Leu	
-15	-10
gcc gtc aac gtg gtc acc acg ctc gtg ctc atc tcc tac tgt ccc acg	161
Ala Val Asn Val Val Thr Thr Leu Val Leu Ile Ser Tyr Cys Pro Thr	
-5	1
gcc acc gaa gag gca cca tac tgg aca tac ctt tta tgt gca ctg gga	209
Ala Thr Glu Glu Ala Pro Tyr Trp Thr Tyr Leu Leu Cys Ala Leu Gly	
10	15
	20
	25

ctt ttt att tac cag tca ctg gat gct att gat ggg aaa caa gcc aga	257
Leu Phe Ile Tyr Gln Ser Leu Asp Ala Ile Asp Gly Lys Gln Ala Arg	
30 35 40	
aga aca aac tct tgt tcc cct tta ggg gag ctc ttt gac cat ggc tgt	305
Arg Thr Asn Ser Cys Ser Pro Leu Gly Glu Leu Phe Asp His Gly Cys	
45 50 55	
gac tct ctt tcc aca gta ttt atg gca gtg gga gct tca att gcc gct	353
Asp Ser Leu Ser Thr Val Phe Met Ala Val Gly Ala Ser Ile Ala Ala	
60 65 70	
cgc tta gga act tat cct gac tgg ttt ttt ttc tgc tct ttt att ggg	401
Arg Leu Gly Thr Tyr Pro Asp Trp Phe Phe Phe Cys Ser Phe Ile Gly	
75 80 85	
atg ttt gtg ttt tat tgc gct cat tgg cag act tat gtt tca ggc atg	449
Met Phe Val Phe Tyr Cys Ala His Trp Gln Thr Tyr Val Ser Gly Met	
90 95 100 105	
ttg aga ttt gga aaa gtg gat gta act gaa att cag ata gct tta gtg	497
Leu Arg Phe Gly Lys Val Asp Val Thr Glu Ile Gln Ile Ala Leu Val	
110 115 120	
att gtc ttt gtg ttg tct gca ttt gga gga gca aca atg tgg gac tat	545
Ile Val Phe Val Leu Ser Ala Phe Gly Gly Ala Thr Met Trp Asp Tyr	
125 130 135	
acg ggc acc agt gtc ttg tca cct gga ctc cac ata gga cta att att	593
Thr Gly Thr Ser Val Leu Ser Pro Gly Leu His Ile Gly Leu Ile Ile	
140 145 150	
ata ctg gca ata atg atc tat aaa aag tca gca act gat gtg ttt gaa	641
Ile Leu Ala Ile Met Ile Tyr Lys Lys Ser Ala Thr Asp Val Phe Glu	
155 160 165	
aag cat cct tgt ctt tat atc cta atg ttt gga tgt gtc ttt gct aaa	689
Lys His Pro Cys Leu Tyr Ile Leu Met Phe Gly Cys Val Phe Ala Lys	
170 175 180 185	
gtc tca caa aaa tta gtg gta gct cac atg acc aaa agt gaa cta tat	737
Val Ser Gln Lys Leu Val Val Ala His Met Thr Lys Ser Glu Leu Tyr	
190 195 200	
ctt caa gac act gtc ttt ttg ggg cca ggt ctt ttg ttt tta gac cag	785
Leu Gln Asp Thr Val Phe Leu Gly Pro Gly Leu Leu Phe Leu Asp Gln	
205 210 215	
tac ttt aat aac ttt ata gac gaa tat gtt gtt cta tgg atg gca atg	833
Tyr Phe Asn Asn Phe Ile Asp Glu Tyr Val Val Leu Trp Met Ala Met	
220 225 230	
gtg att tct tca ttt gat atg gtg ata tac ttt agt gct ttg tgc ctg	881
Val Ile Ser Ser Phe Asp Met Val Ile Tyr Phe Ser Ala Leu Cys Leu	
235 240 245	
caa att tca aga cac ctt cat cta aat ata ttc aag act gca tgt cat	929
Gln Ile Ser Arg His Leu His Leu Asn Ile Phe Lys Thr Ala Cys His	
250 255 260 265	
caa gca cct gaa cag gtt caa gtt ctt tct tca aag agt cat cag aat	977
Gln Ala Pro Glu Gln Val Gln Val Leu Ser Ser Lys Ser His Gln Asn	
270 275 280	
aac atg gat tgaagagact tccgaacact tgctatctct tgctgctgct	1026
Asn Met Asp	
gtttcatgga aggagatatt aaacatttgt ttaattttta tttaagtgtt atacctattt	1086
cagcaaataa aatatttcat tgcttgaaaa aaaaaaaaaa aaa	1129

<210> 109

<211> 778
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 266..586

<220>
 <221> sig_peptide
 <222> 266..307
 <223> Von Heijne matrix
 score 4.534746808071
 seq ILVTVPGVCPAQC/CW

<400> 109
 tagatgtag aattggtatt tgttcttgct ttttggttgc gatggagtta tataactaagt 60
 tacttatact aaggcattag tagtctcata tctgaggagc aattgtatatt ttagttcagc 120
 taaattaatg cctcttttta aatactaact tgtactactt ttgtggctgt gaatggtatc 180
 ttttattgaa ctgaggcagc ttttaaaaga cttgcctgat catttagagc actcccattg 240
 aggttaaatt agacttgaat ctgta atg att ctc gta act gtt cct ggt gtg 292
 Met Ile Leu Val Thr Val Pro Gly Val
 -10
 tgt cca gca caa tgt tgc tgg gca gag cag agg ggc aga ggc tca ggt 340
 Cys Pro Ala Gln Cys Cys Trp Ala Glu Gln Arg Gly Arg Gly Ser Gly
 -5 1 5 10
 atg tac ttc att gac aag tgg gca agg cca tcc tgg gta cca cat tgg 388
 Met Tyr Phe Ile Asp Lys Trp Ala Arg Pro Ser Trp Val Pro His Trp
 15 20 25
 ctt aat gat ctc ttc att gtg aag tcc ggc tac ctc gtt tgc ata aga 436
 Leu Asn Asp Leu Phe Ile Val Lys Ser Gly Tyr Leu Val Cys Ile Arg
 30 35 40
 act aca gta atc agg caa ggc att gtc aga att ggg agg aat aaa atc 484
 Thr Thr Val Ile Arg Gln Gly Ile Val Arg Ile Gly Arg Asn Lys Ile
 45 50 55
 agt gag tct gga agg agt gct ctg tat aca att gca aag aac aaa atg 532
 Ser Glu Ser Gly Arg Ser Ala Leu Tyr Thr Ile Ala Lys Asn Lys Met
 60 65 70 75
 gtc atc ttt aag gta cct gat tgc atg cac tta aat gca gat tat ttt 580
 Val Ile Phe Lys Val Pro Asp Cys Met His Leu Asn Ala Asp Tyr Phe
 80 85 90
 gga gtt tgaaaaggga ctattaatga aatctttctt ttccctcctt tctctttttc 636
 Gly Val
 ctttccccgc cactgattca gtgagctgga gattggatca cagccgaagg agtaaagggtg 696
 ctgcaatgat gttagctgtg gccactgtgg atttttcgca agaacattaa taaactaaaa 756
 acttcaaaaa aaaaaaaaaa aa 778

<210> 110
 <211> 1301
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 59..745

<220>

<221> sig_peptide

<222> 59..160

<223> Von Heijne matrix

score 5.94384548075359

seq LGAAALALLLANT/DV

<400> 110

attcaaaacc	aggctgaaga	ttggaaggaa	gttggccagc	ctcggctgca	ggacagaa		58
atg tct ttc ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc							106
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser							
	-30		-25		-20		
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc							154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Leu Ala							
	-15		-10		-5		
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac							202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr							
	1		5		10		
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc							250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe							
	15		20		25		30
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg							298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val							
	35		40		45		
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc							346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser							
	50		55		60		
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg							394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val							
	65		70		75		
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc							442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe							
	80		85		90		
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa							490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln							
	95		100		105		110
agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac							538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr							
	115		120		125		
aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga							586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly							
	130		135		140		
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga aag cag							634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln							
	145		150		155		
ggc att ctt ctt gag cac cga gaa aaa gaa ttt gga gac aaa gta aac							682
Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn							
	160		165		170		
cta ctt tct gtt ctg gaa gct gct aag atg atc aaa cca cag act ttg							730
Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu							
	175		180		185		190
gcc tca gag aaa aaa tgattgtgtg aaactgccca gctcagggat aaccagggac							785

Ala Ser Glu Lys Lys

195

attcacctgt	gttcatggga	tgtattgttt	ccactcgtgt	ccctaaggag	tgagaaaccc	845
atttatactc	tactctcagt	atggattatt	aatgtatttt	aatattctgt	ttagggccac	905
taaggcaaaa	tagcccaaaa	acaagactga	caaaaatctg	aaaaactaat	gaggattatt	965
aagctaaaaac	ctgggaaata	ggaggtttta	aattgactgc	caggctgggt	gcagtggctc	1025
acacctgtaa	tcccagcact	ttgggaggcc	aaggtgagca	agtcacttga	ggtcgggagt	1085
tcgagaccag	cctgagcaac	atggcgaaac	cccgtctcta	ctaaaaatac	aaaaatcacc	1145
cgggtgtggt	ggcaggcacc	tgtagtccca	gctacccggg	aggctgaggc	aggagaatca	1205
cttgaacctg	ggaggtggag	gttgcggtga	gctgagatca	caccactgta	ttccagcctg	1265
ggtgactgag	actctaacta	aaaaaaaaaa	aaaaaa			1301

<210> 111

<211> 1300

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 59..676

<220>

<221> sig_peptide

<222> 59..160

<223> Von Heijne matrix

score 5.94384548075359

seq LGAAALALLLANT/DV

<400> 111

attcaaaacc	aggctgaaga	ttggaaggaa	gttggccagc	ctcggctgca	ggacagaa	58
atg tct ttc ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc						106
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser						
	-30		-25		-20	
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc						154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Leu Ala						
	-15		-10		-5	
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac						202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr						
	1		5		10	
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc						250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe						
	15		20		25	30
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg						298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val						
	35		40		45	
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc						346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser						
	50		55		60	
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg						394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val						
	65		70		75	
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc						442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe						
	80		85		90	

aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa	490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln	
95 100 105 110	
agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac	538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr	
115 120 125	
aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga	586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly	
130 135 140	
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga agc agg	634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg	
145 150 155	
gca ttc ttc ttg agc acc gag aaa aag aat ttg gag aca aag	676
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys	
160 165 170	
taaacctact ttctgttctg gaagctgcta agatgatcaa accacagact ttggcctcag	736
agaaaaaatg attgtgtgaa actgcccagc tcagggataa ccagggacat tcacctgtgt	796
tcatgggatg tattgtttcc actcgtgtcc ctaaggagtg agaaacccat ttatactcta	856
ctctcagtat ggattattaa tgtatttttaa tattctgttt aggccacta aggcaaaata	916
gccccaaaac aagactgaca aaaatctgaa aaactaatga ggattattaa gctaaaacct	976
gggaaatagg aggtttaaaa ttgactgcca ggctgggtgc agtggctcac acctgtaac	1036
ccagcacttt gggaggccaa ggtgagcaag tcacttgagg tcgggagttc gagaccagcc	1096
tgagcaacat ggcgaaaccc cgtctctact aaaaatacaa aaatcacccg ggtgtggtgg	1156
caggcacctg tagtcccagc taccggggag gctgaggcag gagaatcact tgaacctggg	1216
aggtggaggt tgcggtgagc tgagatcaca ccactgtatt ccagcctggg tgactgagac	1276
tctaactaaa aaaaaaaaaa aaaa	1300

<210> 112

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 15..278

<220>

<221> sig_peptide

<222> 15..146

<223> Von Heijne matrix

score 12.2610572403264

seq PLFLLLLLLGSVTA/DI

<400> 112

gagaggagag gaga atg gcg gcg gaa ggc tgg att tgg cgt tgg ggc tgg	50
Met Ala Ala Glu Gly Trp Ile Trp Arg Trp Gly Trp	
-40 -35	
ggc cgg cgg tgc ctg gga agg cct ggg ctt ctc ggc ccc ggc cct ggc	98
Gly Arg Arg Cys Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly	
-30 -25 -20	
ccc act aca cct ctc ttt ctt ctt ttg ttg ttg ggg tct gtg act gcg	146
Pro Thr Thr Pro Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala	
-15 -10 -5	
gat ata act gac ggc aac att gaa cat ctc aag cgg gag cat tcg ctc	194


```

gcc tca aat ccc acc aac ctt gtc agc acc tcc caa agg cac cgg ccc      223
Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg His Arg Pro
                                -25                                -20                                -15
ttg ctt tca tcc tgt ggc ctc cca cca agc act gcc tca gct gtg cgc      271
Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser Ala Val Arg
                                -10                                -5                                1
agg cta tgc tcc agg gga gtg tta aaa gga tca aat gaa aga agg gat      319
Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu Arg Arg Asp
    5                                10                                15
atg gaa tca ttt tgg aaa cta aat cgt tcc cca ggg tcg gac cga tac      367
Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser Asp Arg Tyr
    20                                25                                30                                35
ctg gag agc cgc gat gcc tct cga ctg agt ggc cgg gac ccc tcc tca      415
Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp Pro Ser Ser
                                40                                45                                50
tgg aca gtc gag gat gtg atg cag ttt gtc cgg gaa gct gat cct cag      463
Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala Asp Pro Gln
                                55                                60                                65
ctt gga ccc cac gct gac ctg ttt cgc aaa cac gag atc gat ggc aag      511
Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile Asp Gly Lys
                                70                                75                                80
gcc ctg ctg ctg ctg cgc agt gac atg atg atg aag tac atg ggc ctg      559
Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr Met Gly Leu
    85                                90                                95
aag ctg ggg cct gca ctc aag ctc tcc tac cac att gac cgg ctg aag      607
Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp Arg Leu Lys
    100                                105                                110                                115
cag ggc aag ttc tgaaccagga gaggcagcct agacaaccaa gtggcagcag      659
Gln Gly Lys Phe
gtgggggcat tcttctagga atgaggggca tcagcccacc ccaggcacct cagtgggggtt      719
ccggggccacc tcaggactcc aagaggctgt gtggagccac cactcctagc cacagctgcc      779
atgataagtc cttccatgaa ggactgagga gggagagtgg ggggtccaggg ctggtgctgc      839
tcttccctca gctctgccgg ggctctaagg tccctctatt tatttctcaa ccctggctgg      899
cctctcacca ggagtttagg ctgaatgcct tccacgtgat ggaggaaaag gccaactctg      959
tctgtgtctt gctgtggcac cccatcgccc cacagctcgt accttctcac cagattcccc      1019
tgaatccaaa ctsgtgggtgc aaacctctac cttttttaca aaaagatctt attgttaatt      1079
tattgtttct ggcacttggg caaacctctgt agttaatact cctccccmac actagacact      1139
gggttttcagg aggagggaga ctgccctgct ttgggtcccca gagaggccct ctgcagatag      1199
gcgtggcccc tcttcagagg aactaccct agggcacttt ctctttgagg tggagagacc      1259
cataaagcct tgaccacatc actccatatg gggaggagaa ggatccctgt caccttctcc      1319
tctcttcacg gggccctttt gcagccctag gcctcatctg tgggaaggga gtccctggct      1379
tatactgccc ccaccacagc tccttgccct ggccagaact gctgtcgaag aaaatcaggc      1439
cggaaggcca agaaggcgct aagggggatg ggagggcagg ttttccaggc tggagtcggt      1499
tccaccact cgctgtcca caggcttctt tgtaagcaag tcagcagcac agctactcac      1559
gctgccatct ggacttattt tatgtcaatc tgtttataaa taaaaaccaa tataggtaaa      1619
aaaaaaaaaa aaaaaa
1634

```

<210> 114
 <211> 693
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 223..417

<220>

<221> sig_peptide

<222> 223..270

<223> Von Heijne matrix

score 4.19788230215007

seq LACVRESTSVAWA/CK

<400> 114

ttagggggcc	tgtcaccag	cacgtgcac	gggggctgtc	ccgggggtca	ggggagggag	60		
gccagcgggc	mgtgtcgggg	tccgccccga	ccccatccac	gaccccgact	cctatccgat	120		
cctatccccg	gccccgctcg	ggcctttccc	cttgcgccct	ggctcggctg	gctcgacgag	180		
cagtaagttc	gtagccgccc	tccgaagccg	ggcgtgcatg	gg atg gca	gag ttg	234		
				Met Ala Glu Leu				
				-15				
gcg tgc	gtg cgt	gag tcc	acc agt	gtg gca	tgg gca	tgt aag	gtg cgc	282
Ala Cys	Val Arg	Glu Ser	Thr Ser	Val Ala	Trp Ala	Cys Lys	Val Arg	
-10			-5			1		
gga ggg	act gca	cct tct	cca tca	ggg gca	gaa ggc	cac gtc	atg ctg	330
Gly Gly	Thr Ala	Pro Ser	Pro Ser	Gly Ala	Glu Gly	His Val	Met Leu	
5		10		15		20		
aac aag	agc cga	gaa gta	gaa tcg	cca gtg	tca agc	cgt cca	cgt tgt	378
Asn Lys	Ser Arg	Glu Val	Glu Ser	Pro Val	Ser Ser	Arg Pro	Arg Cys	
	25			30		35		
ggg atg	ccc act	gtt ccc	cca gga	tca ctc	aag acc	ctg tgact	tggtgg	427
Gly Met	Pro Thr	Val Pro	Pro Gly	Ser Leu	Lys Thr	Leu		
40			45					
tcactgatga	gtggaccaag	tgaagtccac	aagatggctg	ctgtggctcc	aggcatcacg	487		
tccacatgca	aatccatcca	gaggcaggaa	ctgggaatag	gcttggaggt	ggccaggaca	547		
gcaagtgggc	tgtctgtata	aacctcccct	ccacttggga	aggaaaatca	ccccccaagt	607		
cgatcttctg	tccatcttat	tgatcagaga	gcgttataaa	ttcacccatt	aaataatctg	667		
gacaagggga	aaaaaaaaaa	aaaaaa				693		

<210> 115

<211> 784

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 166..732

<220>

<221> sig_peptide

<222> 166..237

<223> Von Heijne matrix

score 6.60662787180923

seq KMVHLLVLSGAWG/MQ

<400> 115

attattgggt	gggggaaacc	cacgagggga	cgcgcccgag	gagggtcgct	gtccacccgg	60
gggcgtggga	gtgaggtacc	agattcagcc	catttggccc	cgacgcctct	gttctcggaa	120
tccgggtgct	gcgattgag	gtcccgggtc	ctaacggact	gcaag atg	gag gaa ggc	177


```

<400> 116
agtacggtgg ccgacgggag tcagacgctg gggatgaatg aaggtgctgg gtgcaggatc 60
aacaaacagt aata atg act gaa tgt aca agt ctt cag ttt gtc agc cct 110
          Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro
          -45          -40
ttt gct ttt gag gca atg cag aag gtg gat gtt gtt tgc ctg gca tct 158
Phe Ala Phe Glu Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser
-35          -30          -25          -20
tta agt gat cca gaa tta aga ctt ctt ctg ccc tgt ttg gta cgg atg 206
Leu Ser Asp Pro Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met
          -15          -10          -5
gca ctt tgt gca cct gct gac cag agc caa agc tgg gct cag gat aag 254
Ala Leu Cys Ala Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys
          1          5          10
aaa ctc atc ctt cgc ctt ctt tct gga gtg gaa gct gtc aac tcc att 302
Lys Leu Ile Leu Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile
          15          20          25
gtt gca ttg ttg tcc gtg gac ttt cat gct tta gaa caa gat gcc agc 350
Val Ala Leu Leu Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser
30          35          40          45
aaa gaa cag cag ctt aga ccg agt ctt gcc ctg ttg ccc agg ctg gag 398
Lys Glu Gln Gln Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu
          50          55          60
tgc ggt ggc gtg atc tcg gct cac tgc aac ctc cac ctc ctg ggt tca 446
Cys Gly Gly Val Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser
          65          70          75
agt gat tct tct gcc tca gtc tcc cga gta gat ggg act aca ggc acg 494
Ser Asp Ser Ser Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr
          80          85          90
cgc cac cat gcc cgg ctt ttt tgt att att agt aga gac gag gtt tca 542
Arg His His Ala Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser
95          100          105
cca tat tgg cca ggc tgg tct cga act ccc aac ctt gtg atc cac ctg 590
Pro Tyr Trp Pro Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu
110          115          120          125
cct cag cct ccc aaa gta ctg gga tta ccg gcg tgagccactg tgctggcct 643
Pro Gln Pro Pro Lys Val Leu Gly Leu Pro Ala
          130          135
atgtggtgga gtatttatta tacgtaggat gtgaatccct gaaatacaca ggcaaactaa 703
atagcatttc agaagtaaca gaacatttta gaacacttta tacatccttt tatagcttat 763
ttcaataaaa gataattttt atacaaaaaa aaaaaaaaaa a 804

```

```

<210> 117
<211> 484
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 30..335

```

```

<220>
<221> sig_peptide

```



```

<222> 30..71
<223> Von Heijne matrix
      score 4.49063834776683
      seq FLTALLWRGRIPG/RQ

<400> 117
gcagagtctt gagcagcgcg gcaggcacc atg ttc ctg act gcg ctc ctc tgg      53
                               Met Phe Leu Thr Ala Leu Leu Trp
                               -10
cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg cgg ccg      101
Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg Arg Pro
      -5              1              5              10
cgg ttc gtg tgc ttg cgc gcc aag cag aac atg atc cgc cgc ctg gag      149
Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg Leu Glu
              15              20              25
atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg acc cgg      197
Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met Thr Arg
              30              35              40
gag cag gag cgc ggc cac gcc gcg gtg cgc agg agg gag gcc ttc gag      245
Glu Gln Glu Arg Gly His Ala Ala Val Arg Arg Arg Glu Ala Phe Glu
      45              50              55
gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga ttc att      293
Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg Phe Ile
      60              65              70
gcg gac cag ctc gac cat ctc aat gtc acc aag aaa tgg tcc      335
Ala Asp Gln Leu Asp His Leu Asn Val Thr Lys Lys Trp Ser
      75              80              85
taatcctgag tcgtcacccct tggattttat ggatcacgga gctgaccatc tttacctggt      395
cctggaactg aaaaactgta gcttgtgtga aaatgagcct ttggaccagt ctttattaaa      455
acaaacaaac acaaaaaaaaa aaaaaaaaaa      484

<210> 118
<211> 985
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..752

<220>
<221> sig_peptide
<222> 21..107
<223> Von Heijne matrix
      score 3.61056351168286
      seq FPLYLLNFLGLWS/WI

<400> 118
gttttttttcc cttctgagca atg gag ctt acc atc ttt atc ctg aga ctg gcc      53
                               Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala
                               -25              -20
att tac atc ctg aca ttt ccc ttg tac ctg ctg aac ttt ctg ggc ttg      101
Ile Tyr Ile Leu Thr Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu
      -15              -10              -5

```

tgg agc tgg ata tgc aaa aaa tgg ttc ccc tac ttc ttg gtg agg ttc	149
Trp Ser Trp Ile Cys Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe	
1 5 10	
act gtg ata tac aac gaa cag atg gca agc aag aag cgg gag ctc ttc	197
Thr Val Ile Tyr Asn Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe	
15 20 25 30	
agt aac ctg cag gag ttt gcg ggc ccc tcc ggg aaa ctc tcc ctg ctg	245
Ser Asn Leu Gln Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu	
35 40 45	
gaa gtg ggc tgt ggc acg ggg gcc aac ttc aag ttc tac cca cct ggg	293
Glu Val Gly Cys Gly Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly	
50 55 60	
tgc agg gtg acc tgt att gac ccc aac ccc aac ttt gag aag ttt ttg	341
Cys Arg Val Thr Cys Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu	
65 70 75	
atc aag agc att gca gag aac cga cac ctg cag ttt gag cgc ttt gtg	389
Ile Lys Ser Ile Ala Glu Asn Arg His Leu Gln Phe Glu Arg Phe Val	
80 85 90	
gta gct gcc ggg gag aac atg cac cag gtg gct gat ggc tct gtg gat	437
Val Ala Ala Gly Glu Asn Met His Gln Val Ala Asp Gly Ser Val Asp	
95 100 105 110	
gtg gtg gtc tgc acc ctg gtg ctg tgc tct gtg aag aac cag gag cgg	485
Val Val Val Cys Thr Leu Val Leu Cys Ser Val Lys Asn Gln Glu Arg	
115 120 125	
att ctc cgc gag gtg tgc aga gtg ctg aga ccg gga ggg gct ttc tat	533
Ile Leu Arg Glu Val Cys Arg Val Leu Arg Pro Gly Gly Ala Phe Tyr	
130 135 140	
ttc atg gag cat gtg gca gct gag tgt tgc act tgg aat tac ttc tgg	581
Phe Met Glu His Val Ala Ala Glu Cys Ser Thr Trp Asn Tyr Phe Trp	
145 150 155	
caa caa gtc ctg gat cct gcc tgg cac ctt ctg ttt gat ggg tgc aac	629
Gln Gln Val Leu Asp Pro Ala Trp His Leu Leu Phe Asp Gly Cys Asn	
160 165 170	
ctg acc aga gag agc tgg aag gcc ctg gag cgg gcc agc ttc tct aag	677
Leu Thr Arg Glu Ser Trp Lys Ala Leu Glu Arg Ala Ser Phe Ser Lys	
175 180 185 190	
ctg aag ctg cag cac atc cag gcc cca ctg tcc tgg gag ttg gtg cgc	725
Leu Lys Leu Gln His Ile Gln Ala Pro Leu Ser Trp Glu Leu Val Arg	
195 200 205	
cct cat atc tat gga tat gct gtg aaa tagtgtgagc tggcaggttaa	772
Pro His Ile Tyr Gly Tyr Ala Val Lys	
210 215	
gagctgaatg gctcaaagaa tttaaagctt cagtgtttaca tttaaaatgc taggtgggtg	832
cctgtaatcc caggtacttg gaaggctgag gcaggagaat ctcttgaacc cagaaggcga	892
aggttgcagt gaaccgagat catgccattg tactctagcc tgggtgacaa gagcaagact	952
ccgtctcaaa aaaaaataaa aaaaaaaaaa aaa	985

<210> 119
 <211> 839
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 185..715

<220>

<221> sig_peptide

<222> 185..253

<223> Von Heijne matrix

score 9.49395175807817

seq SLLFICFFGESFC/IC

<400> 119

```
atattttgct gactggcaag gttatatgaa gtgcttttat tgaagcacca ttttaactaa      60
cagctcctgg tatttttctgc ttcccttcgt aggggaattta gttattttat tttattattt    120
agctaattta gctattttta aatagctaaa ttttagctac ttttttttca attgacaaaag    180
aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc      229
      Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile
                -20                -15                -10
tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca      277
Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr
                -5                1                5
aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa gtt      325
Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val
                10                15                20
aag ggt tct cca tct cac tgc ctg cct tat ctt ctg gat aaa cta tgc      373
Lys Gly Ser Pro Ser His Cys Leu Pro Tyr Leu Asp Lys Leu Cys
25                30                35                40
tgc gac ttt gct aac atg gat ata ttt cag ggt tgt tta tat ctc att      421
Cys Asp Phe Ala Asn Met Asp Ile Phe Gln Gly Cys Leu Tyr Leu Ile
                45                50                55
tat aat tta tta caa gct gtc ttc ttc gtc tta ttt gtt ttg tct gtg      469
Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe Val Leu Ser Val
                60                65                70
cat tac ctg tgg aag aaa tgg aag aaa cac caa aaa aag ctg aaa aag      517
His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys Lys Leu Lys Lys
                75                80                85
caa gcc tcc tta gaa aaa cct ggt aat gat cta gaa agc cca ttg atc      565
Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu Ser Pro Leu Ile
                90                95                100
aac aac att gac caa aca ctc cac aga gtg gca acc aca gca tca gtg      613
Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr Thr Ala Ser Val
105                110                115                120
ata tac aag atc tgg gag cac agg tct cac cat cct tcc tct aag aaa      661
Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro Ser Ser Lys Lys
                125                130                135
att aag cac tgc aaa tta aag aag aag agt aaa gaa gaa gga gcc aga      709
Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu Glu Gly Ala Arg
                140                145                150
aga tac taaataaatg catatgcaaa tgtagcttac tcaattatag atatcacaaa      765
Arg Tyr
agaaatctat catctaagga ttaaaaattg ttctttggaa acctttataa aaaaaaaaga      825
aaaaaaaaaa aaaa      839
```

<210> 120

<211> 583

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 54..527

<220>

<221> sig_peptide

<222> 54..116

<223> Von Heijne matrix

score 6.80928714315144

seq ALXSLNLAPPTVA/AP

<400> 120

```
aacgtcatct aggagcaccg agcagcttgg ctaaaagtaa ggggtgtcgtg ctg atg      56
                                         Met
gcc ctg tgc gca ctg acc cgc gct ctg ccs tct ctg aac ctg gcg ccc      104
Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala Pro
-20                               -15                               -10                               -5
ccg acc gtc gcc gcc cct gcc ccg agt ctg ttc ccc gcc gcc cag atg      152
Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln Met
                               1                               5                               10
atg aac aat ggc ctc ctc caa cag ccc tct gcc ttg atg ttg ctc ccc      200
Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu Pro
                               15                               20                               25
tgc cgc cca gtt ctt act tct gtg gcc ctt aat gcc aac ttt gtg tcc      248
Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val Ser
                               30                               35                               40
tgg aag agt cgt acc aag tac acc att aca cca gtg aag atg agg aag      296
Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg Lys
45                               50                               55                               60
tct ggg ggc cga gac cac aca ggt gct gga aac gtg cgt aga aca gta      344
Ser Gly Gly Arg Asp His Thr Gly Ala Gly Asn Val Arg Arg Thr Val
                               65                               70                               75
ggc cga gta tcc aac gtt gat cat aac aaa cgg gtc att ggc aag gca      392
Gly Arg Val Ser Asn Val Asp His Asn Lys Arg Val Ile Gly Lys Ala
                               80                               85                               90
ggg cgc aac cgc tgg ctg ggc aag agg cct aac agt ggg cgg tgg cac      440
Gly Arg Asn Arg Trp Leu Gly Lys Arg Pro Asn Ser Gly Arg Trp His
95                               100                               105
cgc aag ggg ggc tgg gct ggc cga aag att cgg cca cta ccc ccc atg      488
Arg Lys Gly Gly Trp Ala Gly Arg Lys Ile Arg Pro Leu Pro Pro Met
110                               115                               120
aag agt tac gtg aag ctg cct tct gct tct gcc caa agc tgatatacct      537
Lys Ser Tyr Val Lys Leu Pro Ser Ala Ser Ala Gln Ser
125                               130                               135
gtactctaataaaaatgccccccccccctcaaaaaaaaaa aaaaaa      583
```

<210> 121

<211> 1024

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
 <222> 129..686

<220>
 <221> sig_peptide
 <222> 129..185
 <223> Von Heijne matrix
 score 6.45239823575329
 seq SVFLLMVNGQVES/AQ

<400> 121
 cttcgcgaag gtgtcgtcgc caagaaacgt gtcctgcgcg ctacgccgtc tgtttctagg 60
 gcaacgccgg cgtctcttag caaccgcgcg cggcctagggt gggccccccc ggcacccccca 120
 gacctgcc atg gcg acc gcg agt cct agc gtc ttt cta ctc atg gtc aac 170
 Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn
 -15 -10
 ggg cag gtg gag agc gcc cag ttt cca gag tat gat gac ctc tac tgc 218
 Gly Gln Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys
 -5 1 5 10
 aag tac tgc ttt gtg tac ggc cag gac tgg gcc ccc aca gcg ggt ctg 266
 Lys Tyr Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu
 15 20 25
 gag gag ggg atc tca cag atc aca tcc aag agc caa gat gtg cgg caa 314
 Glu Glu Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln
 30 35 40
 gca ctg gtg tgg aac ttc ccc att gat gtc acc ttt aaa agc acc aac 362
 Ala Leu Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn
 45 50 55
 ccc tac ggc tgg cca cag atc gtg ctc agc gtg tat gga cca gat gtg 410
 Pro Tyr Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val
 60 65 70 75
 ttc ggg aac gat gtg gtt cga ggc tat ggg gcc gtg cac gtg ccc ttc 458
 Phe Gly Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe
 80 85 90
 tca cct ggc cgg cac aaa agg acc atc ccc atg ttt gtc cca gaa tct 506
 Ser Pro Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser
 95 100 105
 acg tct aaa ctg cag aag ttt aca agc tgg ttc atg ggg cgg cgg ccc 554
 Thr Ser Lys Leu Gln Lys Phe Thr Ser Trp Phe Met Gly Arg Arg Pro
 110 115 120
 gag tac aca gac ccc aag gtg gtg gct cag ggt gaa ggc cgg gaa gct 602
 Glu Tyr Thr Asp Pro Lys Val Val Ala Gln Gly Glu Gly Arg Glu Ala
 125 130 135
 atc aca gct ccc cgg aaa gct gtc ttc tct gtc cat ggc ctc acc tca 650
 Ile Thr Ala Pro Arg Lys Ala Val Phe Ser Val His Gly Leu Thr Ser
 140 145 150 155
 ccc agg gca ctg gcc ttg gtc cac atc aag ggg acc tgaagcttcc 696
 Pro Arg Ala Leu Ala Leu Val His Ile Lys Gly Thr
 160 165
 ctgaagcctc tagcctgtgg tgtgcacgta caagcctcag gccccatttg tccagcctgt 756
 cagcagctgg gaaataactaa gtcaccctct tctggttatg ttttaattttc caatttttct 816
 caacattact gaaatgtcta aatgtggaaa agttgacatc attttacagt gaacaccaca 876
 taccaccac ctagatttta ccattaccaa tttcctgttc cgtacttgta tattcacata 936
 tatccaacta ttcacccctg cttcaatcca tcctattttt attgcatttc aaaataaaact 996

gtgaaatcag gaaaaaaaaa aaaaaaaaa

1024

<210> 122
<211> 760
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 165..614

<220>
<221> sig_peptide
<222> 165..305
<223> Von Heijne matrix
score 5.10820788278539
seq ALGLALCSTKALS/VG

<400> 122
aatttccgat gccaggcacc ctcaaggcac agaggctggg gctcatgttg ggggcacttg 60
gcctctccag gcctcgaagg cttctcctgg gctgatgcga gctggggaac gggagggacg 120
gacgtgggag cgagaacgtc acactggagg cagctgggtg cacg atg ggg gac aga 176
Met Gly Asp Arg
-45
gtg aaa ggt agc aag tca aga gcc ttc gtg tca cca tgg cca cac acc 224
Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro Trp Pro His Thr
-40 -35 -30
ccg atg gct tcc ggc ttg agg gac ccc tgg ctg cag ccc aca gcc ctg 272
Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln Pro Thr Ala Leu
-25 -20 -15
ggc ctt gca ctg tgc tct acg aag gcc ctg tcc gtg ggc tct gcc cct 320
Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val Gly Ser Ala Pro
-10 -5 1 5
ttg ccc ccg cga aat tcc aac acc atg gcg gcg gct gcc ctg gct gcc 368
Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala Ala Leu Ala Ala
10 15 20
ccc agc ctg ggc ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc 416
Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr
25 30 35
agc ctc acg gac atg cac gtg gtg gat gta gag ctg agc gga ccc cgg 464
Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg
40 45 50
ggc ccc acg ggc cga agc ttt gct gtg cac acc cgc aga gag aac cct 512
Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro
55 60 65
gcc gag cca ggc gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg 560
Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp
70 75 80 85
cgg agc ctc ctg gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat 608
Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His
90 95 100
ctc tgc tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc 664
Leu Cys
accaccatcc caccctgcc ctgccccact tccccaggtg ctcccttctg actcagtaaa 724

gatcaccgct gcctccctca aaaaaaaaaa aaaaaa 760

<210> 123
<211> 594
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 192..476

<220>
<221> sig_peptide
<222> 192..326
<223> Von Heijne matrix
score 6.60884760057354
seq FILLLLLSGPAEM/SA

<400> 123
actttttattg aaaaagacta cagcaaataca tactgaggtg aatgaagaca gtgaaatgaa 60
ggagaaggca ggtcctcttt atgttttcgc agctggttca aggggttttg ggttttctat 120
ctagggttaa gattgcgtaa tacacagctg gagccataga cattaatgca tgtttatcac 180
acgcaacaac g atg ctg cat cat gtg att aca gct ggg cct gtg ctg ctt 230
Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu
-45 -40 -35
cta cac ctg cct cgc cct gac act tcc acc agg ttg ctg ctg acc tcc 278
Leu His Leu Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser
-30 -25 -20
gtc tct gct ttt atc ctg tta ctg ctg ctt tca gga cca gca gaa atg 326
Val Ser Ala Phe Ile Leu Leu Leu Leu Leu Ser Gly Pro Ala Glu Met
-15 -10 -5
tca gct tcc cag gaa tcc ttc cct gga tct ctg cag caa gaa ata gct 374
Ser Ala Ser Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala
1 5 10 15
tct ctg atc act gta gca ctt ggt tct tta ata tct tta tct tgc tct 422
Ser Leu Ile Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser
20 25 30
acc ttg tta tat ttt tct tgt gaa ctt aaa att ccc tgt gag gac gta 470
Thr Leu Leu Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val
35 40 45
aac ctt tgaaggatg tctcatatct ctgaacctct ttaaaatgcc tagcatccct 526
Asn Leu
50
gtgtgggtgc caattgcttg tgtattgaat taaattgtga ttgttaactt gaaaaaaaaa 586
aaaaaaaaa 594

<210> 124
<211> 559
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..297

```

<220>
<221> sig_peptide
<222> 16..93
<223> Von Heijne matrix
      score 6.65836819891491
      seq FCGSACLLAVIRA/FF

<400> 124
ttacacaggg gataa atg gca gca atc gag att gaa gtc aag cct aac cag      51
          Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln
          -25                -20                -15
ggc ttt tgc ggg agc gca tgc ctt ttg gct gta att cgt gca ttt ttt      99
Gly Phe Cys Gly Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe
          -10                -5                1
ttt aag aaa aac gcc tgc ctt ctg cgt gag att ctc cag agc aaa ctg      147
Phe Lys Lys Asn Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu
          5                10                15
ggc ggc atg ggc cct gtg gtc ttt tcg tac aga ggg ctt cct ctt tgg      195
Gly Gly Met Gly Pro Val Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp
          20                25                30
ctc ttt gcc tgg ttg ttt cca aga tgt act gtg cct ctt act ttc ggt      243
Leu Phe Ala Trp Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly
          35                40                45                50
ttt gaa aac atg agg ggg ttg ggc gtg gta gct tac gcc tgt aat ccc      291
Phe Glu Asn Met Arg Gly Leu Gly Val Val Ala Tyr Ala Cys Asn Pro
          55                60                65
agc act tagggaggcc gaggcgggag gatggcttga ggtccgtagt tgagaccagc      347
Ser Thr
ctggccaaca tgggtgaagcc tgggtctctac aaaaaaataa taacaaaaaat tagccgggtg      407
tgggtggctcg tgccctgtggt cccagctgct ccggtggctg aggcgggagg atctcttgag      467
cttaggcttt tgagctatca tggcgccagt gcactccagc gtgggcaaca gagcgagacc      527
ctgtctctca aaaacaaaaa aaaaaaaaaa aa                                559

<210> 125
<211> 744
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 216..635

<220>
<221> sig_peptide
<222> 216..335
<223> Von Heijne matrix
      score 4.38054120608596
      seq ITLVSAAPGKVIC/EM

<400> 125
gcttcgtcac aagggtgcga tgaaagtcag tgagcaaatc gcggaccacc ggggctgcc      60
gctcgctga ctcccgccct cttgcgtcc taggggcgga gaagggtgcg ggctcttcgc      120
cctttgtgtc ctctctcttt cactaacttc tggactttcc agctcttccg aagttcgttc      180

```



```

ttgcgcaaag cccaaaggct ggaaaaccgt ccacg atg acc agc atg act cag      233
                               Met Thr Ser Met Thr Gln
                               -40                               -35
tct ctg cgg gag gtg ata aag gcc atg acc aag gct cgc aat ttt gag      281
Ser Leu Arg Glu Val Ile Lys Ala Met Thr Lys Ala Arg Asn Phe Glu
                               -30                               -25                               -20
aga gtt ttg gga aag att act ctt gtc tct gct gct cct ggg aaa gtg      329
Arg Val Leu Gly Lys Ile Thr Leu Val Ser Ala Ala Pro Gly Lys Val
                               -15                               -10                               -5
att tgt gaa atg aaa gta gaa gaa gag cat acc aat gca ata ggc act      377
Ile Cys Glu Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr
                               1                               5                               10
ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata tca aca atg      425
Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met
                               15                               20                               25                               30
gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt gtc gat atg      473
Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met
                               35                               40                               45
aac ata acg tac atg tca cct gca aaa tta gga gaa gat ata gtg att      521
Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile
                               50                               55                               60
aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt acc tct gtg      569
Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val
                               65                               70                               75
gat ctg acc aac aag gcc aca gga aaa tta ata gca caa gga aga cac      617
Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His
                               80                               85                               90
aca aaa cac ctg gga aac tgagagaaca gcagaatgac ctaaagaaac      665
Thr Lys His Leu Gly Asn
                               95                               100
ccaacaatga atatcaagta tagatttgac tcaaacaatt gtaatttttg aaataaacta      725
gcaaaaaaaaa aaaaaaaaaa      744

<210> 126
<211> 824
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 164..280

<220>
<221> sig_peptide
<222> 164..268
<223> Von Heijne matrix
      score 5.73290676305402
      seq TLPLCPVTSPVWG/WS

<400> 126
tgtgttcaat cgtgtgaatg gccggcgggc cccctccacg tccccatcct tcgaggggac      60
ccaggagacc tacacagtgg ccacagagga gaatgtccgc tttgtgtccg aaggtagcga      120
gcgggggccag aggggtgcggc ataggctgct gggtcgcaaa acc atg gac ccg gga      175
                               Met Asp Pro Gly

```

```

                                -35
tgg ccc cac ttc aag ctg acc cac agc cgc tgc atg gct gtg ctt ttc      223
Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met Ala Val Leu Phe
      -30                -25                -20
ctt ggc act ctg ccc ttg tgt cct gtg acc agc cct gtg tgg ggc tgg      271
Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro Val Trp Gly Trp
      -15                -10                -5                1
agt cca ggg tgaccatcag gccctgggtg ggcgatgggg tgccctgggac      320
Ser Pro Gly
ctggctcagc ccgactgccc tcctcccaca gcctggcagc aggtgcaaca gcagctggat      380
gggtggcccag ccggtgaggg cgggcccaagg cctgtgcagt acgtggagag gacccccaat      440
ccccggctgc agaactttgt gccattttac ctgacgagt ggtgggcgca gcagttcctg      500
gcgagaatca ccagctgttc ctagtggctg ctgggagggg gcgctgctac acggccgacc      560
tgtcgccagg agagaagcat ggcgccttgc ccaccactg cgcttggtg ggtgccggcc      620
acacctgaag tgccagcatt tggacttttg cacctttttt tcccttggcc cggctgtccc      680
aaccaagctg ccatggccaa gggccgaacc cgtctgacct cagccctgct cactgtgccc      740
agggaccagc gaccagcccc tggggctggc agggaggagc tccaggctaa taaagtggag      800
aaactgtcaa aaaaaaaaaa aaaa      824

```

<210> 127
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..301

<220>
 <221> sig_peptide
 <222> 68..190
 <223> Von Heijne matrix
 score 4.68908216483476
 seq AYLLYILLTGALQ/FG

```

<400> 127
acatccggtg tggtcgacgg gtcctccaag agtttggggc gcggaccgga gtaccttgcg      60
tgcagtt atg tcg gcg tcg gta gtg tct gtc att tcg cgg ttc tta gaa      109
      Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu
            -40                -35                -30
gag tac ttg agc tcc act ccg cag cgt ctg aag ttg ctg gac gcg tac      157
Glu Tyr Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr
      -25                -20                -15
ctg ctg tat ata ctg ctg acc ggg gcg ctg cag ttc ggt tac tgt ctc      205
Leu Leu Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu
      -10                -5                1                5
ctc gtg ggg acc ttc ccc ttc aac tct ttt ctc tcg ggc ttc atc tct      253
Leu Val Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser
            10                15                20
tgt gtg ggg agt ttc atc cta gcg ggt tca ctc ttt gaa ttt cct gga      301
Cys Val Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly
      25                30                35
taagagttct ggagatggca gcttattgga cacatggatt ttcttcagat ttgcacttac      361
tgctagctct gctttttatg caggagaaaa gccagagtt cactgtgtgt cagaacaact      421

```

ttctaacaaa catttattaa tccagcctct gcctttcatt aaatgtaacc ttttgccttc 481
 caaattaaag aactccatgc cactcctcaa aaaaaaaaaa aaaaa 526

<210> 128
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 179..427

<220>
 <221> sig_peptide
 <222> 179..298
 <223> Von Heijne matrix
 score 7.72883276007822
 seq CLVVVMTATLSLA/RP

<400> 128
 aagcgaagag atgggtctgc actttggagg agccggacac tgttgacttt cctgatgtga 60
 aatctacca ggaacaaaac accagtgact gcagcagcag cggcagcgcc tcggttcctg 120
 agcccaccgc aggctgaagg cattgcgcgt agtccatgcc cgtagaggaa gtgtgcag 178
 atg gga tta acg tcc aca tgg aga tat gga aga gga ccg ggg att ggt 226
 Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
 -40 -35 -30 -25
 acc gta acc atg gtc agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc 274
 Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
 -20 -15 -10
 acc atg gca acc ttg tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag 322
 Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
 -5 1 5
 gat acc aca tta gag cca gaa gat gcc atc tca tcc gga gat gat gag 370
 Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
 10 15 20
 gat gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac aac 418
 Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
 25 30 35 40
 aag agt aag taactgccc gctccgatgg tccccgagag aggagcatgg 467
 Lys Ser Lys
 agggaagtgc tgctgtcac ctgtcttctt gtgcactctt ctgcgccatg ctgtgtcccc 527
 cggcccttgc ctttccccgc tgtgtctact ttctgtactt tcaaacctga gaataaacca 587
 gtgttgctgc acataaaaaa aaaaaaaaaa a 618

<210> 129
 <211> 776
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..297

<220>

<221> sig_peptide
 <222> 22..66
 <223> Von Heijne matrix
 score 4.68058603039206
 seq VLAGSLLGPTSRS/AA

<400> 129
 actgcgggac ccaactgcgga t atg gct gtc ttg gct gga tcc ctg ttg ggc 51
 Met Ala Val Leu Ala Gly Ser Leu Leu Gly
 -15 -10
 ccc acg agt agg tcg gca gcg ttg ctg ggt ggc agg tgg ctc cag ccc 99
 Pro Thr Ser Arg Ser Ala Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro
 -5 1 5 10
 cgg gcc tgg ctg ggg ttc cca gac gcc tgg ggc ctc ccc acc ccg cag 147
 Arg Ala Trp Leu Gly Phe Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln
 15 20 25
 cag gcc cgg ggc aag gct cgc ggg aat gag tat cag ccg agc aat atc 195
 Gln Ala Arg Gly Lys Ala Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile
 30 35 40
 aaa cgc aag aac aag cac ggc tgg gtc cgg cgc ctg agc acg ccg gcc 243
 Lys Arg Lys Asn Lys His Gly Trp Val Arg Arg Leu Ser Thr Pro Ala
 45 50 55
 ggc gtg cag gtc atc ctt cgc cga atg ctc aag ggc cgc aag tcg ctg 291
 Gly Val Gln Val Ile Leu Arg Arg Met Leu Lys Gly Arg Lys Ser Leu
 60 65 70 75
 agc cat tgaggatcgc gacgcagtcg gcggggaccc tcatggaagc atcgccctcg 347
 Ser His
 cctcggacct tgccctggcgc tttttttgca gggagctggg gagcaggaac gcctcggacc 407
 tgagtgtctct ccatattgtg ggtttgaagt ctggatggga gccttgccaa gtcccttttt 467
 aggctttttta attaggaagc atttcgaacc tgcgcaacag accaaagaac agtaciaaaga 527
 acatccgtgt acccagtacc ctgactaccg actacctaca acccgctccct gccccatcct 587
 gagttctttt gaagctgatc tcaggcatcg gattattttct tctgtaaata tttcagaatg 647
 tatctctcca agatgagagc tcattaaaag ataattacaa agcttatcac atccaaaaga 707
 attatcaata attttgaaat attattaaac gtgtaataaa tgttcaaagt tcaaaaaaaaa 767
 aaaaaaaaa 776

<210> 130
 <211> 998
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 9..845

<220>
 <221> sig_peptide
 <222> 9..134
 <223> Von Heijne matrix
 score 6.13963522287438
 seq RSLALAAAPSSNG/SP

<400> 130
 aacgaaag atg gcg gcg ccc gta agg cgg acg ctg tta ggg gtg gcg ggg 50

Met Ala Ala Pro Val Arg Arg Thr Leu Leu Gly Val Ala Gly																	
				-40				-35				-30					
ggt	tgg	cgg	cgg	ttc	gag	agg	ctc	tgg	gcc	ggc	agt	cta	agc	tct	cgc	98	
Gly	Trp	Arg	Arg	Phe	Glu	Arg	Leu	Trp	Ala	Gly	Ser	Leu	Ser	Ser	Arg		
				-25				-20				-15					
agc	ctg	gct	ctt	gca	gcc	gca	ccc	tca	agc	aac	gga	tcc	cca	tgg	cgc	146	
Ser	Leu	Ala	Leu	Ala	Ala	Ala	Pro	Ser	Ser	Asn	Gly	Ser	Pro	Trp	Arg		
				-10				-5				1					
ttg	ttg	ggc	gcg	ttg	tgc	ctg	cag	cgg	cca	cct	gta	gtc	tcc	aag	ccg	194	
Leu	Leu	Gly	Ala	Leu	Cys	Leu	Gln	Arg	Pro	Pro	Val	Val	Ser	Lys	Pro		
5					10				15				20				
ttg	acc	cca	ttg	cag	gaa	gag	atg	gcg	tct	cta	ctg	cag	cag	att	gag	242	
Leu	Thr	Pro	Leu	Gln	Glu	Glu	Met	Ala	Ser	Leu	Leu	Gln	Gln	Ile	Glu		
				25				30				35					
ata	gag	aga	agc	ctg	tat	tca	gac	cac	gag	ctt	cgt	gct	ctg	gat	gaa	290	
Ile	Glu	Arg	Ser	Leu	Tyr	Ser	Asp	His	Glu	Leu	Arg	Ala	Leu	Asp	Glu		
				40				45				50					
aac	cag	cga	ctg	gca	aag	aag	aaa	gct	gac	ctt	cat	gat	gaa	gaa	gat	338	
Asn	Gln	Arg	Leu	Ala	Lys	Lys	Lys	Ala	Asp	Leu	His	Asp	Glu	Glu	Asp		
				55				60				65					
gaa	cag	gat	ata	ttg	ctg	gcg	caa	gat	ttg	gaa	gat	atg	tgg	gag	cag	386	
Glu	Gln	Asp	Ile	Leu	Leu	Ala	Gln	Asp	Leu	Glu	Asp	Met	Trp	Glu	Gln		
				70				75				80					
aaa	ttt	cta	cag	ttc	aaa	ctt	gga	gct	cgc	ata	aca	gaa	gct	gat	gaa	434	
Lys	Phe	Leu	Gln	Phe	Lys	Leu	Gly	Ala	Arg	Ile	Thr	Glu	Ala	Asp	Glu		
85					90				95				100				
aag	aat	gac	cga	aca	tcc	ctg	aac	agg	aac	cta	gac	agg	aac	ctt	gtc	482	
Lys	Asn	Asp	Arg	Thr	Ser	Leu	Asn	Arg	Asn	Leu	Asp	Arg	Asn	Leu	Val		
				105				110				115					
ctg	tta	gtc	aga	gag	aag	ttt	gga	gac	cag	gat	gtt	tgg	ata	ctg	ccc	530	
Leu	Leu	Val	Arg	Glu	Lys	Phe	Gly	Asp	Gln	Asp	Val	Trp	Ile	Leu	Pro		
				120				125				130					
cag	gca	gag	tgg	cag	cct	ggg	gag	acc	ctt	cga	gga	aca	gct	gaa	cga	578	
Gln	Ala	Glu	Trp	Gln	Pro	Gly	Glu	Thr	Leu	Arg	Gly	Thr	Ala	Glu	Arg		
				135				140				145					
acc	ctg	gcc	aca	ctc	tca	gaa	aac	aac	atg	gaa	gcc	aag	ttc	cta	gga	626	
Thr	Leu	Ala	Thr	Leu	Ser	Glu	Asn	Asn	Met	Glu	Ala	Lys	Phe	Leu	Gly		
				150				155				160					
aat	gca	ccc	tgt	ggg	cac	tac	aca	ttc	aag	ttc	ccc	cag	gca	atg	cgg	674	
Asn	Ala	Pro	Cys	Gly	His	Tyr	Thr	Phe	Lys	Phe	Pro	Gln	Ala	Met	Arg		
165					170				175				180				
aca	gag	agt	aac	ctc	gga	gcc	aag	gtg	ttc	ttc	ttc	aaa	gca	ctg	cta	722	
Thr	Glu	Ser	Asn	Leu	Gly	Ala	Lys	Val	Phe	Phe	Phe	Lys	Ala	Leu	Leu		
				185				190				195					
tta	act	gga	gac	ttt	tcc	cag	gct	ggg	aat	aag	ggc	cat	cat	gtg	tgg	770	
Leu	Thr	Gly	Asp	Phe	Ser	Gln	Ala	Gly	Asn	Lys	Gly	His	His	Val	Trp		
				200				205				210					
gtc	att	aag	gat	gag	ctg	ggt	gac	tat	ttg	aaa	cca	aaa	tac	ctg	gcc	818	
Val	Ile	Lys	Asp	Glu	Leu	Gly	Asp	Tyr	Leu	Lys	Pro	Lys	Tyr	Leu	Ala		
				215				220				225					
caa	gtt	agg	agg	ttt	gtt	tca	gac	ctc	tgatggg	cgc	agctgcctgt					865	
Gln	Val	Arg	Arg	Phe	Val	Ser	Asp	Leu									
				230				235									
ggacggtgct	cagacaagtc	tgaggattaga	gcctcaagga	cattgtgtga	ttgcctcaca											925	

tttgcaggta atatcaagca gcaaactaaa ttctgagaaa taaacgagtc tattaccaaa 985
 aaaaaaaaaa aaa 998

<210> 131
 <211> 779
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..578

<220>
 <221> sig_peptide
 <222> 27..119
 <223> Von Heijne matrix
 score 4.50637135496675
 seq TALMVGAASLLEG/RP

<400> 131
 atctttctgg actggccctg cagagg atg gca tgc acc act act gcc ccc gcc 53
 Met Ala Cys Thr Thr Thr Ala Pro Ala
 -30 -25
 cag gaa cac atg ctt ctc acc cct ctc act gct ctg atg gtg ggg gct 101
 Gln Glu His Met Leu Leu Thr Pro Leu Thr Ala Leu Met Val Gly Ala
 -20 -15 -10
 gct tct ctg ctt gag ggc cgg cca cag atc tca gct cca tac tcc cga 149
 Ala Ser Leu Leu Glu Gly Arg Pro Gln Ile Ser Ala Pro Tyr Ser Arg
 -5 1 5 10
 gct gca tgt tgc agc cct ggg gca ctg gga tgt cct gca gct cgg gtt 197
 Ala Ala Cys Cys Ser Pro Gly Ala Leu Gly Cys Pro Ala Ala Arg Val
 15 20 25
 ggg att ctg gat ctg atg tat tcc tgg gtt gcc agg aaa gtg ctc agg 245
 Gly Ile Leu Asp Leu Met Tyr Ser Trp Val Ala Arg Lys Val Leu Arg
 30 35 40
 tgc agc aat act ggg ctg cag ggg ctg cac tgt gca cca gct tat gca 293
 Cys Ser Asn Thr Gly Leu Gln Gly Leu His Cys Ala Pro Ala Tyr Ala
 45 50 55
 gca cag ctt ggt atg gac cct ggg agg ggc caa cga gca gga ggg cct 341
 Ala Gln Leu Gly Met Asp Pro Gly Arg Gly Gln Arg Ala Gly Gly Pro
 60 65 70
 gta gag cag aca tac ttc agt ccc atg ggg aag ctg ccc act ctt tcg 389
 Val Glu Gln Thr Tyr Phe Ser Pro Met Gly Lys Leu Pro Thr Leu Ser
 75 80 85 90
 tgg ctg gaa ggc tgt aca gca gtc atg acg ctg gca tct gct tgg ctt 437
 Trp Leu Glu Gly Cys Thr Ala Val Met Thr Leu Ala Ser Ala Trp Leu
 95 100 105
 ctg ggg agc cct cgg gaa act tac aat cat gag aag gtg aag gag aag 485
 Leu Gly Ser Pro Arg Glu Thr Tyr Asn His Glu Lys Val Lys Glu Lys
 110 115 120
 cag tgt cca ttc tcc agt atg gtt ttg ggg gag tat ggc ttc cta cct 533
 Gln Cys Pro Phe Ser Ser Met Val Leu Gly Glu Tyr Gly Phe Leu Pro
 125 130 135
 act gtg gac cac ctg tca act ctg ggc tgt aac atg aga gaa ttg 578

Thr	Val	Asp	His	Leu	Ser	Thr	Leu	Gly	Cys	Asn	Met	Arg	Glu	Leu		
140						145					150					
tgaacttctg	tcttgtttga	gccatggttt	cattctcttt	ttcagccatg	tagcctgtgc										638	
tgtaactcag	taccacatta	gcaactagtg	aaagtcaatg	tgggtaaatt	tgtcattctt										698	
caggtagaa	catttcttcc	ttttattctt	gtgttttttg	ctaaataaac	tgggaaatta										758	
tagtaaaaaa	aaaaaaaaa	a													779	

<210> 132
 <211> 1025
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 408..710

<220>
 <221> sig_peptide
 <222> 408..533
 <223> Von Heijne matrix
 score 5.66440183652506
 seq QLCFHLISWLYSWA/SQ

<400> 132																
atggtttgtt	gtgagttcca	tgtcctcttg	gatcagtcac	tgtggccatg	catgtttggc										60	
cacatgatta	atccagtctg	ggtcatgacc	ttttcttcat	ccaaaacaag	gtgatgggaa										120	
gacaaaaaca	atagctacta	caaacaatag	gagtttataa	ttatgtgctg	atgtattcga										180	
agatgtgttg	acagtcgtga	gtgtgtatcc	taggaaaggc	gagctggact	ctgtctccat										240	
ggtggctctc	accccagggg	cctaggaaca	gcctgtcacc	acacaattac	ttttataacc										300	
ctggagatga	aaatctcctt	gtcctcaaaa	tacttccaga	agaacaacca	gatgggaagg										360	
accttggttg	ggactctttc	cagttcactt	ggggcagagg	gaatttta	atg gct cac										416	
					Met Ala His											
					-40											
gta gct gaa aag gat ggg cta gat tgg gct tca ggc tgc atc cca gga															464	
Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys Ile Pro Gly																
	-35			-30				-25								
ctc caa aca ggg atc tgt ctc ttt ggc tct cag ctc tgc ttt cat ttg															512	
Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys Phe His Leu																
	-20			-15				-10								
agt tgg ctt tat tct tgg gct tca cag tgt ggc ccc aca gca cca gtt															560	
Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr Ala Pro Val																
	-5			1				5								
att gat aaa aag agc tcc cct ttg ctg aca gaa ctg ctg gat ttg gtt															608	
Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu Asp Leu Val																
10		15				20			25							
ctc att ggt cca gac gag gaa ggt atc cag cct caa gtc atc att gtg															656	
Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val Ile Ile Val																
	30			35				40								
gcc agg aag atg gaa tac acc aaa tgg aca ggc ctg gca tgt acc cac															704	
Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala Cys Thr His																
	45			50				55								
aga gac tgagagttgg tgctggtggt tgtggtggca gatgatatta cctgaagaag															760	
Arg Asp																
ggacgaatgg gtgctgggca ggacaaagca tcagctgtcc agttcaggcc tctcctcttt															820	

ccctggtgtc	ttcattttcc	tccgtctccc	tgtgtgccct	taccctctgc	ccaatctcat	880
tactcctggt	cttgggagtt	gccttctgag	gatactccac	tgggggtacc	tgagcctgga	940
ttagagggca	gggggaggat	attgcctagc	caaagtgggt	gttcaataaa	gaaccatttg	1000
gagatggcaa	aaaaaaaaaa	aaaaa				1025

<210> 133
 <211> 607
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 247..501

<220>
 <221> sig_peptide
 <222> 247..306
 <223> Von Heijne matrix
 score 6.43040298500966
 seq LLLVTLVASTVPG/NS

<400> 133	
tgttacaaat attccctatg atctctcctt taaatattct tadcaggata ttggaaattc	60
ttgattttca caactctgct tcagtggcat atgttttagct ttttgtcttc tgaattaatt	120
gggcttctga tggtccttag aggtatcagc tactcagtca gaaaacatac atggggaaga	180
aactgaagtt catgccacaa actgtagcag ctttgggaaca gaagggacca gacaacctca	240
aggaga atg ggc cca aat acc aaa aat tta ctc ttg gtg acc ctt gtt	288
Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val	
-20 -15 -10	
gct tct act gta cca ggc aac tct ctt ggg cag gat ttt act ttt gca	336
Ala Ser Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala	
-5 1 5 10	
cac tta gaa aga tcc tgc acc agg gaa aat cgg tct cct ggg gag gta	384
His Leu Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val	
15 20 25	
ttc cag caa cca tgc aag tct gga ggc ggg ggg gtt gga gaa cca aat	432
Phe Gln Gln Pro Cys Lys Ser Gly Gly Gly Gly Val Gly Glu Pro Asn	
30 35 40	
gcc caa ggg cag cta ctt agc cag cac cca cta cct gcc ttc att aat	480
Ala Gln Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn	
45 50 55	
tgt tct cac ggg cag gcc ttt tgaaccaccc tggtacagaa caccaaccct	531
Cys Ser His Gly Gln Ala Phe	
60 65	
ggtgcttttag gctgtctgtg ccatttctag gcaatgaacg agtagttact gtaccaaccc	591
aaaaaaaaaa aaaaaa	607

<210> 134
 <211> 774
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 333..602

<220>

<221> sig_peptide

<222> 333..416

<223> Von Heijne matrix

score 4.79986448293481

seq VPALPLLSSLCMA/MV

<400> 134

```
ctcttcagtc cggggccttg ttgaacggac tcaccaggaa acgtgacttt cgtgtccgac      60
ctctgctgta tcaggattcg attcttggtg ttaaacaaga caacgctgaa ggctcggtgc      120
agcagccctg caaaggtttt tccagcgctc ttgggaggtg ggctgtgccc tgccctggccc      180
acctggccca cctggcccac cattacctga agggaagcat gaacagcctt tgacgtggga      240
gtggcgactg ctgagaggga actgtctgta cacaagcaat gtagccttat gggacctgag      300
tggagcccca acccacgcag ggcgtgktct tc atg gct ttt cct ggc caa tct      353
                               Met Ala Phe Pro Gly Gln Ser
                               -25

gat acc aag atg cag tgg cca gaa gta cct gca ctt cca ctc ctg tca      401
Asp Thr Lys Met Gln Trp Pro Glu Val Pro Ala Leu Pro Leu Leu Ser
-20                               -15                               -10

agt ctc tgc atg gct atg gtg agg aag agc tct gca ctg ggc aag gaa      449
Ser Leu Cys Met Ala Met Val Arg Lys Ser Ser Ala Leu Gly Lys Glu
-5                               1                               5                               10

gtt ggc cgt cga gtg aag gaa atg gtg atg ctg gtg gcc cct ttc cgg      497
Val Gly Arg Arg Val Lys Glu Met Val Met Leu Val Ala Pro Phe Arg
15                               20                               25

cag tca agt tcc cta tca agg aca ttc agt tct cgg aaa gtg gtg aag      545
Gln Ser Ser Ser Leu Ser Arg Thr Phe Ser Ser Arg Lys Val Val Lys
30                               35                               40

gca cat gct tcc ctg cat ggt gcc cgc ctc tct cca ctc tct aga aat      593
Ala His Ala Ser Leu His Gly Ala Arg Leu Ser Pro Leu Ser Arg Asn
45                               50                               55

att aga ggc taggctgctg ctgtatgtca gggctagtcc ctcttctatg      642
Ile Arg Gly
60

aatccagaat aactctgaag aagccgagta acaggcatga agtgaagaga aatcgctgta      702
acaggaagac agcaaagcag atgctaataa ccacactatt taacgaactg gaaccaacaa      762
aaaaaaaaaa aa      774
```

<210> 135

<211> 611

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 110..376

<220>

<221> sig_peptide

<222> 110..208

<223> Von Heijne matrix

score 3.64796206065748

seq LVPHSPLPGALSS/AP

<220>

<221> misc_feature

<222> 347

<223> n=a, g, c or t

<400> 135

```
tcttgtcaac actgcccact cagcgaggaa gcagccgcga cgccacact tcctgttga      60
gcctgcgag agccagaggc ctcagaagcc acaggaacat ggcctaggc atg gct cag      118
                                     Met Ala Gln
cca gca gcc ccc tcc ctg acg cgg ccc ttc ctg gca gag gcc ccg aca      166
Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu Ala Pro Thr
-30                               -25                -20                -15
gca ctg gtc cca cac agc ccc ctg cct ggg gcc ctg tca agc gcc cct      214
Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser Ser Ala Pro
                               -10                -5                1
ggc ccg aag cag ccc ccg acg gca agc aca ggc ccg gag ctg ctg ctg      262
Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu Leu Leu Leu
                               5                10                15
ctg cct ctt tcc tcc ttc atg ccc tgc ggg gcg gct gca cca gcc agg      310
Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala Pro Ala Arg
                               20                25                30
gtg tca tca cag cgg gct act cct agg gat aag ccc ncc ggt ccc ctc      358
Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa Gly Pro Leu
35                               40                45                50
atc cct ggc cag tgt ccc tgacccccat ctactccttc ctggggactt      406
Ile Pro Gly Gln Cys Pro
                               55
ctcagcgcca gccattggc gctgcggtg cccgcattcca ggccctgcg caggccctgt      466
gctagcgtgt tcgcaccagg aacgcaggtg ctgggctgtc ggggaggcct caggccacct      526
ccaggaacag aacacagttt taagtttgat tttttttatt tcaaaatgct ttgcaattaa      586
atgaattact gttcaaaaaa aaaaaa      611
```

<210> 136

<211> 925

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 22..417

<220>

<221> sig_peptide

<222> 22..66

<223> Von Heijne matrix
score 5.47092708754574
seq RVLCPAAGAVRA/LR

<400> 136

```
agtcgaggag tcaaggcagc a atg aat cgt gtc ttg tgt gcc ccg gcg gcc      51
                                     Met Asn Arg Val Leu Cys Ala Pro Ala Ala
                                     -15                -10
```

```

ggg gcc gtc cgg gcg ctg agg ctc ata ggc tgg gct tcc cga agc ctt      99
Gly Ala Val Arg Ala Leu Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu
-5                               1                               5                               10
cat ccg ttg ccc ggt tcc cgg gat cgg gcc cac cct gcc gcc gag gaa      147
His Pro Leu Pro Gly Ser Arg Asp Arg Ala His Pro Ala Ala Glu Glu
                               15                               20                               25
gag gac gac cct gac cgc ccc att gag ttt tcc tcc agc aaa gcc aac      195
Glu Asp Asp Pro Asp Arg Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn
                               30                               35                               40
cct cac cgc tgg tgc gtg ggc cat acc atg gga aag gga cat cag cgg      243
Pro His Arg Trp Ser Val Gly His Thr Met Gly Lys Gly His Gln Arg
                               45                               50                               55
ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg atc      291
Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu Ile
60                               65                               70                               75
atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg aga      339
Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg
                               80                               85                               90
cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag cct      387
Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro
                               95                               100                               105
gag act cca gct gcc tac aga gcg aga act tgacggggtg cccgctgggg      437
Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr
                               110                               115
ctggcaggaa gggagccgac agccgccctt cggatttgat gtcacgtttg cccgtgactg      497
tcctggctat gcgtgcgtcc tcagactga aggacttgcc tggtggtatgg ggcacttgcc      557
tatgctgatt cgcgtgaagg cggagcagaa tctcagcaga tcggaaactg ctccctgcct      617
ggctcttgat gtccaaggat tccatcggca agacttctca gatccttggg gaaggtttca      677
gttgactgt atgctgttgg atttgccaag tctttgtata acataatcat gtttccaaag      737
cacttctggt gacacttgtc atccagtgtt agtttgcagg taatttgctt tctgagatag      797
aatatctggc agaagtgtga aactgtattg catgctgcgg cctgtgcaag gaacacttcc      857
acatgtgagt ttacacaac aacaaatgaa aataaatttt aattttataa taacacacac      917
aaaaaaaaa                                925

<210> 137
<211> 674
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..367

<220>
<221> sig_peptide
<222> 62..103
<223> Von Heijne matrix
      score 4.49063834776683
      seq FLTALLWRGRIPG/RQ

<400> 137
acgccacggc gtctgctggc ggccgcggag acgcagagtc ttgagcagcg cggcaggcac      60
c atg ttc ctg act gcg ctc ctc tgg cgc gcc cgc att ccc gcc cgt cag      109
Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln

```

	-10	-5	1	
tgg atc ggg aag cac cgg cgg ccg cgg ttc gtg tgc ttg cgc gcc aag				157
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys				
5 10 15				
cag aac atg atc cgc cgc ctg gag atc gat gcg gag aac cat tac tgg				205
Gln Asn Met Ile Arg Arg Leu Glu Ile Asp Ala Glu Asn His Tyr Trp				
20 25 30				
ctg agc atg ccc tac atg acc cgg gag cag gag cgc ggc cac gcc gsg				253
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa				
35 40 45 50				
dtg cgc agg agg gag gcc ttc gag gcc ata aag gcg gcc gcc act tcc				301
Xaa Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser				
55 60 65				
aag ttc ccc ccg cat aga ttc att gcg gac cag ctc gac cat ctc aat				349
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn				
70 75 80				
gtc acc aag aaa tgg tcc taatcctgag tagtcaccct tggattttat				397
Val Thr Lys Lys Trp Ser				
85				
ggatcacgga gctgaccatc tttacctggt cctggaactg aaaaactgta gcttgtgtga				457
aaatgagcct ttggaccagt ctttattaaa acaaacaaac atgagtagtc tgcataatcga				517
atatctagag ctctaaaccc cccaataactt aaaagtctaa ttgctgtcct gtggtttcat				577
tagtctgata ggaagatagg gatttcctca gtcacagatg atattttgaa ggaaagctgc				637
aataaagcca caatgattcg aaaaaaaaaa aaaaaaa				674

<210> 138
 <211> 1725
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 107..1618

<220>
 <221> sig_peptide
 <222> 107..178
 <223> Von Heijne matrix
 score 6.19650168602189
 seq LGLYSLVLSGALA/YA

<400> 138	
agagctcagc cggtcgcacg gacggacagt tggaagccgg accccagagc ctgaggtggg	60
cagtgtgccca gggtccttg cggcctcctc aagccctgtc caggct atg ggc atc	115
	Met Gly Ile
aag aca gca ttg ccg gcg gct gag ctg ggc ctc tac tct ctg gtg ctg	163
Lys Thr Ala Leu Pro Ala Ala Glu Leu Gly Leu Tyr Ser Leu Val Leu	
-20 -15 -10	
agt ggg gcc ctg gcc tat gct ggc cgg ggc ctc ctt gag gct tca caa	211
Ser Gly Ala Leu Ala Tyr Ala Gly Arg Gly Leu Leu Glu Ala Ser Gln	
-5 1 5 10	
gat ggg gcc cac agg aag gcc ttc cgg gag tct gtg cga cct ggc tgg	259
Asp Gly Ala His Arg Lys Ala Phe Arg Glu Ser Val Arg Pro Gly Trp	
15 20 25	

gag tac att ggc cgg aag atg gat gtg gct gac ttc gag tgg gtg atg	307
Glu Tyr Ile Gly Arg Lys Met Asp Val Ala Asp Phe Glu Trp Val Met	
30 35 40	
tgg ttc acc tcc ttt cgc aac gtc atc atc ttt gcc ctc tcc gga cat	355
Trp Phe Thr Ser Phe Arg Asn Val Ile Ile Phe Ala Leu Ser Gly His	
45 50 55	
gtg ctg ttt gct aaa ctc tgc acg atg gtt gcc cca aag ctc cgc tcc	403
Val Leu Phe Ala Lys Leu Cys Thr Met Val Ala Pro Lys Leu Arg Ser	
60 65 70 75	
tgg atg tat gct gtg tac ggg gcc ttg gct gtg atg ggc aca atg ggc	451
Trp Met Tyr Ala Val Tyr Gly Ala Leu Ala Val Met Gly Thr Met Gly	
80 85 90	
cct tgg tac ctg ctg ctg ctg ctt ggt cac tgt gtg ggc ctc tat gtg	499
Pro Trp Tyr Leu Leu Leu Leu Leu Gly His Cys Val Gly Leu Tyr Val	
95 100 105	
gcc tcg ctt ttg ggc cag ccc tgg ctc tgt ctt ggc ctt ggc ttg gcc	547
Ala Ser Leu Leu Gly Gln Pro Trp Leu Cys Leu Gly Leu Gly Leu Ala	
110 115 120	
agc ctg gcc tcc ttc aag atg gac ccc cta atc tct tgg cag agc ggg	595
Ser Leu Ala Ser Phe Lys Met Asp Pro Leu Ile Ser Trp Gln Ser Gly	
125 130 135	
ttt gta aca ggc act ttt gat ctt caa gag gtg ctg ttt cat ggg ggc	643
Phe Val Thr Gly Thr Phe Asp Leu Gln Glu Val Leu Phe His Gly Gly	
140 145 150 155	
agc agc ttc aca gtg ctg cgt tgc acc agc ttt gca ctg gag agc tgt	691
Ser Ser Phe Thr Val Leu Arg Cys Thr Ser Phe Ala Leu Glu Ser Cys	
160 165 170	
gcc cac cct gac cgc cac tac tcc tta gct gac ctg ctc aag tac agc	739
Ala His Pro Asp Arg His Tyr Ser Leu Ala Asp Leu Leu Lys Tyr Ser	
175 180 185	
ttc tac ctg ccc ttc ttc ttc ttc ggg ccc atc atg acc ttt gat cgc	787
Phe Tyr Leu Pro Phe Phe Phe Phe Gly Pro Ile Met Thr Phe Asp Arg	
190 195 200	
ttc cat gct cag gtg agc cag gtg gag cca gtg aga cgc gag ggt gag	835
Phe His Ala Gln Val Ser Gln Val Glu Pro Val Arg Arg Glu Gly Glu	
205 210 215	
ctg tgg cac atc cga gcc cag gca ggc cta agc gtg gtg gcc atc atg	883
Leu Trp His Ile Arg Ala Gln Ala Gly Leu Ser Val Val Ala Ile Met	
220 225 230 235	
gcc gtc gac atc ttc ttt cac ttc ttc tac atc ctc act atc ccc agc	931
Ala Val Asp Ile Phe Phe His Phe Phe Tyr Ile Leu Thr Ile Pro Ser	
240 245 250	
gac ctc aag ttc gcc aac cgc ctc cca gac att gcc ctc gct ggc cta	979
Asp Leu Lys Phe Ala Asn Arg Leu Pro Asp Ile Ala Leu Ala Gly Leu	
255 260 265	
gcc tat tca aac ctg gtg tat gac tgg gtg aag gcg gcc gtc ctc ttt	1027
Ala Tyr Ser Asn Leu Val Tyr Asp Trp Val Lys Ala Ala Val Leu Phe	
270 275 280	
ggg gtt gtc aac act gtg gca tgc ctc gac cac ctg gac cca ccc cag	1075
Gly Val Val Asn Thr Val Ala Cys Leu Asp His Leu Asp Pro Pro Gln	
285 290 295	
cct ccc aag tgc atc acc gca ctc tac gtc ttt gcg gaa acg cac ttt	1123
Pro Pro Lys Cys Ile Thr Ala Leu Tyr Val Phe Ala Glu Thr His Phe	
300 305 310 315	

gac cgt ggc atc aac gac tgg ctt tgc aaa tat gtg tat aac cac att	1171
Asp Arg Gly Ile Asn Asp Trp Leu Cys Lys Tyr Val Tyr Asn His Ile	
320 325 330	
ggt ggg gag cat tcc gct gtg atc cca gag ctg gca gcc aca gtg gcc	1219
Gly Gly Glu His Ser Ala Val Ile Pro Glu Leu Ala Ala Thr Val Ala	
335 340 345	
aca ttt gcc atc acc aca ctg tgg ctt ggg cct tgt gac att gtc tac	1267
Thr Phe Ala Ile Thr Thr Leu Trp Leu Gly Pro Cys Asp Ile Val Tyr	
350 355 360	
ctg tgg tca ttc ctt aac tgc ttt ggc ctc aac ttt gag ctc tgg atg	1315
Leu Trp Ser Phe Leu Asn Cys Phe Gly Leu Asn Phe Glu Leu Trp Met	
365 370 375	
caa aaa ctg gca gag tgg ggg ccc cta gca cga att gag gcc tct ctg	1363
Gln Lys Leu Ala Glu Trp Gly Pro Leu Ala Arg Ile Glu Ala Ser Leu	
380 385 390 395	
tca gtg cag atg tcc cgt agg gtc cgg gcc ctg ttt gga gcc atg aac	1411
Ser Val Gln Met Ser Arg Arg Val Arg Ala Leu Phe Gly Ala Met Asn	
400 405 410	
ttc tgg gcc atc atc atg tac aac ctt gtg agc ctg aac agc ctc aaa	1459
Phe Trp Ala Ile Ile Met Tyr Asn Leu Val Ser Leu Asn Ser Leu Lys	
415 420 425	
ttc aca gag ctg gtt gcc cgg cgc ctg cta ctc aca ggg ttc ccc cag	1507
Phe Thr Glu Leu Val Ala Arg Arg Leu Leu Leu Thr Gly Phe Pro Gln	
430 435 440	
acc acg ctg tcc atc ctg ttt gtc acc tac tgt ggc gtc cag ctg gta	1555
Thr Thr Leu Ser Ile Leu Phe Val Thr Tyr Cys Gly Val Gln Leu Val	
445 450 455	
aag gag cgt gag cga acc ttg gca ctg gag gag gag cag aag cag gac	1603
Lys Glu Arg Glu Arg Thr Leu Ala Leu Glu Glu Glu Gln Lys Gln Asp	
460 465 470 475	
aaa gag aag ccg gag taggagggag cgggtagagg gatgggctct gctcagctat	1658
Lys Glu Lys Pro Glu	
480	
tcttgggcca gatggggcct gaccgataga ataaaagact tttctacaac aaaaaaaaaa	1718
aaaaaaaa	1725

<210> 139
 <211> 1474
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 16..471

<220>
 <221> sig_peptide
 <222> 16..93
 <223> Von Heijne matrix
 score 5.809301698725
 seq FCVCVIAIGVVQA/LI

<400> 139
 tacacgtttt cggtta atg gtg acc ttc cct gat gtg cct ctg ggc atc ttc 51

	Met	Val	Thr	Phe	Pro	Asp	Val	Pro	Leu	Gly	Ile	Phe	
	-25						-20				-15		
ttg ttc tgt gtg tgt gtg atc gcc atc ggg gtc gtg cag gca ctg att													99
Leu Phe Cys Val Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile													
	-10						-5				1		
gta ggg tac gca ttc cac ttc ccg cac ctg ctg agc ccg cag atc cag													147
Val Gly Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln													
	5					10				15			
cgc tct gcc cac agg gct ctg tac cga cga cac gtc ctg ggc atc gtc													195
Arg Ser Ala His Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val													
	20				25				30				
ctc caa ggc ccg gcc ctg tgc ttt gca gcg gcc atc ttc tct ctc ttc													243
Leu Gln Gly Pro Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe													
	35			40			45			50			
ttt gtc ccc ttg tct tac ctg ctg atg gtg act gtc atc ctc ctc ccc													291
Phe Val Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro													
			55			60			65				
tat gtc agc aag gtc acc ggc tgg tgc aga gac agg ctc ctg ggc cac													339
Tyr Val Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His													
		70			75			80					
agg gag ccc tcg gct cac cca gtg gaa gtc ttc tcg ttt gac ctc cac													387
Arg Glu Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His													
	85			90			95						
gag cca ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac													435
Glu Pro Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr													
	100			105			110						
gcc atc gtg gcc acg ctt ctc atc ctg gac atc tgg tgaggacccc													481
Ala Ile Val Ala Thr Leu Leu Ile Leu Asp Ile Trp													
	115		120			125							
gcgtcacctg cccagctat cagggtggcca atgtgtcttg agtccctggc gtctcatcct													541
ggaaacccca gaaaggcaca ggggtcttgg ctccaccctc ctctggatgc ctagagtttt													601
gtgtgaggtc agggcagccc ccacttcagg gaggacaacc ttcccggcgg cccctccctt													661
cccagcggcc cctcccttcc cagaggctcc caccccaagc acagccgagg atgggggtgcc													721
aggggtgaggt cagcaccagc agccaactgc tctcctcact cctctcagag gggctcagca													781
gccatgggta tccccctgcc ccaggcctca cccctgcccc aacaccagcc cctcctagtc													841
cctagtcctt cccattccct ccggctccct cccagtgcct cccatcgctt cgcagccctt													901
tctgctccct ttggttggt gttgcttctt tccagcgtct gctcctccgc ggctcatct													961
gcctcttctg ctgttagagc gcgcgtctcg tctcagtcgt cacgtttttg gtttttgtgg													1021
ggtttttttt tttttttttt tttgagacag tctgtctgtg tcgcccaggc tggagtatag													1081
tggtcaagc tcagctcact gcaacctccg cctcccaggc tcaagcaatt ctctgcctc													1141
agcctcccaa gtagttggga ttacaagcac ccaccacat gccagctaa ctttttgcac													1201
ttttaataga gatgaggttt caccaagttg gccaggctgg tcttgaactc ctgacctcag													1261
gtgatctgcc cacctcggcc tcccaaagtg ctgggattac aggtgtaagc caccgtgccc													1321
ggccatcgta atgtttgaat ttgctttttt acatcttcca tctttttgga gtgtcttggt													1381
ccctcgtcac agttcagcac tgtgaccacc ttgggggttag acactatggg tttatatcct													1441
gtacttgata ttctccaaaa aaaaaaaaaa aaa													1474

<210> 140
 <211> 653
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 222..374

<220>

<221> sig_peptide

<222> 222..299

<223> Von Heijne matrix

score 4.28353322771141

seq ILFKFSLCPYAAA/LS

<400> 140

taataatggtt	gttaaattat	tgccttctca	tctgcgtgtc	tcttatgttc	tgcttaaaga	60
gattgtcagt	ttgttcaagc	tctttttagt	tggtgtcctc	ccagtgccta	gctttgagct	120
ttgtacacgg	tagttattga	gttgagtaac	atagtttggt	ctgagtcatt	tgttccacat	180
gcttgaagac	ttggcttaac	ctagtagata	ataggaaaga	a atg gaa atg ctc ttt		236
				Met Glu Met Leu Phe		
				-25		

gat gaa aga gcc cct ctc tta ttc atc ctt ttt	aaa ttt tct ttg tgc	284
Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe	Lys Phe Ser Leu Cys	
-20	-15	-10

cca tat gca gca gct ctc agc aaa cct ata ttt	ggc agt gtg gcc tgt	332
Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe	Gly Ser Val Ala Cys	
-5	1	5

atg act aaa gaa atc ctg gcc agg cac ggt ggc	tca cgc ctg	374
Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly	Ser Arg Leu	
15	20	25

taatcccagc	actttgggag	gccgaggcgg	gtggattacg	aggtcaggag	attgagacca	434
tccctggctaa	catggcgaaa	ccccatctct	acgaaaaata	caaaaaaaaa	aattagccgg	494
gcatcatggc	ggcgccctgt	agtcttagct	actcaggagg	ctgaggcagg	agaatggcgt	554
gaacccggga	ggcgagcctt	gcagtgagcc	gagattgcgc	cactgcactc	cagcctgggg	614
caacagagca	agactccgtc	tcaaaaaaaaa	aaaaaaaaaa			653

<210> 141

<211> 1490

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 59..274

<220>

<221> sig_peptide

<222> 59..127

<223> Von Heijne matrix

score 7.37647149292058

seq LGLCSLLVGAEAE/PS

<400> 141

agacagaggc	agggcttgcg	acggaagtgg	cctctctgct	tctgcagggc	tggggaag	58
atg ctg cgt cca gcg tta ccg tgg ctg tac ctt	ggc ctc tgc agc ctc	106				
Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu	Gly Leu Cys Ser Leu					
-20	-15	-10				
ctg gtg ggg gag gca gag gcc ccg agc ccc	gtg gat ccg ctg gag cgg	154				
Leu Val Gly Glu Ala Glu Ala Pro Ser Pro	Val Asp Pro Leu Glu Arg					

-5	1	5	
agc cgg ccg tac gcg gtg ctg cga ggg cag aac ctg gtg ttg atg gga			202
Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly			
10	15	20	25
acc att ttc agc atc ctg ctg gtg act gtc atc ctt atg gca ttt tgt			250
Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys			
	30	35	40
gtc tac aag ccc att cgg cgt cgg tgacagccag acaagttctt caatgagtat			304
Val Tyr Lys Pro Ile Arg Arg Arg			
45			
ttgggaatag gataagttgt gttgcacaca ggccagtggg gaagttggaa ccaaaacttt			364
cctacttgga aatgaccttt ggtctggaca gttggtaaata gctaaatgaa ttagaagaaa			424
acatgtacta gacattatatt tttcctaaca ctgtagcgca aataattggc ccctgagtc			484
gcttctcagt gtttctgact gtacttggtt aaagtaagac ctgaaagctc caaaggctcag			544
tgtaaagatg gagtgttcat gagaaagaaa acatggtaac cttgtgagtg cctgtaagaa			604
ccacactgta aagaactcat cattaatgct tgaaaatggt attaagaagg agacttacca			664
tgacagacatt ccctatttaa gaaccatttg gttacagtgg gttagaatc acagatTTTT			724
TTTTTTaatc tcacctgagt tagcctagaa tgcgctgggt gcaaagtggg gtcagctgtg			784
gggatcttgg gccctcggtc ctcacctgca tcctgccctg cactcagggtg ctccccctga			844
agtcaggggtc acatcaggta gacctgttac tatatgcacc tttggcctgg aatgctctga			904
agttggactg gaaatgttac taggttggcc tgttacaaaa aggaccccat cctgcttaaa			964
cacattgatc tcccttgccc tgcatttgag tctttctagc ccacgggtctg aaacttgagg			1024
cagctttcca gatttggaat gtaaaaggct cagtgggcac tctgttcac cctgggtggg			1084
gagggcccag ccaacagaag tgcattgtcca ctgtgcgggc cagtgtgtgt ttacacaaat			1144
ttcatctcag ctttgaaaat gctgctatta gtttccactg ttggtgaact ggattttttc			1204
ctcctattga aatgatactt tcatacttat aaagctgtcg tcaatattta tttcaagggtg			1264
ctagatttaa ttttgattat aaattgaaat gcttatcttg tgttcaagca cagcactgat			1324
tttaacaacc tgcatttaaat gtgaagtaac cgaagtagga tactgtaact gtgtaaggat			1384
tttgtttgta atcttgtaac attgaaccat tgaaatgttc agttctttgc ttttgagcaa			1444
aacgtcaatt aaaactaaag taaaatctta aaaaaaaaaa aaaaaa			1490

<210> 142
 <211> 661
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 158..442

<220>
 <221> sig_peptide
 <222> 158..301
 <223> Von Heijne matrix
 score 7.53908709538105
 seq FVILLLFIFTVVS/LV

<400> 142	
aaaaacagac gataccatcg cttcagcagc atcctctcag acaagagcca ctatttctga	60
ttcagatcac ctgtcatcga agtttaaaga aggggaaaca ggagacagaa atacactgaa	120
ccaaaaagat tcaaaagagc aagtggaatc tctaaga atg gct tcc agc cac tgg	175
	Met Ala Ser Ser His Trp

	-45	
aat gaa acc act acc tct gtt tat cag tac ctt ggt ttt caa gtt caa		223

Asn	Glu	Thr	Thr	Thr	Ser	Val	Tyr	Gln	Tyr	Leu	Gly	Phe	Gln	Val	Gln		
		-40					-35				-30						
aaa	att	tac	cct	ttc	cat	gac	aac	tgg	aac	act	gcc	tgc	ttt	gtc	atc	271	
Lys	Ile	Tyr	Pro	Phe	His	Asp	Asn	Trp	Asn	Thr	Ala	Cys	Phe	Val	Ile		
	-25					-20				-15							
ctg	ctt	tta	ttt	ata	ttt	aca	gtg	gta	tct	tta	gtg	gtg	ctg	gct	ttc	319	
Leu	Leu	Leu	Phe	Ile	Phe	Thr	Val	Val	Ser	Leu	Val	Val	Leu	Ala	Phe		
-10				-5					1					5			
ctt	tat	gaa	gtg	ctt	gac	tgc	tgc	tgc	tgt	gta	aaa	aac	aaa	acc	gtg	367	
Leu	Tyr	Glu	Val	Leu	Asp	Cys	Cys	Cys	Cys	Val	Lys	Asn	Lys	Thr	Val		
		10				15					20						
aaa	gac	ttg	aaa	agt	gaa	ccc	aac	cct	ctt	aga	agt	atg	atg	gac	aac	415	
Lys	Asp	Leu	Lys	Ser	Glu	Pro	Asn	Pro	Leu	Arg	Ser	Met	Met	Asp	Asn		
	25					30					35						
atc	aga	aaa	cgt	gaa	act	gaa	gtg	gtc	taacactcta	tagaagatga						462	
Ile	Arg	Lys	Arg	Glu	Thr	Glu	Val	Val									
	40					45											
acaaaatctc	tgaaagcagc	tcaacctctt	ctgagaaaaa	aaatatattc	tgaggccaac											522	
tgttgctaca	aaacaaattc	tgactgaatg	tttaaaacat	ttctagtaga	aggggaaaaa											582	
aaagttaaac	atgcactggt	tgtgtgtata	gccatttcat	taaatataca	gtaaaacttc											642	
ataaaaaaaaa	aaaaaaaaa															661	

<210> 143
 <211> 1789
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..454

<220>
 <221> sig_peptide
 <222> 5..64
 <223> Von Heijne matrix
 score 6.64507667657896
 seq LLPLLSLLVGAWL/KL

<400>	143																
cctg	atg	gcc	cgg	cat	ggg	tta	ccg	ctg	ctg	ccc	ctg	ctg	tcg	ctc	ctg	49	
	Met	Ala	Arg	His	Gly	Leu	Pro	Leu	Leu	Pro	Leu	Leu	Ser	Leu	Leu		
	-20				-15					-10							
gtc	ggc	gcg	tgg	ctc	aag	cta	gga	aat	gga	cag	gct	act	agc	atg	gtc	97	
Val	Gly	Ala	Trp	Leu	Lys	Leu	Gly	Asn	Gly	Gln	Ala	Thr	Ser	Met	Val		
-5				1				5					10				
caa	ctg	cag	ggt	ggg	aga	ttc	ctg	atg	gga	aca	aat	tct	cca	gac	agc	145	
Gln	Leu	Gln	Gly	Gly	Arg	Phe	Leu	Met	Gly	Thr	Asn	Ser	Pro	Asp	Ser		
		15				20					25						
aga	gat	ggt	gaa	ggg	cct	gtg	cgg	gag	gcg	aca	gtg	aaa	ccc	ttt	gcc	193	
Arg	Asp	Gly	Glu	Gly	Pro	Val	Arg	Glu	Ala	Thr	Val	Lys	Pro	Phe	Ala		
	30					35					40						
atc	gac	ata	ttt	cct	gtc	acc	aac	aaa	gat	ttc	agg	gat	ttt	gtc	agg	241	
Ile	Asp	Ile	Phe	Pro	Val	Thr	Asn	Lys	Asp	Phe	Arg	Asp	Phe	Val	Arg		
	45					50					55						

gag aaa aag tat cgg aca gaa gct gag atg ttt gga tgg agc ttt gtc	289
Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val	
60 65 70 75	
ttt gag gac ttt gtc tct gat gag ctg aga aac aaa gcc acc cag cca	337
Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro	
80 85 90	
atg aag gtc aag ttt acc cat ggg gga act ggt tcc agc caa acc gca	385
Met Lys Val Lys Phe Thr His Gly Thr Gly Ser Ser Gln Thr Ala	
95 100 105	
cca acc tgt ggc agg gaa agt tcc cca agg gag aca aag ctg agg atg	433
Pro Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met	
110 115 120	
gct tcc atg gag tct ccc cag tgaatgcttt ccccgcccag aacaactacg	484
Ala Ser Met Glu Ser Pro Gln	
125 130	
ggctctatga cctcctgggg aacgtgtggg agtggacagc atcacccgtac caggctgctg	544
agcaggacat gcgcgtcctc cggggggcat cctggatcga cacagctgat ggctctgcca	604
atcacccggc ccgggtcacc accaggatgg gcaacactcc agattcagcc tcagacaacc	664
tcggtttccg ctgtgctgca gacgcaggcc ggccgccagg ggagctgtaa gcagccgggt	724
ggtgacaagg agaaaagcct tctaggggtca ctgtcattcc ctggccatgt tgcaaacagc	784
gcaattccaa gctcgagagc ttcagcctca ggaaagaact tccccctccc tgtctcccat	844
ccctctgtgg caggcgccctc tcaccagggc aggagaggac tcagcctcct gtgttttgga	904
gaagggggccc aatgtgtgtt gacgatggct gggggccagg tgtttctgtt agaggccaag	964
tattattgac acaggattgc aaacacacaa acaattggaa cagagcactc tgaaaggcca	1024
ttttttaagc attttaaaat ctattctctc cccctttctc cctggatgat tcaggaagct	1084
gacattgttt cctcaaggca gaattttcct ggttctgttt tctcagccag ttgctgtgga	1144
aggagaatgc tttctttgtg gcctcatctg tggtttcgtg tccctctgaa ggaaactagt	1204
ttccactgtg taacaggcag acatgtaact atttaaagca cagttcagtc ctaaaagggt	1264
ctgggagaac cagatgatgt actaggtgaa gcattgcatt gtgggaatca caaagcaaat	1324
agtactccag aaagacaaat atcagaagct tcctattctt tttttttttt tttttttttt	1384
ttgagacagg gtctttctct gttgcccagg ctagagtgca ctggtgatca cggctcactc	1444
tagccttgaa ttccctgggc caagcaattc tcccacctca gcctcctgag tagctgggac	1504
tacaagtgtg caccaccatg cctggctaatt tttttgaatt tttgtagtga tgggatctcg	1564
ctctgttgcc cagggtggtc tcgaactcct ggccctcaagc gatcctccca cctcgacctc	1624
ccaaagtgtc gggattacag gtgtgagcca cctcgccctgg gcccccttct ccatatgcct	1684
ccaaaaacat gtccctggag agtagcctgc tcccacactg tcactggatg tcatggggcc	1744
aataaaatct cctgcaattg tgtatctcaa aaaaaaaaaa aaaaa	1789

<210> 144
 <211> 2006
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 241..1302

<400> 144	
tagtgccgga gccccgccag agccccgactt cagccccagc cagatcccgc gtcaacggag	60
gcggaacggc ggaccccgtc ccttggcagc atcggagcac cggcgggtga aggcaaggctc	120
cctggactgg tcatatacct cttgtggccc tggcagaatc aagatgaggc cctgtcatgc	180
ctccccagtg aggcctacag tctgagcaga cagcatggcc tgccactggc agtgaacacc	240
atg tct gca gga ggt ggc cgg gcc ttt gct tgg caa gtg ttc ccc ccc	288
Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro	

1	5	10	15	
atg ccc act tgc cgg gtc tat ggc aca gtg gca cac caa gat ggg cac				336
Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His				
20	25	30		
ctg ctg gtg ttg ggg ggt tgt ggc cgg gct gga ctg ccc ctg gac act				384
Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr				
35	40	45		
gct gag aca ctg gac atg gcc tcg cac aca tgg ctg gca ctg gca ccc				432
Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro				
50	55	60		
ctg ccc act gcc cgg gct ggt gca gct gcg gta gtt ctg ggc aag cag				480
Leu Pro Thr Ala Arg Ala Gly Ala Ala Val Val Leu Gly Lys Gln				
65	70	75	80	
gtg cta gtg gtg tgt ggt gtg gat gag gtc cag agc ccg gta gct gct				528
Val Leu Val Val Cys Gly Val Asp Glu Val Gln Ser Pro Val Ala Ala				
85	90	95		
gta gag gcc ttc ctg atg gat gag ggc cgc tgg gag cgt cgg gcc acc				576
Val Glu Ala Phe Leu Met Asp Glu Gly Arg Trp Glu Arg Arg Ala Thr				
100	105	110		
ctc cct caa gca gcc atg ggg gtt gca act gtg gag aga gat ggt atg				624
Leu Pro Gln Ala Ala Met Gly Val Ala Thr Val Glu Arg Asp Gly Met				
115	120	125		
gtg tat gct ctg ggg gga atg ggc cct gac acg gcc ccc cag gcc cag				672
Val Tyr Ala Leu Gly Gly Met Gly Pro Asp Thr Ala Pro Gln Ala Gln				
130	135	140		
gta cgt gtg tat gac ccc cgt cgg gac tgc tgg ctt tcg cta ccc tcc				720
Val Arg Val Tyr Asp Pro Arg Arg Asp Cys Trp Leu Ser Leu Pro Ser				
145	150	155	160	
atg ccc aca ccc tgc tat ggg gcc tcc acc ttc ctg cac ggg aac aag				768
Met Pro Thr Pro Cys Tyr Gly Ala Ser Thr Phe Leu His Gly Asn Lys				
165	170	175		
atc tat gtc ctg ggg ggc cgc cag ggc aag ctc ccg gtg act gct ttt				816
Ile Tyr Val Leu Gly Gly Arg Gln Gly Lys Leu Pro Val Thr Ala Phe				
180	185	190		
gaa gcc ttt gat ctg gag gcc cgt aca tgg acc cgg cat cca agc cta				864
Glu Ala Phe Asp Leu Glu Ala Arg Thr Trp Thr Arg His Pro Ser Leu				
195	200	205		
ccc agc cgt cgg gcc ttt gct ggc tgc gcc atg gct gaa ggc agc gtc				912
Pro Ser Arg Arg Ala Phe Ala Gly Cys Ala Met Ala Glu Gly Ser Val				
210	215	220		
ttt agc ctg ggt ggc ctg cag cag cct ggg ccc cac aac ttc tac tct				960
Phe Ser Leu Gly Gly Leu Gln Gln Pro Gly Pro His Asn Phe Tyr Ser				
225	230	235	240	
cgc cca cac ttt gtc aac act gtg gag atg ttt gac ctg gag cat ggg				1008
Arg Pro His Phe Val Asn Thr Val Glu Met Phe Asp Leu Glu His Gly				
245	250	255		
tcc tgg acc aaa ttg ccc cgc agc ctg cgc atg agg gat aag agg gca				1056
Ser Trp Thr Lys Leu Pro Arg Ser Leu Arg Met Arg Asp Lys Arg Ala				
260	265	270		
gac ttt gtg gtt ggg tcc ctt ggg ggc cac att gtg gcc att ggg ggc				1104
Asp Phe Val Val Gly Ser Leu Gly Gly His Ile Val Ala Ile Gly Gly				
275	280	285		
ctt gga aac cag cca tgt cct ttg ggc tct gtg gag agc ttt agc ctt				1152
Leu Gly Asn Gln Pro Cys Pro Leu Gly Ser Val Glu Ser Phe Ser Leu				

290	295	300	
gca cgg cgg cgc tgg gag gca ttg cct gcc atg ccc act gcc cgc tgc			1200
Ala Arg Arg Arg Trp Glu Ala Leu Pro Ala Met Pro Thr Ala Arg Cys			
305	310	315	320
tcc tgc tct agt ctg cag gct ggg ccc cgg ctg ttt gtt att ggg ggt			1248
Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly			
	325	330	335
gtg gcc cag ggc ccc agt caa gcc gtg gag gca ctg tgt ctg cgt gat			1296
Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp			
	340	345	350
ggg gtc tgaaggcttg gtgggagctg tccactggag cagctcattg ccagaggcag			1352
Gly Val			
ctatttctat ggctcctttt gctgctgagg acactcactg tggctctgtg ggatgagaga			1412
ggcatggggg tgagcacttg aaacactgcc ttggggcctt gggttagggg agcctttgtc			1472
tttagtgcag gacacacata tgcttacacc tacctttatc accattcgtt catgaatcat			1532
gcctagctcc atccttgccc tgggacctac taggccttcc atccaactgg gaaatgggga			1592
gaagcaaagc tggcctcatg ctcttcaggg tcagttccta tctggagttg accaggccta			1652
ccccagttgc cattcctgaa aaatctcagc tgccaggctg cctttagggg ccctgcagac			1712
ccaggagagt tgagaggggtg ggggacacac acagaataga gaggatgtgg gaactgccag			1772
agggccggag cgcaggagtt caagtggagg aatgctggct ttgagccctc tacactgctg			1832
gttgatgac cttggacaag tcacttcacc tctctgtgcc tcagcatcct catctataaa			1892
tggggatctc tgaaaccttc ctaccctacc tacctcacag ggctgttgtg aggacccagg			1952
gagtttggat gtggaagtaa aagtgtgtgct aaaaccgaaa aaaaaaaaaa aaaa			2006

<210> 145
 <211> 1096
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 15..635

<400> 145	
atccaaggcgc caag atg gcg ctg ctt ttt gca cgt tct ttg cgc ttg tgc	50
Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys	
1 5 10	
cgc tgg gga gcc aaa cga ttg gga gtt gcc tcc aca gag gcc cag aga	98
Arg Trp Gly Ala Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg	
15 20 25	
ggc gtc agt ttc aaa ctg gaa gaa aaa acc gcc cac agc agc ctg gca	146
Gly Val Ser Phe Lys Leu Glu Lys Thr Ala His Ser Ser Leu Ala	
30 35 40	
ctc ttc aga gat gat acg ggt gtc aaa tat ggc ttg gtg gga ttg gag	194
Leu Phe Arg Asp Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu	
45 50 55 60	
ccc acc aag gtg gcc ttg aat gtg gag cgc ttc cgg gag tgg gca gtg	242
Pro Thr Lys Val Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val	
65 70 75	
gtg ctg gca gac aca gcg gtc acc agt ggc aga cac tac tgg gaa gtg	290
Val Leu Ala Asp Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val	
80 85 90	
aca gtg aag cgc tcc cag cag ttc cgg ata gga gtg gca gat gtg gac	338
Thr Val Lys Arg Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp	

95	100	105	
atg tcc cgg gat agc tgc att ggt gtt gat gat cgt tcc tgg gtg ttc			386
Met Ser Arg Asp Ser Cys Ile Gly Val Asp Asp Arg Ser Trp Val Phe			
110	115	120	
acc tat gcc cag cgc aag tgg tac acc atg ttg gcc aac gag aaa gcc			434
Thr Tyr Ala Gln Arg Lys Trp Tyr Thr Met Leu Ala Asn Glu Lys Ala			
125	130	135	140
cca gtt gag ggt att ggg cag cca gag aag gtg ggg ctg ttg ctg gag			482
Pro Val Glu Gly Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu			
145	150	155	
tat gag gcc cag aag ctg agc ctg gtg gat gtg agc cag gtc tct gtg			530
Tyr Glu Ala Gln Lys Leu Ser Leu Val Asp Val Ser Gln Val Ser Val			
160	165	170	
gtt cac acg cta cag aca gat ttc cgg ggt cca gtg gtg cct gcc ttt			578
Val His Thr Leu Gln Thr Asp Phe Arg Gly Pro Val Val Pro Ala Phe			
175	180	185	
gct ctc tgg gat ggg gag ctg ctg acc cat tca ggg ctt gag gtg ccc			626
Ala Leu Trp Asp Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro			
190	195	200	
gag ggc ctc tagtatgtcc attactggag tccctaataca cgcctttggc			675
Glu Gly Leu			
205			
cagcctcctt ttgaaagtgt ccgaagcctt tttactttgc ctcaagcaac ctctagctcc			735
cacaattcag tggtgggtcc tctgtgcaat atcatgatca tcttcctcat cccctacctt			795
gtgaaagcta ggcatacagc caaaccctcc ttttccccac ccaccaacac tactgccaat			855
ttcctaggct accatgggtg tatcttcctt gacctgttc cttcagtccc tctgcctccc			915
tttgcccagg cctttctcag actgtattcc atcctggggt cttatcattc agctttgttt			975
gaatttatta atcaccatga tacctctccc tccctttgtc cacatgtaac ttgttcttgg			1035
ggctctacca gatggctgaa gagtaaattcc tttctacctc tggcaaaaaa aaaaaaaaaa			1095
a			1096

<210> 146
 <211> 1666
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 109..738

<400> 146	
cccagcgttc ctctccggc ccaggtcac cgccagcacg cgctgtctc ccgtctgcgc	60
gagtccacgc agtccccag gcccttcacc agcacagcag cagcaggc atg gca gca	117
Met Ala Ala	
1	
agc gtg gag cag cgc gag ggc acc atc cag gtg cag ggc cag gcc ctc	165
Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly Gln Ala Leu	
5 10 15	
ttc ttc cga gag gcc ctg ccc ggc agt ggg cag gct cgc ttc tct gta	213
Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg Phe Ser Val	
20 25 30 35	
ctg ctg ctg cat ggt att cgc ttc tcc tcc gag acc tgg cag aac ctg	261
Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp Gln Asn Leu	
40 45 50	

ggt aca ctg cac agg ctg gcc cag gct ggc tac cgg gct gtg gcc att	309
Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala Val Ala Ile	
55 60 65	
gac ctg cca ggt ctg ggg cac tcc aag gaa gca gca gcc cct gcc cct	357
Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala Pro Ala Pro	
70 75 80	
att ggg gag ctg gcc cct ggc agc ttc ctg gcg gct gtg gtg gat gcc	405
Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val Val Asp Ala	
85 90 95	
ttg gag ctg ggc ccc ccg gtt gtg atc agt cca tca ctg agt ggc atg	453
Leu Glu Leu Gly Pro Val Val Ile Ser Pro Ser Leu Ser Gly Met	
100 105 110 115	
tac tcc ctg ccc ttc ctc acg gcc cct ggc tcc cag ctc ccg ggc ttt	501
Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu Pro Gly Phe	
120 125 130	
gtg cca gtg gcc ccc atc tgc act gac aaa atc aat gct gcc aac tat	549
Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala Ala Asn Tyr	
135 140 145	
gcc agt gtg aag act cca gct ctg att gta tat gga gac cag gac ccc	597
Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp Gln Asp Pro	
150 155 160	
atg ggt cag acc agc ttt gag cac ctg aag cag ctg ccc aac cac cgg	645
Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro Asn His Arg	
165 170 175	
gtg ctg atc atg aag ggg gcg ggg cac ccc tgt tac ctg gac aaa cca	693
Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu Asp Lys Pro	
180 185 190 195	
gag gag tgg cat aca ggg ctg ctg gac ttc ctg cag ggg ctc cag	738
Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly Leu Gln	
200 205 210	
tgaagcccag cactgctgca ggggggtgggc tgccctgacctg ctctgagctc tctcttgccac	798
gctctctctt ctctcccagg ctctggctca tgcacatgca acaggtgcgt ctgtctatat	858
gtctgggttc ttgtcttttg tggctctgtt gtcttttcta cctctttctc ttgcagtgat	918
agactgaggg ggtaaaatca agagaaaaaa ctctcaggaa tcaaggaaca taatcctgtg	978
gagggtaatc cattacatga gcttctcctg ttcttccact ttccctgcctg gctttcactc	1038
cttcccctgc tctgcccagc ctttccctcc caccactcc tacttctgca aatgccctga	1098
aggccagccc ttaccccac acccacttcc ccacctcctt aggccccaga tacatacatg	1158
cccacatgca cgcttacatg tttagagcca tccttgtttc caaatatgac ccttcgcttg	1218
agggcaactg cataggtaca tctaactctg gactggcatg cacattgtca tgtgcagctt	1278
tgcataataca cacatgcata catgagcctc cacacaagca cttgcacaca tgtggactcc	1338
taaccatgct aacctcactg gctgggaagg tggggacccc atggggccagc ccttgaggga	1398
ggcccttttg caaggcttag ggtgtggcca gccctgaaag ctacttggac acaggtttca	1458
gtgggccccca gcccagaagt gacccccaga aagggagggc caccgctttg cccctgctt	1518
ttacccttcc ttctgggtgc tctacacctc aggttaccag gcctgaggca tctcagccaa	1578
gcttggtttcc tgctctgagg cttgtggggg gggagccaga gtggaggtcg gtgaaataaa	1638
gtgatgcaat taaaaaaaaa aaaaaaaaaa	1666

<210> 147
 <211> 1687
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 21..1145

<400> 147

gtttctccgg acttcgagcc atg gcg gtg acg gaa gcg agc ctg ttg cgc cag	53
Met Ala Val Thr Glu Ala Ser Leu Leu Arg Gln	
1 5 10	
tgc ccc ctg ctt ctg ccc cag aac cgg tcg aaa acc gtg tat gag gga	101
Cys Pro Leu Leu Leu Pro Gln Asn Arg Ser Lys Thr Val Tyr Glu Gly	
15 20 25	
ttc atc tcg gct cag gga aga gac ttc cac ctt agg ata gtg ttg cct	149
Phe Ile Ser Ala Gln Gly Arg Asp Phe His Leu Arg Ile Val Leu Pro	
30 35 40	
gaa gat tta caa ctg aag aat gca aga tta tta tgt att tgg cag ctg	197
Glu Asp Leu Gln Leu Lys Asn Ala Arg Leu Leu Cys Ile Trp Gln Leu	
45 50 55	
aga aca ata ctt agt gga tac cat cga ata gta caa cag aga atg cag	245
Arg Thr Ile Leu Ser Gly Tyr His Arg Ile Val Gln Gln Arg Met Gln	
60 65 70 75	
cac tct cct gat cta atg agc ttt atg atg gag ttg aag atg ctt ttg	293
His Ser Pro Asp Leu Met Ser Phe Met Met Glu Leu Lys Met Leu Leu	
80 85 90	
gaa gtt gcc tta aag aat aga caa gag ctg tat gca cta cct cct cct	341
Glu Val Ala Leu Lys Asn Arg Gln Glu Leu Tyr Ala Leu Pro Pro Pro	
95 100 105	
ccc cag ttc tac tca agc ctt att gaa gag ata gga act ctt ggt tgg	389
Pro Gln Phe Tyr Ser Ser Leu Ile Glu Glu Ile Gly Thr Leu Gly Trp	
110 115 120	
gat aaa ctt gtg tat gcg gat acc tgc ttc agt acc atc aag tta aaa	437
Asp Lys Leu Val Tyr Ala Asp Thr Cys Phe Ser Thr Ile Lys Leu Lys	
125 130 135	
gca gaa gat gct tct ggt aga gag cat tta atc act ctc aag ttg aag	485
Ala Glu Asp Ala Ser Gly Arg Glu His Leu Ile Thr Leu Lys Leu Lys	
140 145 150 155	
gca aag tat cct gca gaa tca cca gat tat ttt gtg gat ttt cct gtt	533
Ala Lys Tyr Pro Ala Glu Ser Pro Asp Tyr Phe Val Asp Phe Pro Val	
160 165 170	
cca ttt tgt gcc tcc tgg aca cct cag agc tcc tta ata agc att tat	581
Pro Phe Cys Ala Ser Trp Thr Pro Gln Ser Ser Leu Ile Ser Ile Tyr	
175 180 185	
agt cag ttt ttg gca gca ata gaa tca cta aag gca ttc tgg gat gtt	629
Ser Gln Phe Leu Ala Ala Ile Glu Ser Leu Lys Ala Phe Trp Asp Val	
190 195 200	
atg gat gaa atc gat gag aag acc tgg gta ctt gag cca gaa aaa cct	677
Met Asp Glu Ile Asp Glu Lys Thr Trp Val Leu Glu Pro Glu Lys Pro	
205 210 215	
cca cgg agt gca aca gca cgc aga att gca tta ggt aat aat gtt tcc	725
Pro Arg Ser Ala Thr Ala Arg Arg Ile Ala Leu Gly Asn Asn Val Ser	
220 225 230 235	
ata aat ata gag gta gac ccc agg cat cct act atg ctt cct gag tgc	773
Ile Asn Ile Glu Val Asp Pro Arg His Pro Thr Met Leu Pro Glu Cys	
240 245 250	
ttc ttt ctt gga gct gac cat gtg gta aaa ccc ctg gga att aag ctg	821
Phe Phe Leu Gly Ala Asp His Val Val Lys Pro Leu Gly Ile Lys Leu	
255 260 265	

agc agg aac ata cat ttg tgg gat cca gaa aat agt gtg tta caa aat	869
Ser Arg Asn Ile His Leu Trp Asp Pro Glu Asn Ser Val Leu Gln Asn	
270 275 280	
ttg aaa gat gtt tta gaa att gat ttt cca gct cgt gct atc ctg gaa	917
Leu Lys Asp Val Leu Glu Ile Asp Phe Pro Ala Arg Ala Ile Leu Glu	
285 290 295	
aaa tct gat ttt act atg gat tgt gga att tgt tat gct tat caa ctt	965
Lys Ser Asp Phe Thr Met Asp Cys Gly Ile Cys Tyr Ala Tyr Gln Leu	
300 305 310 315	
gac ggt acc att cct gat caa gtg tgt gat aat tcc cag tgt gga caa	1013
Asp Gly Thr Ile Pro Asp Gln Val Cys Asp Asn Ser Gln Cys Gly Gln	
320 325 330	
cct ttc cat caa ata tgc tta tat gag tgg ctg aga gga cta cta act	1061
Pro Phe His Gln Ile Cys Leu Tyr Glu Trp Leu Arg Gly Leu Leu Thr	
335 340 345	
agt aga cag agt ttt aac atc ata ttt ggt gaa tgt cca tat tgt agt	1109
Ser Arg Gln Ser Phe Asn Ile Ile Phe Gly Glu Cys Pro Tyr Cys Ser	
350 355 360	
aag cca att acc tta aaa atg tct gga agg aaa cac tgaaataaga	1155
Lys Pro Ile Thr Leu Lys Met Ser Gly Arg Lys His	
365 370 375	
atacaacatt tcggtgaaga gctggaaact taaaaaatta tcaaaaggaa ttttggatc	1215
atcttcagag aaaaaataaa gcaagraata ctaacatcaa aaggacaggt atgatgatgc	1275
gataataata aacatctgcg tttgtctctt cactaagagt aaactgggaa attgtaggcc	1335
aaagtccagt tgaactttct aagtctgtga tccccgtgct gactgtggaa gtgtatttat	1395
accaagatgg agatcttgac ttcttgaata tatctggact ggtaaaatct tgatgaggct	1455
cataaaatga gtttgggaat tgtgtatagc tgattttttg tgggaaactg tttacttcat	1515
tcaaagggtc ttgagactct tgatatttct gtcttctcct tgtgctttcc tatggaaaaa	1575
atacatatat agtttagttt gtttagacgtg agttatccaa gtattttattt tgtgtagtgt	1635
gtaagaatgc taaataaaat gttatacagg aaaaaaaaaa aaaaatgcga aa	1687

<210> 148
 <211> 1747
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..1596

<400> 148	
gttgggcggc cggtagctgt tgctgttggg ggacccctc attcctgccg ctgccgtccc	60
tgctgcctc atg gcg gcc atc gga gtt cac ctg ggc tgc acc tca gcc tgt	111
Met Ala Ala Ile Gly Val His Leu Gly Cys Thr Ser Ala Cys	
1 5 10	
gtg gcc gtc tat aag gat ggc cgg gct ggt gtg gtt gca aat gat gcc	159
Val Ala Val Tyr Lys Asp Gly Arg Ala Gly Val Val Ala Asn Asp Ala	
15 20 25 30	
ggt gac cga gtt act cca gct gtt gtt gct tac tca gaa aat gaa gag	207
Gly Asp Arg Val Thr Pro Ala Val Val Ala Tyr Ser Glu Asn Glu Glu	
35 40 45	
att gtt gga ttg gca gca aaa caa agt aga ata aga aat att tca aat	255
Ile Val Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn	
50 55 60	

aca gta atg aaa gta aag cag atc ctg ggc aga agc tcc agt gat cca	303
Thr Val Met Lys Val Lys Gln Ile Leu Gly Arg Ser Ser Ser Asp Pro	
65 70 75	
caa gct cag aaa tac atc gcg gaa agt aaa tgt tta gtc att gaa aaa	351
Gln Ala Gln Lys Tyr Ile Ala Glu Ser Lys Cys Leu Val Ile Glu Lys	
80 85 90	
aat ggg aaa tta cga tat gaa ata gat act gga gaa gaa aca aaa ttt	399
Asn Gly Lys Leu Arg Tyr Glu Ile Asp Thr Gly Glu Glu Thr Lys Phe	
95 100 105 110	
ggt aac cca gaa gat gtt gcc aga ctg ata ttt agt aaa atg aaa gaa	447
Val Asn Pro Glu Asp Val Ala Arg Leu Ile Phe Ser Lys Met Lys Glu	
115 120 125	
acg gca cat tct gta ttg ggc tca gat gca aat gat gta gtt att act	495
Thr Ala His Ser Val Leu Gly Ser Asp Ala Asn Asp Val Val Ile Thr	
130 135 140	
gtc ccg ttt gat ttt gga gaa aag caa aaa aat gct ctt gga gaa gca	543
Val Pro Phe Asp Phe Gly Glu Lys Gln Lys Asn Ala Leu Gly Glu Ala	
145 150 155	
gct aga gct gct gga ttt aat gtt ttg cga tta att cac gaa ccg tct	591
Ala Arg Ala Ala Gly Phe Asn Val Leu Arg Leu Ile His Glu Pro Ser	
160 165 170	
gca gct ctt ctt gct tat gga att gga caa gac tcc cct act gga aaa	639
Ala Ala Leu Leu Ala Tyr Gly Ile Gly Gln Asp Ser Pro Thr Gly Lys	
175 180 185 190	
agc aat att ttg gtg ttt aag ctt gga gga aca tcc tta tct ctc agc	687
Ser Asn Ile Leu Val Phe Lys Leu Gly Gly Thr Ser Leu Ser Leu Ser	
195 200 205	
gtc atg gaa gtt aac agt gga ata tat cgg gtt ctt tca aca aac act	735
Val Met Glu Val Asn Ser Gly Ile Tyr Arg Val Leu Ser Thr Asn Thr	
210 215 220	
gat gat aac atc ggt ggt gca cat ttc aca gaa acc tta gca cag tat	783
Asp Asp Asn Ile Gly Gly Ala His Phe Thr Glu Thr Leu Ala Gln Tyr	
225 230 235	
cta gct tct gag ttc caa aga tcc ttc aaa cat gat gtg aga gga aat	831
Leu Ala Ser Glu Phe Gln Arg Ser Phe Lys His Asp Val Arg Gly Asn	
240 245 250	
gcg cga gcc atg atg aaa tta acg aac agt gct gaa gta gcg aaa cat	879
Ala Arg Ala Met Met Lys Leu Thr Asn Ser Ala Glu Val Ala Lys His	
255 260 265 270	
tct ttg tca acc ttg gga agt gcc aac tgt ttt ctt gac tca tta tat	927
Ser Leu Ser Thr Leu Gly Ser Ala Asn Cys Phe Leu Asp Ser Leu Tyr	
275 280 285	
gaa ggt caa gat ttt gat tgc aat gtg tcc aga gca aga ttt gaa ctt	975
Glu Gly Gln Asp Phe Asp Cys Asn Val Ser Arg Ala Arg Phe Glu Leu	
290 295 300	
ctt tgt tct cca ctt ttt aat aag tgt ata gaa gca atc aga gga ctc	1023
Leu Cys Ser Pro Leu Phe Asn Lys Cys Ile Glu Ala Ile Arg Gly Leu	
305 310 315	
tta gat caa aat gga ttt aca aca gat gat atc aac aag gtt gtc ctt	1071
Leu Asp Gln Asn Gly Phe Thr Thr Asp Asp Ile Asn Lys Val Val Leu	
320 325 330	
tgt gga ggg tct tct cga atc cca aag cta cag caa ctg att aaa gat	1119
Cys Gly Gly Ser Ser Arg Ile Pro Lys Leu Gln Gln Leu Ile Lys Asp	
335 340 345 350	

ctt ttc cca gct gtt gag ctt ctc aat tct atc cct cct gat gaa gtg	1167
Leu Phe Pro Ala Val Glu Leu Leu Asn Ser Ile Pro Pro Asp Glu Val	
355 360 365	
atc cct att ggt gca gct ata gaa gca gga att ctt att ggg aaa gaa	1215
Ile Pro Ile Gly Ala Ala Ile Glu Ala Gly Ile Leu Ile Gly Lys Glu	
370 375 380	
aac ctg ttg gtg gaa gac tct ctt atg ata gag tgt tca gcc aga gat	1263
Asn Leu Leu Val Glu Asp Ser Leu Met Ile Glu Cys Ser Ala Arg Asp	
385 390 395	
att tta gtt aag ggt gtg gac gaa tca gga gcc agt aga ttc aca gtg	1311
Ile Leu Val Lys Gly Val Asp Glu Ser Gly Ala Ser Arg Phe Thr Val	
400 405 410	
ctg ttt cca tca ggg act cct ttg cca gct cga aga caa cac aca ttg	1359
Leu Phe Pro Ser Gly Thr Pro Leu Pro Ala Arg Arg Gln His Thr Leu	
415 420 425 430	
caa gcc cct gga agc ata tct tca gtg tgc ctt gaa ctc tat gag tct	1407
Gln Ala Pro Gly Ser Ile Ser Ser Val Cys Leu Glu Leu Tyr Glu Ser	
435 440 445	
gat ggg aag aac tct gcc aaa gag gaa acc aag ttt gca cag gtt gta	1455
Asp Gly Lys Asn Ser Ala Lys Glu Glu Thr Lys Phe Ala Gln Val Val	
450 455 460	
ctc cag gat tta gat aaa aaa gaa aat gga tta cgt gat ata tta gct	1503
Leu Gln Asp Leu Asp Lys Lys Glu Asn Gly Leu Arg Asp Ile Leu Ala	
465 470 475	
gtt ctt act atg aaa agg gat gga tct tta cat gtg aca tgc aca gat	1551
Val Leu Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp	
480 485 490	
caa gaa act gga aaa tgt gaa gca atc tct att gag ata gca tct	1596
Gln Glu Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser	
495 500 505	
tagtggtttta gagaaatcaa gaattttttaa aaacaagaat atcaacattt gggtttgtgt	1656
ataagtgggtg tttgtattaa aatacttttt caatgaactg tataaactat gttttattaa	1716
actacaatat atcagtaaaa aaaaaaaaaa a	1747

<210> 149
 <211> 658
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 129..362

<400> 149	
agtcaggaaa atgaagctga acatcaagtc ccagcaagaa aagaaggaaa aggaatgcc	60
agcagtcatg ttagcagttt gaaggggctg gagcaagatg gaatcaggaa taaggagtca	120
gtggggacc atg tac aac act gga aga cac gta tcc ctt cgc ctg gac aag	170
Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys	
1 5 10	
gag cac ttg gtc aac ata tct gga ggg ccc atg aca tac agc cac cgg	218
Glu His Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg	
15 20 25 30	
ctg gag gag atc cga cta cac ttt ggg agt gag gac agc caa ggg tgc	266
Leu Glu Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser	

	35	40	45	
gag cac ctc ctc aat gga cag gcc ttc tct ggg gag ctt caa gag agg				314
Glu His Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg				
	50	55	60	
gat ttg ttc atc ttg ttg act tct gta tca gga cat ctg ccc gat aca				362
Asp Leu Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr				
	65	70	75	
tagaaaaagt ctgctgaccc ctgaattaca gtatgagcca ttcggaatgc atttctcttt				422
aaaagtcttc gcctcattca gtgtctggaa cacagtgggt gctccccaat aggtgacacc				482
ttcctcaagt ttccttggga gaacagactc aatgtcggat ccacaaagga gacctgcaca				542
tacctaacc cttatttctgc agaagctgaa ggctgtatta tctattgctt gcataataaa				602
tattgcataa cgacaacaat agtaaaaaaa aaaaaaaaaa gaaaaaaaaa aaaaaa				658

<210> 150

<211> 2045

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 109..594

<400> 150

attattacta caggaaaaac tggtctcttc tgtggcacag agaaccctgc ttcaaagcag	60
aagtagcagt tccggagtcc agctggctaa aactcatccc agaggata atg gca acc	117
	Met Ala Thr
	1
cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg gtg	165
His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met Val	
	5 10 15
ggc aca gtg gct gtc act gtc atg cct cag tgg ata gtg tcg gcc ttc	213
Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val Ser Ala Phe	
	20 25 30 35
att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg tgg	261
Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu Trp	
	40 45 50
atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc tat	309
Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr	
	55 60 65
gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga ctg	357
Asp Ser Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu	
	70 75 80
atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc atc	405
Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala Ile	
	85 90 95
ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg aag	453
Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val Lys	
	100 105 110 115
gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc atg	501
Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met	
	120 125 130
gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga gat	549
Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp	
	135 140 145

ttc tat aac cca ata gtg aat gtt gcc caa aaa cgt gag ctt gga	594
Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly	
150 155 160	
taagctctct acttaggatg gaccacggca ctggtgctga ttgttggagg agctctgttc	654
tgctgcgttt tttgttgcaa cgaaaagagc agtagctaca gatactcgat accttcccat	714
cgcacaaccc aaaaaagtta tcacaccgga aagaagtcac cgagcgtcta ctccagaagt	774
cagtatgtgt agttgtgtat gtttttttaa ctttactata aagccatgca aatgacaaaa	834
atctatatta ctttctcaaa atggaccca aagaaacttt gatttactgt tcttaactgc	894
ctaactctaa ttacaggaac tgtgcatcag ctatttatga ttctataagc tatttcagca	954
gaatgagata ttaaattccaa tgctttgatt gttctagaaa gtatagtaat ttgttttcta	1014
aggtgggttca agcatctact ctttttatca tttacttcaa aatgacattg ctaaagactg	1074
cattattttta ctactgtaat ttctccacga catagcatta tgtacataga tgagtgtaac	1134
atztatatct cacatagaga catgcttata tggttttatt taaaatgaaa tgccagtcca	1194
ttacactgaa taaatagaac tcaactattg cttttcaggg aaatcatgga tagggttgaa	1254
gaaggttact attaatgttt taaaaacagc ttagggatta atgtcctcca tttataatga	1314
agattaaaaat gaaggcttta atcagcattg taaaggaaat tgaatggctt tctgatatgc	1374
tggttttttag ctaggaggtt agaaatccta acttctttat cctcttctcc cagaggcttt	1434
ttttttcttg tgtattaaat taacattttt aaaaagcaga tattttgtca aggggctttg	1494
cattcaaaact gcttttccag ggctatactc agaagaaaga taaaagtgtg atctaagaaa	1554
aagtgatggg tttaggaaaag tgaaaatatt tttgtttttg tatttgaaga agaatgatgc	1614
attttgacaa gaaatcatat atgtatggat atattttaat aagtatttga gtacagactt	1674
tgaggtttca tcaatataaa taaaagagca gaaaaatatg tcttggtttt catttgctta	1734
ccaaaaaaac aacaacaaaa aaagtgtgcc tttgagaact tcacctgctc ctatgtgggt	1794
acctgagtca aaattgtcat ttttgttctg tgaaaaataa atttccttct tgtaccattt	1854
ctgttttagtt ttactaaaat ctgtaaatatc tgtatttttc tgtttattcc aaatttgatg	1914
aaactgacaa tccaatttga aagtttgtgt cgacgtctgt ctagcttaaa tgaatgtgtt	1974
ctatttgctt tatacattta tattaataaa ttgtacattt ttctaattat ttggaaaaaa	2034
aaaaaaaaa a	2045

<210> 151
 <211> 788
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 150..587

<400> 151	
attttcaaat ttaccctctt gtgacttgta agccatgcaa ttcgtagggc taaatatgca	60
gttggttcgat ttcacggttt ggaatctctt gtcaaggagc tgggactctt caattaatct	120
gacatttcac aaatccaaaa ttgccgtgg atg aac tct tta ctt cac ttc ggg	173
Met Asn Ser Leu Leu His Phe Gly	
1 5	
ata ttg ctg gag ctg agt ctc ctg aaa cag ttt aag tct gta tat gtt	221
Ile Leu Leu Glu Leu Ser Leu Leu Lys Gln Phe Lys Ser Val Tyr Val	
10 15 20	
cct gga aat cat acc cac cag gca tct tat aag cca ttg ttg aag caa	269
Pro Gly Asn His Thr His Gln Ala Ser Tyr Lys Pro Leu Leu Lys Gln	
25 30 35 40	
gtt gtg gag gaa ata ttt cat ccc gag agg cca gat tcc gtt gat att	317
Val Val Glu Glu Ile Phe His Pro Glu Arg Pro Asp Ser Val Asp Ile	
45 50 55	
gaa cac atg tct tca ggc ctc act gat ctc ctt aaa act gga ttt agc	365

Glu His Met Ser Ser Gly Leu Thr Asp Leu Leu Lys Thr Gly Phe Ser	
60 65 70	
atg ttc atg aag gtg agc cgg cct cat cct agt gac tac ccc ctc ctg	413
Met Phe Met Lys Val Ser Arg Pro His Pro Ser Asp Tyr Pro Leu Leu	
75 80 85	
atc ctc ttt gtg gta ggt ggg gtc aca gtc tct gaa gtg aaa atg gtc	461
Ile Leu Phe Val Val Gly Gly Val Thr Val Ser Glu Val Lys Met Val	
90 95 100	
aaa gat ctt gtg gca tcg ttg aag cca gga acc cag gta atc gtg ctg	509
Lys Asp Leu Val Ala Ser Leu Lys Pro Gly Thr Gln Val Ile Val Leu	
105 110 115 120	
tcc aca cga ctc ctg aag cca ctt aac att cct gag ctg tta ttt gca	557
Ser Thr Arg Leu Leu Lys Pro Leu Asn Ile Pro Glu Leu Leu Phe Ala	
125 130 135	
act gac cga ctg cat cca gac ctt ggc ttc tgagcatccg ctâagaagat	607
Thr Asp Arg Leu His Pro Asp Leu Gly Phe	
140 145	
aagacctact caagctggaa atgccgatgc aattttctgc caccactcca aatactcctc	667
cacaaccagc gtccctgtca ctaattgcca gaatgatgga attctgcctg aagggtcttg	727
atacctactc agtgaggtac stttgcttgg attgctgtga ttccaaaaaa aaaaaaaaaa	787
a	788

<210> 152
 <211> 1931
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 173..847

<400> 152	
actggatact atctggccag aagtagcaaa gcagctctta tttgaaaaac cactggggttc	60
cgagttcatt actacaggaa aaactgttct cttctgtggc acagagaacc ctgcttcaaa	120
gcagaagtag cagttccgga gtccagctgg ctaaaactca tcccagagga ta atg gca	178
Met Ala	
1	
acc cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg	226
Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met	
5 10 15	
gtg ggc aca gtg gct gtc act gtc atg cct cag tgg aga gtg tcg gcc	274
Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala	
20 25 30	
ttc att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg	322
Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu	
35 40 45 50	
tgg atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc	370
Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile	
55 60 65	
tat gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga	418
Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly	
70 75 80	
ctg atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc	466
Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala	

85	90	95	
atc ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg			514
Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val			
100	105	110	
aag gct cac att ctg ctg acg gct gga atc atc ttc atc atc gcg ggc			562
Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Ala Gly			
115	120	125	130
atg gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga			610
Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg			
135	140	145	
gat ttc tat aac cca ata gtg aat gtt gcc caa aaa cgt gag ctt gga			658
Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly			
150	155	160	
gaa gct ctc tac tta gga tgg acc acg gca ctg gtg ctg att gtt gga			706
Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly			
165	170	175	
gga gct ctg ttc tgc tgc gtt ttt tgt tgc aac gaa aag agc agt agc			754
Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser			
180	185	190	
tac aga tac tcg ata cct tct cat cgc aca acc caa aaa agt tat cac			802
Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His			
195	200	205	210
acc gga aag aag tca ccg agc gtc tac tcc aga agt cag tat gtg			847
Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val			
215	220	225	
tagttgtgta tgttttttta actttactat aaagctatgc aaatgacaaa aatctatatt			907
actttctcaa aatggacccc aaagaaactt tgatttactg ttcttaactg cctaacttta			967
attacaggaa ctgtgcatca gctatttatg attctataag ctatttcagc agaatgagat			1027
attaaatcca atgctttgat tgttctagaa agtatagtaa tttgttttct aaggtgggttc			1087
aagcatctac tctttttatc atttacttca aaatgacatt gctaaagact gcattatatt			1147
actactgtaa tttctccatg acatagcatt atgtacatag atgagtgtaa catttatatc			1207
tcacatagag acatgcttat atgggttttat ttaaaatgaa atgccagtcc attacactga			1267
ataaatagaa ctcaactatt gcttttcagg gaaatcatgg ataggggtga agaaggttac			1327
tattaattgt ttaaaaacag cttagggatt aatgtcctcc atttataatg aagattaaaa			1387
tgaaggcttt aatcagcatt gtaaaggaaa ttgaatggct ttctgatatg ctgtttttta			1447
gcctaggagt tagaaatcct aacttcttta tcctcttctc ccagaggctt tttttttctt			1507
gtgtattaaa ttaacatttt taaaaagcag atattttgtc aaggggcttt gcattcaaac			1567
tgcttttcca gggctatact cagaagaaag ataaaagtgt gatctaagaa aaagtgatgg			1627
tttttaggaaa gtgaaaatat ttttggtttt gtatttgaag aagaatgatg cattttgaca			1687
agaaatcata tatgtatgga tatattttta taagtatttg agtacagact ttgaggtttc			1747
atcaatataa ataaaagagc agaaaaatat gtcttggttt tcatttgctt accaaaaaaa			1807
caacaacaaa aaaagttgtc ctttgagaac ttcacctgct cctatgtggg tacctgagtc			1867
aaaattgtca tttttgttct gtgaaaaata aatttccttc ttgtaccaa aaaaaaaaaa			1927
aaaa			1931

<210> 153
 <211> 514
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 100..441

<400> 153
ataccaggca ctttagaacc agagactctg ctgcttttcc tgggcagggc ctgcttgctc 60
cagctctcaa gtctgacttg catctacact gcgggcaag atg cgg ctg caa gac 114
Met Arg Leu Gln Asp
1 5
cgc atc gcc acg ttc ttc ttc cca aaa ggc atg atg ctc acc acg gct 162
Arg Ile Ala Thr Phe Phe Pro Lys Gly Met Met Leu Thr Thr Ala
10 15 20
gcg ctg atg ctc ttc ttc tta cac ctg ggc atc ttc atc aga gac gtg 210
Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile Phe Ile Arg Asp Val
25 30 35
cac aac ttc tgc atc acc tac cac tat gac cac atg agc ttt cac tac 258
His Asn Phe Cys Ile Thr Tyr His Tyr Asp His Met Ser Phe His Tyr
40 45 50
acg gtc gtc ctg atg ttc tcc cag gtg atc agc atc tgc tgg gct gcc 306
Thr Val Val Leu Met Phe Ser Gln Val Ile Ser Ile Cys Trp Ala Ala
55 60 65
atg ggg tca ctc tat gct gag atg aca gaa aac aat gct caa cgg agc 354
Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn Asn Ala Gln Arg Ser
70 75 80 85
cat gtt ctt caa ccg cct gtc ctt gga gtt tct ggc cat cga gta ccg 402
His Val Leu Gln Pro Pro Val Leu Gly Val Ser Gly His Arg Val Pro
90 95 100
gga gga gca cca ctg agg cct ggg gag tcg gaa cag ggc taaggagggg 451
Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu Gln Gly
105 110
gaagcaaaag gctgcctcgg gtgtttttaat aaagttgttg tttattccaa aaaaaaaaaa 511
aaa 514

<210> 154
<211> 1183
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 32..1132

<400> 154
acttctttcc tgcctctgat tccgggctgt c atg gcg acc ccc aac aat ctg 52
Met Ala Thr Pro Asn Asn Leu
1 5
acc ccc acc aac tgc agc tgg tgg ccc atc tcc gcg ctg gag agc gat 100
Thr Pro Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp
10 15 20
gcg gcc aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc 148
Ala Ala Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro
25 30 35
gcc cat tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc 196
Ala His Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser
40 45 50 55
ttc agc tcg cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg 244
Phe Ser Ser Gln Lys Val Arg Leu Val Ile Ala Glu Lys Gly Leu Val
60 65 70

tgc gag gag cgg gac gtg agc ctg cca cag agc gag cac aag gag ccc	292
Cys Glu Glu Arg Asp Val Ser Leu Pro Gln Ser Glu His Lys Glu Pro	
75 80 85	
tgg ttc atg cgg ctc aac ctg ggc gag gag gtg ccc gtc atc atc cac	340
Trp Phe Met Arg Leu Asn Leu Gly Glu Glu Val Pro Val Ile Ile His	
90 95 100	
cgc gac aac atc atc agt gac tat gac cag atc att gac tat gtg gag	388
Arg Asp Asn Ile Ile Ser Asp Tyr Asp Gln Ile Ile Asp Tyr Val Glu	
105 110 115	
cgc acc ttc aca gga gag cac gtg gtg gcc ctg atg ccc gag gtg ggc	436
Arg Thr Phe Thr Gly Glu His Val Val Ala Leu Met Pro Glu Val Gly	
120 125 130 135	
agc ctg cag cac gca cgg gtg ctg cag tac cgg gag ctg ctg gac gca	484
Ser Leu Gln His Ala Arg Val Leu Gln Tyr Arg Glu Leu Leu Asp Ala	
140 145 150	
ctg ccc atg gat gcc tac acg cat ggc tgc atc ctg cat ccc gag ctc	532
Leu Pro Met Asp Ala Tyr Thr His Gly Cys Ile Leu His Pro Glu Leu	
155 160 165	
acc acc gac tcc atg atc ccc aag tac gcc acg gcc gag atc cgc aga	580
Thr Thr Asp Ser Met Ile Pro Lys Tyr Ala Thr Ala Glu Ile Arg Arg	
170 175 180	
cat tta gcc aat gcc acc acg gac ctc atg aaa ctg gac cat gaa gag	628
His Leu Ala Asn Ala Thr Thr Asp Leu Met Lys Leu Asp His Glu Glu	
185 190 195	
gag ccc cag ctc tcc gag ccc tac ctt tct aaa caa aag aag ctc atg	676
Glu Pro Gln Leu Ser Glu Pro Tyr Leu Ser Lys Gln Lys Lys Leu Met	
200 205 210 215	
gtc aag atc ttg gag cat gat gat gtg agc tac ctg aag aag atc ctc	724
Val Lys Ile Leu Glu His Asp Asp Val Ser Tyr Leu Lys Lys Ile Leu	
220 225 230	
ggg gaa ctg gcc atg gtg ctg gac cag att gag gcg gag ctg gag aag	772
Gly Glu Leu Ala Met Val Leu Asp Gln Ile Glu Ala Glu Leu Glu Lys	
235 240 245	
agg aag ctg gag aac gag ggg cag aaa tgc gag ctg tgg ctc tgt ggc	820
Arg Lys Leu Glu Asn Glu Gly Gln Lys Cys Glu Leu Trp Leu Cys Gly	
250 255 260	
tgt gcc ttc acc ctc gct gat gtc ctc ctg gga gcc acc ctg cac cgc	868
Cys Ala Phe Thr Leu Ala Asp Val Leu Leu Gly Ala Thr Leu His Arg	
265 270 275	
ctc aag ttc ctg gga ctg tcc aag aaa tac tgg gaa gat ggc agc cgg	916
Leu Lys Phe Leu Gly Leu Ser Lys Lys Tyr Trp Glu Asp Gly Ser Arg	
280 285 290 295	
ccc aac ctg cag tcc ttc ttt gag agg gtc cag aga cgc ttt gcc ttc	964
Pro Asn Leu Gln Ser Phe Phe Glu Arg Val Gln Arg Arg Phe Ala Phe	
300 305 310	
cgg aaa gtc ctg ggt gac atc cac acc acc ctg ctg tgc gcc gtc atc	1012
Arg Lys Val Leu Gly Asp Ile His Thr Thr Leu Leu Ser Ala Val Ile	
315 320 325	
ccc aat gct ttc cgg ctg gtc aag agg aaa ccc cca tcc ttc ttc ggg	1060
Pro Asn Ala Phe Arg Leu Val Lys Arg Lys Pro Pro Ser Phe Phe Gly	
330 335 340	
gcg tcc ttc ctc atg ggc tcc ctg ggt ggg atg ggc tac ttt gcc tac	1108
Ala Ser Phe Leu Met Gly Ser Leu Gly Gly Met Gly Tyr Phe Ala Tyr	
345 350 355	

tgg tac ctc aag aaa aaa tac atc tagggccagg cctggggcctt ggtgtctgac 1162
 Trp Tyr Leu Lys Lys Lys Tyr Ile

360 365
 tgtcaaaaaa aaaaaaaaaa a 1183

<210> 155
 <211> 1545
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 160..996

<400> 155
 acacagcatg catttcttca acaagcgact cagaaggcac ttgcacatcg ttgctgttct 60
 gcctctttgc ttcagcatga ttaccagag gcgcacccgt gccgtggcct gcccgtcgtc 120
 tatgcacccg tgctgtggcg tgcccgtcgt ctgtgtggc atg cct gtc tgt gca 174
 Met Pro Val Cys Ala
 1 5
 ccc gtg ctg tgg cgt gcc cgt cgt ctg tgt ggc atg cct gtc tgt gca 222
 Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly Met Pro Val Cys Ala
 10 15 20
 ccc gtg ccg tgg cgt gcc cgt cgt ctg tgc acc cgt gct gtg gtg tgc 270
 Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr Arg Ala Val Val Cys
 25 30 35
 cct tcg tct gtt cct ttt att gcc ggg cag ggt tgc acc cac atg tgc 318
 Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly Cys Thr His Met Cys
 40 45 50
 aag cca gcg acg gac ccc agg ttc acc cgt tca ccg ctg gct gga ggc 366
 Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser Pro Leu Ala Gly Gly
 55 60 65
 gtg atc ctg ggt gtg gcc ctg tgg ctc cgc cat gac ccg cag acc acc 414
 Val Ile Leu Gly Val Ala Leu Trp Leu Arg His Asp Pro Gln Thr Thr
 70 75 80 85
 aac ctc ctg tat ctg gag ctg gga gac aag ccc gcg ccc aac acc ttc 462
 Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro Ala Pro Asn Thr Phe
 90 95 100
 tat gta ggc atc tac atc ctc atc gct gtg ggc gct gtc atg atg ttc 510
 Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly Ala Val Met Met Phe
 105 110 115
 gtt ggc ttc ctg ggc tgc tac ggg gcc atc cag gaa tcc cag tgc ctg 558
 Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln Glu Ser Gln Cys Leu
 120 125 130
 ctg ggg acg ttc ttc act tgc ctg gtc atc ctg ttt gcc tgt gag gtg 606
 Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu Phe Ala Cys Glu Val
 135 140 145
 gcc gcc ggc atc tgg ggc ttt gtc aac aag gac cag atc gcc aag gat 654
 Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp Gln Ile Ala Lys Asp
 150 155 160 165
 gtg aag cag ttc tat gac cag gcc cta cag cag gcc gtg gtg gat gat 702
 Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln Ala Val Val Asp Asp
 170 175 180
 gac gcc aac aac gcc aag gct gtg gtg aag acc ttc cac gag acg ctt 750

Asp	Ala	Asn	Asn	Ala	Lys	Ala	Val	Val	Lys	Thr	Phe	His	Glu	Thr	Leu	
			185					190					195			
gac	tgc	tgt	ggc	tcc	agc	aca	ctg	act	gct	ttg	acc	acc	tca	gtg	ctc	798
Asp	Cys	Cys	Gly	Ser	Ser	Thr	Leu	Thr	Ala	Leu	Thr	Thr	Ser	Val	Leu	
		200					205					210				
aag	aac	aat	ttg	tgt	ccc	tcg	ggc	agc	aac	atc	atc	agc	aac	ctc	ttc	846
Lys	Asn	Asn	Leu	Cys	Pro	Ser	Gly	Ser	Asn	Ile	Ile	Ser	Asn	Leu	Phe	
		215					220					225				
aag	gag	gac	tgc	cac	cag	aag	atc	gat	gac	ctc	ttc	tcc	ggg	aag	ctg	894
Lys	Glu	Asp	Cys	His	Gln	Lys	Ile	Asp	Asp	Leu	Phe	Ser	Gly	Lys	Leu	
230					235					240					245	
tac	ctc	atc	ggc	att	gct	gcc	atc	gtg	gtc	gct	gtg	atc	atg	atc	ttc	942
Tyr	Leu	Ile	Gly	Ile	Ala	Ala	Ile	Val	Val	Ala	Val	Ile	Met	Ile	Phe	
				250					255					260		
gag	atg	atc	ctg	agc	atg	gtg	ctg	tgc	tgt	ggc	atc	cgg	aac	agc	tcc	990
Glu	Met	Ile	Leu	Ser	Met	Val	Leu	Cys	Cys	Gly	Ile	Arg	Asn	Ser	Ser	
			265					270					275			
gtg	tac	tgaggccccg	cagctctggc	cacagggacc	tctgcagtgc	cccctaagtg										1046
Val	Tyr															
acccggacac	ttccgagggg	gccatcacccg	cctgtgtata	taacgtttcc	ggtattactc											1106
tgctacacgt	agccttttta	cttttggggt	tttgtttttg	ttctgaactt	tcctgttacc											1166
ttttcagggc	tgacgtcaca	tgtaggtggc	gtgtatgagt	ggagacgggc	ctgggtcttg											1226
gggactggag	ggcaggggtc	cttctgccct	ggggtcccag	ggtgctctgc	ctgctcagcc											1286
aggcctctcc	tgggagccac	tcgcccagag	actcagcttg	gccaacttgg	ggggctgtgt											1346
ccaccagccc	cgcccgtcct	gtgggctgca	cagctcacct	tggtccctcc	tgccccggtt											1406
cgagagccga	gtctgtgggc	actctctgcc	ttcatgcacc	tgctctttct	aacacgtcgc											1466
cttcaactgt	aatcacaca	tcctgactcc	gtcatttaat	aaagaaggaa	catcaggcat											1526
gcaaaaaaaaa	aaaaaaaaa															1545

<210> 156
 <211> 1068
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 11..529

<400> 156	
gaagcacgga	atg tgt ctc ctg ctg ggg gcc acg ggc gtc ggg aag acg
	Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr
	1 5 10
ctg ctg gtg	aaa cgg ctg cag gag gtg agc tcc cgg gat ggg aaa ggc
Leu Leu Val	Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly
	15 20 25
gac ctg ggg	gag ccg ccc ccg aca cgg ccc acg gtg ggc acc aat ctt
Asp Leu Gly	Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu
	30 35 40 45
act gac atc	gtg gca cag aga aag atc acc atc cgg gag ctt ggg ggg
Thr Asp Ile	Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly
	50 55 60
tgc atg ggc	ccc atc tgg tcc agt tac tat gga aac tgc cgt tct ctc
Cys Met Gly	Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu
	65 70 75

ctg ttt gtg atg gac gcc tct gac ccc acc cag ctc tct gca tcc tgt	289
Leu Phe Val Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys	
80 85 90	
gtg cag ctc tta ggt ctc ctt tct gca gaa caa ctt gca gaa gca tcg	337
Val Gln Leu Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser	
95 100 105	
gtg ctg ata ctc ttc aat aaa atc gac cta ccc tgt tac atg tcc acg	385
Val Leu Ile Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr	
110 115 120 125	
gag gag atg aag tca tta atc agg ctt cca gac atc att gct tgt gcc	433
Glu Glu Met Lys Ser Leu Ile Arg Leu Pro Asp Ile Ile Ala Cys Ala	
130 135 140	
aag cag aac atc acc acg gca gaa atc agc gcc cgt gaa ggc act ggc	481
Lys Gln Asn Ile Thr Thr Ala Glu Ile Ser Ala Arg Glu Gly Thr Gly	
145 150 155	
tta gca ggg gtg ctg gcc tgg ctc cag gcc acc cac aga gcc aac gat	529
Leu Ala Gly Val Leu Ala Trp Leu Gln Ala Thr His Arg Ala Asn Asp	
160 165 170	
tgactgcacg gcagaggcgc agctggcctg agctggggag aggtggcaga gggcagtatg	589
gcttttgctgc caatagtttc ttctcacagg ggcagaataa cccaaagtaa ccctacatga	649
tggggctctg tgctgggatg caatgatgtg taaactgagg catgtggaga tggaagttga	709
catctggcct ctgaaaaaag tgtccccagg ggctaggcat ggtggctcac acctgtaatc	769
ccagcacttt gagaggccga ggcgggtgta tcacctgagg tcgggagttc gagactagcc	829
tgaccaacat ggagaaaccc tgttcttact aaaaatacaa aattagctgg gtgtgctggt	889
gcatgcctgt aatctcagct acttgggagg ctgagacagg agaatccctt gaacctggga	949
ggtggagggt gcagtgagtc gagatcatgc cattgcactg cacctgggca acaagagtga	1009
aactccgtct taaaaaatat aagaaataaa aaaataaaaa cctaaaaaaaa aaaaaaaaaa	1068
<210> 157	
<211> 1097	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 135..749	
<400> 157	
aacgaaacgg taaccagccc tgggaagccc gcaagaggcc tcagcgggtgg ccgtccgagc	60
gccgagaggt gagggtgccc ccgcctcacc tgcagagggg ccgttccggg ctcgaaccgg	120
gcaccttccg gaaa atg gcg gct gcc agg ccc agc ctg ggc mga gtc ctc	170
Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu	
1 5 10	
cca gga tcc tct gtc ctg ttc ctg tgt gac atg cag gag aag ttc cgc	218
Pro Gly Ser Ser Val Leu Phe Leu Cys Asp Met Gln Glu Lys Phe Arg	
15 20 25	
cac aac atc gcc tac ttc cca cag atc gtc tca gtg gct gcc cgc atg	266
His Asn Ile Ala Tyr Phe Pro Gln Ile Val Ser Val Ala Ala Arg Met	
30 35 40	
ctc aag gtg gcc cgg ctg ctt gag gtg cca gtc atg ctg acg gag cag	314
Leu Lys Val Ala Arg Leu Leu Glu Val Pro Val Met Leu Thr Glu Gln	
45 50 55 60	
tac cca caa ggc ctg ggc ccc acg gtg ccc gag ctg ggg act gag ggc	362
Tyr Pro Gln Gly Leu Gly Pro Thr Val Pro Glu Leu Gly Thr Glu Gly	

	65	70	75	
ctt cgg ccg ctg gcc aag acc tgc ttc agc atg gtg cct gcc ctg cag				410
Leu Arg Pro Leu Ala Lys Thr Cys Phe Ser Met Val Pro Ala Leu Gln				
	80	85	90	
cag gag ctg gac agt cgg ccc cag ctg cgc tct gtg ctg ctc tgt ggc				458
Gln Glu Leu Asp Ser Arg Pro Gln Leu Arg Ser Val Leu Leu Cys Gly				
	95	100	105	
att gag gca cag gcc tgc atc ttg aac acg acc ctg gac ctc cta gac				506
Ile Glu Ala Gln Ala Cys Ile Leu Asn Thr Thr Leu Asp Leu Leu Asp				
	110	115	120	
cgg ggg ctg cag gtc cat gtg gtg gtg gac gcc tgc tcc tca cgc agc				554
Arg Gly Leu Gln Val His Val Val Val Asp Ala Cys Ser Ser Arg Ser				
	125	130	135	140
cag gtg gac cgt ctg gtg gct ctg gcc cgc atg aga cag agt ggt gcc				602
Gln Val Asp Arg Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala				
	145	150	155	
ttc ctc tcc acc agc gaa ggg ctc att ctg cag ctt gtg ggc gat gcc				650
Phe Leu Ser Thr Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala				
	160	165	170	
gtc cac ccc cag ttc aag gag atc cag aaa ctc atc aag gag ccc gcc				698
Val His Pro Gln Phe Lys Glu Ile Gln Lys Leu Ile Lys Glu Pro Ala				
	175	180	185	
cca gac agc gga ctg ctg ggc ctc ttc caa ggc cag aac tcc ctc ctc				746
Pro Asp Ser Gly Leu Leu Gly Leu Phe Gln Gly Gln Asn Ser Leu Leu				
	190	195	200	
cac tgaactccaa ccctgccttg agggaagacc accctcctgt caccgcggacc				799
His				
205				
tcagtgggaag cccgttcccc ccatccctgg atcccaagag tgggtgcgatc caccaggagt				859
gccgccccct tgtggggggg ggcaggggtgc tgccttccca ttggacagct gctcccggaa				919
atgcaaata gactcctgga aactgggtgg gaattggctg agccaagatg gaggcggggc				979
tcggcccccg gccacttcac ggggcgggaa ggggagggga agaagagtct cagactgtgg				1039
gacacggact cgcagaataa acatatatgt ggctgtggac caaaaaaaaa aaaaaaaa				1097
<210> 158				
<211> 894				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> 98..637				
<400> 158				
ctttggggcc gaagtgggcg tgcggctcgc gctgttcgcg gccttcctgg tgacggagct				60
gctccccccg ttccagagac tcatccagcc ggaggag atg tgg ctc tac cgg aac				115
		Met Trp Leu Tyr Arg Asn		
		1	5	
ccc tac gtg gag gcg gag tat ttc ccc acc aag ccg atg ttt gtt att				163
Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile				
	10	15	20	
gca ttt ctc tct cca ctg tct ctg atc ttc ctg gcc aaa ttt ctc aag				211
Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys				
	25	30	35	

aag gca gac aca aga gac agc aga caa gcc tgc ctg gct gcc agc ctt	259
Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu	
40 45 50	
gcc ctg gct ctg aat ggc gtc ttt acc aac aca ata aaa ctg atc gta	307
Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val	
55 60 65 70	
ggg agg cca cgc cca gat ttc ttc tac cgc tgc ttc cct gat ggg cta	355
Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu	
75 80 85	
gcc cat tct gac ttg atg tgt aca ggg gat aag gac gtg gtg aat gag	403
Ala His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn Glu	
90 95 100	
ggc cga aag agc ttc ccc agt gga cat tct tcc ttt gca ttt gct ggt	451
Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly	
105 110 115	
ctg gcc ttt gcg tcc ttc tac ctg gca ggg aag tta cac tgc ttc aca	499
Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr	
120 125 130	
cca caa ggc cgt ggg aaa tct tgg agg ttc tgt gcc ttt ctg tca cct	547
Pro Gln Gly Arg Gly Lys Ser Trp Arg Phe Cys Ala Phe Leu Ser Pro	
135 140 145 150	
cta ctt ttt gca gct gtg att gca ctg tcc cgc aca tgt gac tac aag	595
Leu Leu Phe Ala Ala Val Ile Ala Leu Ser Arg Thr Cys Asp Tyr Lys	
155 160 165	
cat cac tgg caa gat ctg ctc aaa tgc acc aac act gcc aag	637
His His Trp Gln Asp Leu Leu Lys Cys Thr Asn Thr Ala Lys	
170 175 180	
tgactaaggt agaaaagaaa aatgacaggt atcgctcatct gaaggacaga tgaatctttt	697
tctgccccctt cttcacaatg gaatataagg aacaattatg ggatgtcatc agaatggatg	757
ccataggacc tacagctccc tttctcttta ttgtgattat actttaata tgacattgtc	817
ttttatgtgt atgttcctat attttcaatg tatctttttc cttcagtaaa cctgatattc	877
aaaaaaaaa aaaaaaa	894

<210> 159
 <211> 703
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 221..670

<400> 159	
aaggaagcgc cgcccccttc tacggctacg ggaaggatcg tccagtggct gaggctggac	60
agagcacaga caaaagataa aaagcaagat ttgagagagg ttcttgatc aactggctca	120
atctgcttag ttctacaaag tggagtttct gggcatcatt cttcatttct gtacacaaag	180
tgctgtgaag ctcaagaaga aatagctctg cacaggaacg atg tgc act gcc cta	235
Met Cys Thr Ala Leu	
1 5	
ctg ctt ctt tat cta aga tgg tgt ttc aac tta aaa ctt gtg aat gtg	283
Leu Leu Leu Tyr Leu Arg Trp Cys Phe Asn Leu Lys Leu Val Asn Val	
10 15 20	
aaa tat gag cca aaa gac tct ctc ggc cct gaa atg acc ttt gta gca	331
Lys Tyr Glu Pro Lys Asp Ser Leu Gly Pro Glu Met Thr Phe Val Ala	

	25		30		35	
gat gct gcc aga ggc ccc ctg tta tcc tcc ctg gac tct cca gct aac						379
Asp Ala Ala Arg Gly Pro Leu Leu Ser Ser Leu Asp Ser Pro Ala Asn						
	40		45		50	
ctg atg tca act gcc agt gtg tgc atc tcc tta cct gag ggc tgt tct						427
Leu Met Ser Thr Ala Ser Val Cys Ile Ser Leu Pro Glu Gly Cys Ser						
	55		60		65	
ggt ggc agg agt cct tgc tac tca cag aaa tgg cca cca gaa gtg cca						475
Gly Gly Arg Ser Pro Cys Tyr Ser Gln Lys Trp Pro Pro Glu Val Pro						
70		75		80		85
gaa aaa tta acc tcc ctt ggc cag cag tcc tca acc agc tcc ctc act						523
Glu Lys Leu Thr Ser Leu Gly Gln Gln Ser Ser Thr Ser Ser Leu Thr						
	90		95		100	
gac act gat gtg cag gtg tct cct atg ctg gtt gct gga gtc aac cac						571
Asp Thr Asp Val Gln Val Ser Pro Met Leu Val Ala Gly Val Asn His						
	105		110		115	
agc agc agc ctt ctt gac aac ata ccc ttc act ggc tgc ctt cct ttc						619
Ser Ser Ser Leu Leu Asp Asn Ile Pro Phe Thr Gly Cys Leu Pro Phe						
	120		125		130	
cat ctc tct tct tca ctc ccc tac cta tgt ctc cta ggc tct ccc ttc						667
His Leu Ser Ser Ser Leu Pro Tyr Leu Cys Leu Leu Gly Ser Pro Phe						
	135		140		145	
aaa taaacagctt gcacttgaaa aaaaaaaaaa aaa						703
Lys						
150						

<210> 160
 <211> 849
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 165..674

<400> 160	
aaaactgagg cctgggagca ggaacctgta ggcagcgctt gagggtagcg ggatagcagc	60
tgcaagcgcg cgtgggaggc gggggctctg ggcggaacaa aaatcacagg atgtcagagg	120
atgtttcccg ggaagaactg ggataaagga aggggtcccg cacc atg gag gac ccg	176
	Met Glu Asp Pro
	1
aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt	224
Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser	
5	10 15 20
ccc cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc	272
Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys	
	25 30 35
acc cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac	320
Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His	
	40 45 50
atg aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg	368
Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly	
	55 60 65
gtc ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa	416

Val	Leu	Phe	Ile	Cys	Phe	Thr	Cys	Ala	Arg	Ser	Phe	Pro	Ser	Ser	Lys	
70						75				80						
gcc	cta	atc	acc	cac	cag	cgc	agc	cac	ggc	cca	gcc	gcc	aag	ccc	acc	464
Ala	Leu	Ile	Thr	His	Gln	Arg	Ser	His	Gly	Pro	Ala	Ala	Lys	Pro	Thr	
85					90				95					100		
ctg	ccg	gtt	gca	acc	act	act	gcc	cag	ccc	acc	ttc	cct	tgt	cct	gac	512
Leu	Pro	Val	Ala	Thr	Thr	Thr	Ala	Gln	Pro	Thr	Phe	Pro	Cys	Pro	Asp	
				105					110					115		
tgt	ggc	aag	acc	ttt	ggg	cag	gct	gtt	tct	ctg	agg	cgg	cac	cgc	cag	560
Cys	Gly	Lys	Thr	Phe	Gly	Gln	Ala	Val	Ser	Leu	Arg	Arg	His	Arg	Gln	
			120				125					130				
atg	cat	gag	gtc	cgt	gcc	cct	cct	ggc	acc	ttc	gcc	tgc	aca	gag	tgc	608
Met	His	Glu	Val	Arg	Ala	Pro	Pro	Gly	Thr	Phe	Ala	Cys	Thr	Glu	Cys	
			135				140					145				
ggc	cag	gac	ttt	gct	cag	gaa	gca	ggg	ctg	cat	caa	cac	tac	att	cgg	656
Gly	Gln	Asp	Phe	Ala	Gln	Glu	Ala	Gly	Leu	His	Gln	His	Tyr	Ile	Arg	
			150				155				160					
cat	gcc	cgg	ggg	gag	ctc	tgagtgcagc	ttaagcctct	ccacggtgac								704
His	Ala	Arg	Gly	Glu	Leu											
165					170											
gggtggctct	gtggctggtg	ggactcaccc	atgatatggg	gtgcaggaac	tctggggggcc											764
ctgaaggatt	tgcttccttc	ccctgggaag	gcagagggct	cttaataaag	aggaccaga											824
agattctcaa	aaaaaaaaaa	aaaaa														849

<210> 161

<211> 846

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 165..671

<400> 161

aaaactgagg	cctgggagca	ggaacctgta	ggcagcgctt	gagggtagcg	ggatagcagc		60
tgcaagcgcg	cgtgggaggc	gggggctctg	ggcggaacaa	aatcacagg	atgtcagagg		120
atgtttcccg	ggaagaactg	ggataaagga	agggctccag	cacc atg	gag gac ccg		176
				Met	Glu Asp Pro		
				1			
aac cct	gaa gag	aac atg	aag cag	cag gat	tca ccc	aag gag	aga agt
Asn Pro	Glu Glu	Asn Met	Lys Gln	Gln Asp	Ser Pro	Lys Glu	Arg Ser
5		10		15		20	
ccc cag	ccc agg	agg caa	cat ctg	cca cct	ggg ggc	ccc gaa	gtg cac
Pro Gln	Pro Arg	Arg Gln	His Leu	Pro Pro	Gly Gly	Pro Glu	Val His
		25		30		35	
ccg ctg	cct cat	cac ctt	cgc aga	ttc caa	ggt cca	gga gcg	tca cat
Pro Leu	Pro His	His Leu	Arg Arg	Phe Gln	Val Pro	Gly Ala	Ser His
		40		45		50	
gaa gcg	gga gca	ccc agc	gga ctt	cgt ggc	cca gaa	gct gca	ggg ggt
Glu Ala	Gly Ala	Pro Ser	Gly Leu	Arg Gly	Pro Glu	Ala Ala	Gly Gly
		55		60		65	
cct ctt	cat ctg	ctt cac	ctg cgc	ccg ctc	ctt ccc	ctc ctc	caa agc
Pro Leu	His Leu	Leu His	Leu Arg	Pro Leu	Leu Leu	Leu Leu	Gln Ser
		70		75		80	

cct aat cac cca cca gcg cag cac ggt cca gcc gcc aag ccc acc ctg	464
Pro Asn His Pro Pro Ala Gln His Gly Pro Ala Ala Lys Pro Thr Leu	
85 90 95 100	
ccg gtt gca acc act act gcc cag ccc acc ttc cct tgt cct gac tgt	512
Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys	
105 110 115	
ggc aag acc ttt ggg cag gct gtt tct ctg agg cgg cac cgc cag atg	560
Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln Met	
120 125 130	
cat gag gtc cgt gcc cct cct ggc acc ttc gcc tgc aca gag tgc ggt	608
His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys Gly	
135 140 145	
cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg cat	656
Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg His	
150 155 160	
gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacggtgac ggggtggctct	711
Ala Arg Gly Glu Leu	
165	
gtggctggta ggactcaccc atgatatggg gtgcaggaac tctggggggcc ctgaaggatt	771
tgcttccttc ccctgggaag gcagagggct cttaataaag aggaccaga agattctcaa	831
aaaaaaaaaa aaaaa	846

<210> 162
 <211> 1176
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..1128

<400> 162	
ctttcctgcc tctgattccg ggctgtc atg gcg acc ccc aac aat ctg acc ccc	54
Met Ala Thr Pro Asn Asn Leu Thr Pro	
1 5	
acc aac tgc agc tgg tgg ccc atc tcc gcg ctg gag agc gat gcg gcc	102
Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp Ala Ala	
10 15 20 25	
aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc gcc cat	150
Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro Ala His	
30 35 40	
tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc ttc agc	198
Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser Phe Ser	
45 50 55	
tcg cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg tgc gag	246
Ser Gln Lys Val Arg Leu Val Ile Ala Glu Lys Gly Leu Val Cys Glu	
60 65 70	
gag cgg gac gtg agc ctg cca cag agc gag cac aag gag ccc tgg ttc	294
Glu Arg Asp Val Ser Leu Pro Gln Ser Glu His Lys Glu Pro Trp Phe	
75 80 85	
atg cgg ctc aac ctg ggc gag gag gtg ccc gtc atc atc cac cgc gac	342
Met Arg Leu Asn Leu Gly Glu Glu Val Pro Val Ile Ile His Arg Asp	
90 95 100 105	
aac atc atc agt gac tat gac cag atc att gac tat gtg gag cgc acc	390

Asn	Ile	Ile	Ser	Asp	Tyr	Asp	Gln	Ile	Ile	Asp	Tyr	Val	Glu	Arg	Thr		
				110					115					120			
ttc	aca	gga	gag	cac	gtg	gtg	gcc	ctg	atg	ccc	gag	gtg	ggc	agc	ctg	438	
Phe	Thr	Gly	Glu	His	Val	Val	Ala	Leu	Met	Pro	Glu	Val	Gly	Ser	Leu		
			125					130					135				
cag	cac	gca	cgg	gtg	ctg	cag	tac	cgg	gag	ctg	ctg	gac	gca	ctg	ccc	486	
Gln	His	Ala	Arg	Val	Leu	Gln	Tyr	Arg	Glu	Leu	Leu	Asp	Ala	Leu	Pro		
		140					145					150					
atg	gat	gcc	tac	acg	cat	ggc	tgc	atc	ctg	cat	ctc	gag	ctc	acc	acc	534	
Met	Asp	Ala	Tyr	Thr	His	Gly	Cys	Ile	Leu	His	Leu	Glu	Leu	Thr	Thr		
	155					160					165						
gac	tcc	atg	atc	ccc	aag	tac	gcc	acg	gcc	gag	atc	cgc	aga	cat	tta	582	
Asp	Ser	Met	Ile	Pro	Lys	Tyr	Ala	Thr	Ala	Glu	Ile	Arg	Arg	His	Leu		
170					175					180					185		
gcc	aat	gcc	acc	acg	gac	ctc	atg	aaa	ctg	gac	cat	gaa	gag	gag	ccc	630	
Ala	Asn	Ala	Thr	Thr	Asp	Leu	Met	Lys	Leu	Asp	His	Glu	Glu	Glu	Pro		
			190					195						200			
cag	ctc	tcc	gag	ccc	tac	ctt	tct	aaa	caa	aag	aag	ctc	atg	gcc	aag	678	
Gln	Leu	Ser	Glu	Pro	Tyr	Leu	Ser	Lys	Gln	Lys	Lys	Leu	Met	Ala	Lys		
			205					210					215				
atc	ttg	gag	cat	gat	gat	gtg	agc	tac	ctg	aag	aag	atc	ctc	ggg	gaa	726	
Ile	Leu	Glu	His	Asp	Asp	Val	Ser	Tyr	Leu	Lys	Lys	Ile	Leu	Gly	Glu		
	220					225						230					
ctg	gcc	atg	gtg	ctg	gac	cag	att	gag	gcg	gag	ctg	gag	aag	agg	aag	774	
Leu	Ala	Met	Val	Leu	Asp	Gln	Ile	Glu	Ala	Glu	Leu	Glu	Lys	Arg	Lys		
	235					240					245						
ctg	gag	aac	gag	ggg	cag	aaa	tgc	gag	ctg	tgg	ctc	tgt	ggc	tgt	gcc	822	
Leu	Glu	Asn	Glu	Gly	Gln	Lys	Cys	Glu	Leu	Trp	Leu	Cys	Gly	Cys	Ala		
250				255				260					265				
ttc	acc	ctc	gct	gat	gtc	ctc	ctg	gga	gcc	acc	ctg	cac	cgc	ctc	aag	870	
Phe	Thr	Leu	Ala	Asp	Val	Leu	Leu	Gly	Ala	Thr	Leu	His	Arg	Leu	Lys		
			270					275					280				
ttc	ctg	gga	ctg	tcc	aag	aaa	tac	tgg	gaa	gat	ggc	agc	cgg	ccc	aac	918	
Phe	Leu	Gly	Leu	Ser	Lys	Lys	Tyr	Trp	Glu	Asp	Gly	Ser	Arg	Pro	Asn		
		285					290					295					
ctg	cag	tcc	ttc	ttt	gag	agg	gtc	cag	aga	cgc	ttt	gcc	ttc	cgg	aaa	966	
Leu	Gln	Ser	Phe	Phe	Glu	Arg	Val	Gln	Arg	Arg	Phe	Ala	Phe	Arg	Lys		
	300					305					310						
gtc	ctg	ggt	gac	atc	cac	acc	acc	ctg	ctg	tcg	gcc	gtc	atc	ccc	aat	1014	
Val	Leu	Gly	Asp	Ile	His	Thr	Thr	Leu	Leu	Ser	Ala	Val	Ile	Pro	Asn		
	315					320					325						
gct	ttc	cgg	ctg	gtc	aag	agg	aaa	ccc	cca	tcc	ttc	ttc	ggg	gcg	tcc	1062	
Ala	Phe	Arg	Leu	Val	Lys	Arg	Lys	Pro	Pro	Ser	Phe	Phe	Gly	Ala	Ser		
330				335				340					345				
ttc	ctc	atg	ggc	tcc	ctg	ggt	ggg	atg	ggc	tac	ttt	gcc	tac	tgg	tac	1110	
Phe	Leu	Met	Gly	Ser	Leu	Gly	Gly	Met	Gly	Tyr	Phe	Ala	Tyr	Trp	Tyr		
			350				355					360					
ctc	aag	aaa	aaa	tac	atc	tagggccagg	cctggggcctt	ggtgtctgac								1158	
Leu	Lys	Lys	Lys	Tyr	Ile												
			365														
aaaaaamaaa	aaaaaaaa															1176	

<210> 163
<211> 1084

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 135..194

```

<400> 163
aacgaaacgg taaccagccc tgggaagccc gcaagaggcc tcagcgggtgg ccgtccgagc      60
gccgagaggt gaggggtgccc ccgcctcacc tgcagagggg ccgttccggg ctcgaaccgg      120
gcaccttccg gaaa atg gcg gct gcc agg ccc agc ctg ggc cga gtc ctc      170
               Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu
                   1             5             10
cca gga tcc tct cct gtt cct gtg tgacatgcag gagaagttcc gccacaacat      224
Pro Gly Ser Ser Pro Val Pro Val
                   15             20
cgcctacttc ccacagatcg tctcagtggc tgcccgcgatg ctcaagggtgg cccgggtgct      284
tgaggtgcca gtcagtctga cggagcagta cccacaaggc ctgggcccga cggtgcccga      344
gctggggact gagggccttc ggccgctggc caagacctgc ttcagcatgg tgcttgcctt      404
gcagcaggag ctggacagtc ggccccagct gcgctctgtg ctgctctgtg gcattgaggc      464
acaggcctgc atcttgaaca cgaccttga cctcctagac cgggggctgc aggtccatgt      524
ggtggtggac gcctgtctct caccagcca ggtggaccgg ctggtggctc tggcccgcct      584
gagacagagt ggtgccttcc tctccaccag cgaagggttc attctgcagc ttgtgggcga      644
tgccgtccac cccagttca aggagatcca gaaactcatc aaggagcccg cccagacag      704
cggactgctg ggctcttcc aaggccagaa ctccctctc cactgaactc caacctgcc      764
ttgagggaag accacctcc tgtcaccgg acctcagtgg aagcccgttc ccccatccc      824
tggatcccaa gagtgggtgc atccaccagg agtgccgccc ccttgggggg ggcagggtgc      884
tgcttccca ttggacagct gctcccgaa atgcaaatga gactcctgga aactgggtgg      944
gaattggctg agccaagatg gaggcggggc tcggccccgg gccacttcac ggggcgggaa      1004
ggggagggga agaagagtct cagactgtgg gacacggact cgcagaataa acatatatgt      1064
ggcaaaaaaa aaaaaaaaaa                                     1084

```

<210> 164
<211> 1793
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 173..847

```

<400> 164
gsmggrrggc attacctaga acatcstaac cgaarratta tttgaaaaac cactgggttc      60
cgagttcatt actacaggaa aaactgttct cttctgtggc acagagaacc ctgcttcaaa      120
gcagaagtag cagttccgga gtccagctgg ctaaaactca tcccagagga ta atg gca      178
               Met Ala
                   1
acc cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg      226
Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met
                   5             10             15
gtg ggc aca gtg gct gtc act gtc atg cct cag tgg aga gtg tcg gcc      274
Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala
                   20             25             30
ttc att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg      322

```

Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu	
35 40 45 50	
tgg atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc	370
Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile	
55 60 65	
tat gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga	418
Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly	
70 75 80	
ctg atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc	466
Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala	
85 90 95	
atc ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg	514
Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val	
100 105 110	
aag gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc	562
Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly	
115 120 125 130	
atg gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga	610
Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg	
135 140 145	
gat ttc tat aac tca ata gtg aat gtt gcc caa aaa cgt gag ctt gga	658
Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly	
150 155 160	
gaa gct ctc tac tta gga tgg acc acg gca ctg gtg ctg att gtt gga	706
Glu Ala Leu Tyr Leu Gly Trp Thr Ala Leu Val Leu Ile Val Gly	
165 170 175	
gga gct ctg ttc tgc tgc gtt ttt tgt tgc aac gaa aag agc agt agc	754
Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser	
180 185 190	
tac aga tac tcg ata cct tcc cat cgc aca acc caa aaa agt tat cac	802
Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His	
195 200 205 210	
acc gga aag aag tca ccg agc gtc tac tcc aga agt cag tat gtg	847
Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val	
215 220 225	
tagttgtgta tgttttttta actttactat aaagccatgc aaatgacaaa aatctatatt	907
actttctcaa aatggacccc aaagaaactt tgattttactg ttcttaactg cctaacttta	967
attacaggaa ctgtgcatca gctattttatg attctataag ctatttcagc agaatgagat	1027
attaaaccca atgctttgat tgttctagaa agtattgtaa tttgttttct aaggtggttc	1087
aagcatctac tctttttatc atttacttca aaatgacatt gctaaagact gcattattct	1147
actactgtaa tttctccacg acatagcatt atgtacatag atgagtgtaa catttatatc	1207
tcacatagag acatgcttat atggttttat ttaaaatgaa atgccagtcc attacactga	1267
ataaatagaa ctcaactatt gctttttcagg gaaatcatgg atagggttga agaaggttac	1327
tattaattgt ttaaaaacag cttatggatt aatgtcctcc atttataatg aagattaaaa	1387
tgaaggcttt aatcagcatt gtaaaggaaa ttgaatggct ttctgatatg ctgtttttta	1447
gcctaggagt tagaaatcct aacttcttta tcctcttctc ccagaggctt tttttttctt	1507
gtgtattaaa ttaacatttt taaaaagcag atattttgtc aaggggcttt gcattcaaac	1567
tgcttttcca gggctatact cagaagaaag ataaaagtgt gatctaagaa aaagtgatgg	1627
tttttaggaaa gtgaaaatat ttttgttttt gtatttgaa aagaatgatg cattttgaca	1687
agaaatcata tatgtatgta tatattttta taagtatttg agtacagact ttgaggtttc	1747
atcaatataa ataaaagagc agaaaagtaa aaaaaaaaa aaaaaa	1793

<210> 165
<211> 1849

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 8..1141

<220>
 <221> misc_feature
 <222> 1707
 <223> n=a, g, c or t

<400> 165
 cggttgcc atg gat cct ggg gac gac tgg ctg gtg gaa tcc ttg cgc ttg 49
 Met Asp Pro Gly Asp Asp Trp Leu Val Glu Ser Leu Arg Leu
 1 5 10
 tac cag gat ttc tat gca ttc gac ctg tca gga gcc act cga gtc ctt 97
 Tyr Gln Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu
 15 20 25 30
 gaa tgg att gat gac aaa gga gtc ttt gtt gct ggc tat gaa agc ctg 145
 Glu Trp Ile Asp Asp Lys Gly Val Phe Val Ala Gly Tyr Glu Ser Leu
 35 40 45
 aaa aag aat gaa att ctt cat ctg aaa tta cct ctc aga ctt tct gta 193
 Lys Lys Asn Glu Ile Leu His Leu Lys Leu Pro Leu Arg Leu Ser Val
 50 55 60
 aag gaa aac aag ggc tta ttc cca gaa aga gat ttc aaa gtg cgc cat 241
 Lys Glu Asn Lys Gly Leu Phe Pro Glu Arg Asp Phe Lys Val Arg His
 65 70 75
 gga gga ttt tca gac agg tct atc ttt gat cta aag cat gtg cca cat 289
 Gly Gly Phe Ser Asp Arg Ser Ile Phe Asp Leu Lys His Val Pro His
 80 85 90
 acc aga ttg ctg gtt acc agt ggc ctt cca ggt tgt tat ctg cag gtg 337
 Thr Arg Leu Leu Val Thr Ser Gly Leu Pro Gly Cys Tyr Leu Gln Val
 95 100 105 110
 tgg cag gtt gca gag gac agt gat gtc att aaa gct gtc agc acc att 385
 Trp Gln Val Ala Glu Asp Ser Asp Val Ile Lys Ala Val Ser Thr Ile
 115 120 125
 gct gtg cat gag aaa gag gag agt ctc tgg cct agg gtg gcc gtc ttc 433
 Ala Val His Glu Lys Glu Glu Ser Leu Trp Pro Arg Val Ala Val Phe
 130 135 140
 tcc aca ttg gca ccc gga gtc ctc cat ggg gcg agg ctc cga agt ctg 481
 Ser Thr Leu Ala Pro Gly Val Leu His Gly Ala Arg Leu Arg Ser Leu
 145 150 155
 cag gtc gtt gat ctg gag tcc cgg aag acc acg tac acc tca gat gtc 529
 Gln Val Val Asp Leu Glu Ser Arg Lys Thr Thr Tyr Thr Ser Asp Val
 160 165 170
 agt gac agt gag gag ctg agt agc ctg cag gtc cta gat gcg gac acc 577
 Ser Asp Ser Glu Glu Leu Ser Ser Leu Gln Val Leu Asp Ala Asp Thr
 175 180 185 190
 ttt gcc ttc tgc tgt gct tcg ggc cgg ctg ggg ctt gtt gac acc cgg 625
 Phe Ala Phe Cys Cys Ala Ser Gly Arg Leu Gly Leu Val Asp Thr Arg
 195 200 205
 cag aag tgg gca ccg ttg gag aat cgc agc cct ggc cct ggg tct ggt 673
 Gln Lys Trp Ala Pro Leu Glu Asn Arg Ser Pro Gly Pro Gly Ser Gly

	210		215		220	
gga gag aga tgg tgt gct gaa gtt ggg agc tgg ggc cag ggc cct ggg						721
Gly Glu Arg Trp Cys Ala Glu Val Gly Ser Trp Gly Gln Gly Pro Gly						
	225		230		235	
ccc agc att gcc agc ctt agc tca gat ggg cgt ctt tgt ctt ctt gac						769
Pro Ser Ile Ala Ser Leu Ser Ser Asp Gly Arg Leu Cys Leu Leu Asp						
	240		245		250	
ccc cgg gat ctc tgc cat cct gtg agc tca gtc cag tgc cca gta tcc						817
Pro Arg Asp Leu Cys His Pro Val Ser Ser Val Gln Cys Pro Val Ser						
	255		260		265	
gta cct agc cct gac cca gag ctg ctg cga gtg act tgg gcc cca ggc						865
Val Pro Ser Pro Asp Pro Glu Leu Leu Arg Val Thr Trp Ala Pro Gly						
	275		280		285	
ctg aag aat tgc ttg gcc atc tca ggt ttt gat ggt aca gtc cag gtc						913
Leu Lys Asn Cys Leu Ala Ile Ser Gly Phe Asp Gly Thr Val Gln Val						
	290		295		300	
tat gat gcc aca tct tgg gat gga aca cgg agc caa gat gga aca cgg						961
Tyr Asp Ala Thr Ser Trp Asp Gly Thr Arg Ser Gln Asp Gly Thr Arg						
	305		310		315	
agc caa gta gaa cct ctc ttc act cac aga ggt cac atc ttc cta gat						1009
Ser Gln Val Glu Pro Leu Phe Thr His Arg Gly His Ile Phe Leu Asp						
	320		325		330	
gga aat ggg atg gac cct gct cct ttg gtc acc acc cac acc tgg cat						1057
Gly Asn Gly Met Asp Pro Ala Pro Leu Val Thr Thr His Thr Trp His						
	335		340		345	
ccc tgc aga cca agg act ttg tta tca gca aca aat gat gcc tct ctg						1105
Pro Cys Arg Pro Arg Thr Leu Leu Ser Ala Thr Asn Asp Ala Ser Leu						
	355		360		365	
cat gtg tgg gac tgg gtg gac ctt tgt gcc ccc cgc tgacaccagc						1151
His Val Trp Asp Trp Val Asp Leu Cys Ala Pro Arg						
	370		375			
atctttccat ctaggcctct agaaagggga ggagctgctg tagtagcaag ggtgctgatg						1211
taggactcaa gtgactacca gtccctgtta ccagctgtgt ggccttgggc aagtctgcca						1271
gcgtcactta gcctcagttt ccttatctgt aaaatgagga tagtaagaac tacctcgtag						1331
tgatattgcg aagggttagaa gaaacgcatg gcataattac ttggtagcta ttgttagatc						1391
tgggagtgtg aaatggtagc gttttgtccc tgtcttcaca ctatcatagg gagaatcaaa						1451
agagctaaca aatataaaca tgctttgtga atttttttaa agaaaaaaat gtaggggggc						1511
caataaacat gaaaaaatcc cagccctagt agcaattaag gaaatagcaa aacaggattt						1571
ctgctcctct tgaggggggc tcatgggaac acaggtgcac tttcccacac ttgtcccccc						1631
aggtgactag gttcaagaga catttgcttt tgggtggcccc acaaacattt ccttttgagg						1691
gcccatagtg aatatntaaa gtgtgctgga catggtggct catgcctgta atcccagcac						1751
tttcagaggc tgaggtgggc agattgcttg agctgaggag tttgagacca gcctgggcaa						1811
catagcaaga tcccttcccc aaaaaaaaaa aaaaaaaa						1849

<210> 166
 <211> 1748
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 136..264

<400> 166

attattttgaa aaaccactgg gttccgagtt cattactaca ggaaaaactt tctcttctgt	60
ggcacagaga accctgcttc aaagcagaag tagcagttcc ggagtccagc tggctaaaac	120
tcatcccaga ggata atg gca acc cat gcc tta gaa atc gct ggg ctg ttt	171
Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe	
1 5 10	
ctt ggt ggt gtt gga atg gtg ggc aca gtg gct gtc act gtc atg cct	219
Leu Gly Gly Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro	
15 20 25	
cag tgg aga gtg tgc gcc ttc att gaa aac aac atc gtg gtt ttt	264
Gln Trp Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe	
30 35 40	
taaaaacttct gggaaggact gtggatgaat tgcgtgaggc aggctaacat caggatgcag	324
tgcaaaatct atgattccct gctggctctt tctccggacc tacaggcagc cagaggactg	384
atgtgtgctg cttccgtgat gtccttcttg gctttcatga tggccatcct tggcatgaaa	444
tgcaccaggt gcacggggga caatgagaag gtgaaggctc acattctgct gacggctgga	504
atcatcttca tcatcacggg catgggtggtg ctcatccctg tgagctgggt tgccaatgcc	564
atcatcagag atttctataa ctcaatagtg aatgttgccc aaaaacgtga gcttggagaa	624
gctctctact taggatggac cacggcactg gtgctgattg ttggaggagc tctgttctgc	684
tgcgtttttt gttgcaacga aaagagcagt agctacagat actcgatacc ttcccatcgc	744
acaacccaaa aaagttatca caccggaaaag aagtcaccga gcgtctactc cagaagtcag	804
tatgtgtagt tgtgtatgtt tttttaactt tactataaag ccatgcaaat gacaaaaatc	864
tatattactt tctcaaaatg gaccccaaag aaactttgat ttactgttct taactgccta	924
atcttaatta caggaactgt gcatcagcta tttatgattc tataagctat ttcagcagaa	984
tgagatatta aaccgaatgc tttgattgtt ctgaaagta tagtaatttg ttttctaagg	1044
tggktcaagc atctactctt tttatcattt acttcaaaat gacattgcta aagactgcat	1104
tattttacta ctgtaatttc tccacgacat agcattatct acatagatga gtgtaacatt	1164
tatatctcac atagagacat gcttatatgg ttkcatttaa aatgaaatgc cagtccatta	1224
cactgaataa atagaactca actattgctt ttcagggaaa tcatggatag ggttgaagaa	1284
ggttactatt aattgtttta aaacagctta gggattaatg tcctccattt ataatgaaga	1344
ttaaaatgaa ggctttaatc agcattgtaa aggaaattga atggctttct gatatgctgt	1404
tttttagcct aggagttaga aatcctaact tctttatcct cttctcccag aggctttttt	1464
tttcttgtgt attaaattaa cattttttaa aagcagatat tttgtcaagg ggctttgcat	1524
tcaaactgct tttccagggc tatactcaga agaaagataa aagtgtgatc taagaaaaag	1584
tgatgggttt aggaaagtga aaatattttt gtttttgtat ttgaagaaga atgatgcatt	1644
ttgacaagaa atcatatatg tatggatata ttttaataag tatttgagta cagactttga	1704
ggtttcatca atataaataa aagagcaaaa aaaaaaaaaa aaaa	1748

<210> 167
 <211> 1275
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 14..1048

<400> 167	
agaggttggg aag atg gcg tgg cga ggc tgg gcg cag aga ggc tgg ggc	49
Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly	
1 5 10	
tgc ggc cag gcg tgg ggt gcg tgc gtg ggc ggc cgc agc tgc gag gag	97
Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu	
15 20 25	
ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac	145

Leu	Thr	Ala	Val	Leu	Thr	Pro	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn	
30						35					40					
ttc	ttt	att	caa	caa	aaa	tgc	gga	ttc	aga	aaa	gca	ccc	agg	aag	gtt	193
Phe	Phe	Ile	Gln	Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val	
45					50					55					60	
gaa	cct	cga	aga	tca	gac	cca	ggg	aca	agt	ggt	gaa	gca	tac	aag	aga	241
Glu	Pro	Arg	Arg	Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg	
				65					70						75	
agt	gct	ttg	att	cct	cct	gtg	gaa	gaa	aca	gtc	ttt	tat	cct	tct	ccc	289
Ser	Ala	Leu	Ile	Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro	
			80					85					90			
tat	cct	ata	agg	agt	ctc	ata	aaa	cct	tta	ttt	ttt	act	gtt	ggg	ttt	337
Tyr	Pro	Ile	Arg	Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe	
		95					100					105				
aca	ggc	tgt	gca	ttt	gga	tca	gct	gct	att	tgg	caa	tat	gaa	tca	ctg	385
Thr	Gly	Cys	Ala	Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu	
	110					115					120					
aaa	tcc	agg	gtc	cag	agt	tat	ttt	gat	ggt	ata	aaa	gct	gat	tgg	ttg	433
Lys	Ser	Arg	Val	Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu	
	125				130					135					140	
gat	agc	ata	aga	cca	caa	aaa	gaa	gga	gac	ttc	aga	aag	gag	att	aac	481
Asp	Ser	Ile	Arg	Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn	
				145					150					155		
aag	tgg	tgg	aat	aac	cta	agt	gat	ggc	cag	cgg	act	gtg	aca	ggt	att	529
Lys	Trp	Trp	Asn	Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile	
			160					165					170			
ata	gct	gca	aat	gtc	ctt	gta	ttc	tgt	tta	tgg	aga	gta	cct	tct	ctg	577
Ile	Ala	Ala	Asn	Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu	
		175					180					185				
cag	cgg	aca	atg	atc	aga	tat	ttc	aca	tcg	aat	cca	gcc	tca	aag	gtc	625
Gln	Arg	Thr	Met	Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val	
	190					195					200					
ctt	tgt	tct	cca	atg	ttg	ctg	tca	aca	ttc	agt	cat	ttc	tcc	tta	ttt	673
Leu	Cys	Ser	Pro	Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe	
	205				210					215					220	
cac	atg	gca	gca	aat	atg	tat	gtt	ttg	tgg	agc	ttc	tct	tcc	agc	ata	721
His	Met	Ala	Ala	Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile	
			225						230					235		
gtg	aac	att	ctg	ggt	caa	gag	cag	ttc	atg	gca	gtg	tac	cta	tct	gca	769
Val	Asn	Ile	Leu	Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala	
			240					245					250			
ggt	gtt	att	tcc	aat	ttt	gtc	agt	tac	gtg	ggt	aaa	gtt	gcc	aca	gga	817
Gly	Val	Ile	Ser	Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly	
		255					260					265				
aga	tat	gga	cca	tca	ctt	ggt	gca	gcc	ctg	aaa	gcc	att	atc	gcc	atg	865
Arg	Tyr	Gly	Pro	Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met	
	270					275					280					
gat	aca	gca	gga	atg	atc	ctg	gga	tgg	aaa	ttt	ttt	gat	cat	gcg	gca	913
Asp	Thr	Ala	Gly	Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala	
	285				290					295					300	
cat	ctt	ggg	gga	gct	ctt	ttt	gga	ata	tgg	tat	gtt	act	tac	ggt	cat	961
His	Leu	Gly	Gly	Ala	Leu	Phe	Gly	Ile	Trp	Tyr	Val	Thr	Tyr	Gly	His	
			305					310						315		
gaa	ctg	att	tgg	aag	aac	agg	gag	ccg	cta	gtg	aaa	atc	tgg	cat	gaa	1009

Glu	Leu	Ile	Trp	Lys	Asn	Arg	Glu	Pro	Leu	Val	Lys	Ile	Trp	His	Glu			
								320							325			330
ata	agg	act	aat	ggc	ccc	aaa	aaa	gga	ggg	ggc	tct	aag	taaa	actggg		1058		
Ile	Arg	Thr	Asn	Gly	Pro	Lys	Lys	Gly	Gly	Gly	Ser	Lys						
							335							340			345	
attggacagt			agtgggtgc			cat ctggttcctt			g ccgcctgaga			gccccaggag			acatcggtcta		1118	
gagtgaccat			ggctatgctc			ccgtctggaa			gatgccagca			tgtggcctcc			cacttttttc		1178	
agctgtgtcc			cccagtc			ccgt gtcttttag			aatgtgaatg			atgataaagt			tgtgaaataa		1238	
aggtttctat			ctagtttgca			aaaaaaaaaaaa			aaaaaaaa								1275	

```
<210> 168
<211> 1023
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> 70..777
```

<400> 168																
aataggtccg gttccggggg cgcgtggtg cagcggggcc cgcgtggtgc ctctgaggc																60
ggcccccg atg aag aga tct ggg aac ccg gga gcc gag gta acg aac agc																111
Met Lys Arg Ser Gly Asn Pro Gly Ala Glu Val Thr Asn Ser																
1 5 10																
tcg gtg gca ggg cct gac tgc tgc gga ggc ctc ggc aat att gat ttt																159
Ser Val Ala Gly Pro Asp Cys Cys Gly Gly Leu Gly Asn Ile Asp Phe																
15 20 25 30																
aga cag gca gac ttc tgc gtt atg acc cgg ctg ctg ggc tac gtg gac																207
Arg Gln Ala Asp Phe Cys Val Met Thr Arg Leu Leu Gly Tyr Val Asp																
35 40 45																
ccc ctg gat ccc agc ttt gtg gct gcc gtc atc acc atc acc ttc aat																255
Pro Leu Asp Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn																
50 55 60																
ccg ctc tac tgg aat gtg gtt gca cga tgg gaa cac aag acc cgc aag																303
Pro Leu Tyr Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys																
65 70 75																
ctg agc agg gcc ttc gga tcc ccc tac ctg gcc tgc tac tct cta agc																351
Leu Ser Arg Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser																
80 85 90																
atc acc atc ctg ctc ctg aac ttc ctg cgc tcg cac tgc ttc acg cag																399
Ile Thr Ile Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln																
95 100 105 110																
gcc atg ctg agc cag ccc agg atg gag agc ctg gac acc ccc gcg gcc																447
Ala Met Leu Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala																
115 120 125																
tac agc ctg gtc ctc gca ctc ctg gga ctg ggc gtc gtg ctc gtg ctc																495
Tyr Ser Leu Val Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu																
130 135 140																
tcc agc ttc ttt gca ctg ggg ttc gct gga act ttc cta ggt gat tac																543
Ser Ser Phe Phe Ala Leu Gly Phe Ala Gly Thr Phe Leu Gly Asp Tyr																
145 150 155																
ttc ggg atc ctc aag gag gcg aga gtg acc gtg ttc ccc ttc aac atc																591
Phe Gly Ile Leu Lys Glu Ala Arg Val Thr Val Pro Phe Asn Ile																
160 165 170																

ctg gac aac ccc atg tac tgg gga agc aca gcc aac tac ctg ggc tgg	639
Leu Asp Asn Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp	
175 180 185 190	
gcc atc atg cac gcc agc ccc acg ggc ctg ctc ctg acg gtg ctg gtg	687
Ala Ile Met His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val	
195 200 205	
gcc ctc acc tac ata gtg gct ctc cta tac gaa gag ccc ttc acc gct	735
Ala Leu Thr Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala	
210 215 220	
gag atc tac cgg cag aaa gcc tcc ggg tcc cac aag agg agc	777
Glu Ile Tyr Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser	
225 230 235	
tgattgagct gcaacagctt tgctgaaggc ctggccagcc tcctggcctg ccccaagtgg	837
caggccctgc gcagggcgag aatgggtgcct gctgctcagg gctcgccccc ggctgtgggt	897
gccccagtgc cttggaacct gctgccttgg ggaccctgga cgtgccgaca tatggccatt	957
gagctccaac ccacacattc ccattcacca ataaaggcac cctgacctca aaaaaaaaaa	1017
aaaaaa	1023
<210> 169	
<211> 1085	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 38..400	
<400> 169	
aacaattcat gaagttgaag aaaagacact gtcagaa atg aac aca gaa gcg gag	55
Met Asn Thr Glu Ala Glu	
1 5	
caa cag ctt ctc cat cac gcc aga aat ggc aat gct gaa gaa gta aga	103
Gln Gln Leu Leu His His Ala Arg Asn Gly Asn Ala Glu Glu Val Arg	
10 15 20	
caa cta tta gag acc atg gcg agt aat gaa gtg att gct gac att aat	151
Gln Leu Leu Glu Thr Met Ala Ser Asn Glu Val Ile Ala Asp Ile Asn	
25 30 35	
tgc aaa gga aga agt aag tct aac ttg ggc tgg aca ccc cta cat ctg	199
Cys Lys Gly Arg Ser Lys Ser Asn Leu Gly Trp Thr Pro Leu His Leu	
40 45 50	
gca tgc tat ttt gga cac aga caa gtg gtc cag gat ctg ttg aag gct	247
Ala Cys Tyr Phe Gly His Arg Gln Val Val Gln Asp Leu Leu Lys Ala	
55 60 65 70	
ggg gca gaa gtg aat gtg ttg aat gac atg gga gac acg ccg ctt cat	295
Gly Ala Glu Val Asn Val Leu Asn Asp Met Gly Asp Thr Pro Leu His	
75 80 85	
cga gct gcc ttt aca gga cga aag gtg aaa atc att cta tgt tca atg	343
Arg Ala Ala Phe Thr Gly Arg Lys Val Lys Ile Ile Leu Cys Ser Met	
90 95 100	
ttt gta agt gag gta ttt gga gga gta gtt acc att gtt ttc tct gtt	391
Phe Val Ser Glu Val Phe Gly Gly Val Val Thr Ile Val Phe Ser Val	
105 110 115	
ata acc atc tgaccagcaa ccgaagaaag ccacacaaaa aaatgtatac	440
Ile Thr Ile	

120
accagcactt tgggtcaaaa ggccacagga tcttttgagt ctgacagtga ggtccagtac 500
taagggtcatg gagaccccca ctctgtagca tccctgtgag gagatcattc cgtttctgct 560
tgtgtactcc agcaatgggg aactcctgat tattcttttt ttttaaaaaa aaatagcttc 620
attgaggtat aacttacatt gcataaactt cacctgtgat attgtgaaat atatatatttg 680
tctttgacct tgtacactaa agatgtacaa aaagatgact ggcaaccctt ggcttcagga 740
tgggggctgg tcaccagaaa gaccaaggca ggactagggg gttgggactt tcagccgaac 800
tttgcaacct ccaggaggag tagaggggct gaaggggaaa tggctcgcta atggccagtg 860
gtttcatcaa tcatgcctat ttaatggaac ctccataaaa acctgaaagg acagggttct 920
aggagctcct gggtagctga acacgtggag gttcttgaat gatcacacc agggagggca 980
tgggtgctct gtgcccttc tccatgcctt gctttatgta tctcttcac tgtatccttt 1040
gtaataaagc agtaaacatg ttttctgaa aaaaaaaaaa aaaaa 1085

<210> 170
<211> 776
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..572

<400> 170
atatgtcatc agggcccccg cctgggaggt gtgctgccag agattttgcc tcttcaagggt 60
ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
1 5 10 15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
20 25 30
gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
35 40 45
ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
50 55 60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
65 70 75
ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
80 85 90 95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
100 105 110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
115 120 125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
130 135 140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
145 150 155

gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga	592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp	
160 165 170	
gaggagggac gccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt	652
cacccaatg ggaccaccct cctgggtccc ctgggtgccg ttttccttag aaatcagaga	712
aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagcaaaaaa	772
aaaa	776

<210> 171
 <211> 1219
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 160..867

<400> 171	
gtagttagga gtctggagtc gtgagccgga gtcagaactg cgtctcgcca cccaggcgcg	60
ggtttccgga ggacagccaa caagcgatgc tgccgcgcgc gtttcctgat tggttgtggg	120
tggctacctc ttcgttctga ttggccgcta gtgagcaag atg ctg agc aag ggt	174
Met Leu Ser Lys Gly	
1 5	
ctg aag cgg aaa cgg gag gag gag gag gag aag gaa cct ctg gca gtc	222
Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys Glu Pro Leu Ala Val	
10 15 20	
gac tcc tgg tgg cta gat cct ggc cac aca gcg gtg gca cag gca ccc	270
Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala Val Ala Gln Ala Pro	
25 30 35	
ccg gcc gtg gcc tct agc tcc ctc ttt gac ctc tca gtg ctc aag ctc	318
Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu Ser Val Leu Lys Leu	
40 45 50	
cac cac agc ctg cag cag agt gag ccg gac ctg cgg cac ctg gtg ctg	366
His His Ser Leu Gln Gln Ser Glu Pro Asp Leu Arg His Leu Val Leu	
55 60 65	
gtc gtg aac act ctg cgg cgc atc cag gcg tcc atg gca ccc gcg gct	414
Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser Met Ala Pro Ala Ala	
70 75 80 85	
gcc ctg cca cct gtg cct agc cca cct gca gcc ccc agt gtg gct gac	462
Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Pro Ser Val Ala Asp	
90 95 100	
aac tta ctg gca agc tcg gac gct gcc ctt tca gcc tcc atg gcc agc	510
Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser Ala Ser Met Ala Ser	
105 110 115	
ctc ctg gag gac ctc agc cac att gag ggc ctg agt cag gct ccc caa	558
Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu Ser Gln Ala Pro Gln	
120 125 130	
ccc ttg gca gac gag ggg cca cca ggc cgt agc atc ggg gga gca gcg	606
Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser Ile Gly Gly Ala Ala	
135 140 145	
ccc agc ctg ggt gcc ttg gac ctg ctg ggc cca gcc act ggc tgt cta	654
Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro Ala Thr Gly Cys Leu	
150 155 160 165	
ctg gac gat ggg ctt gag ggc ctg ttt gag gat att gac acc tct atg	702

Leu	Asp	Asp	Gly	Leu	Glu	Gly	Leu	Phe	Glu	Asp	Ile	Asp	Thr	Ser	Met	
			170						175					180		
tat	gac	aat	gaa	ctt	tgg	gca	cca	gcc	tct	gag	ggc	ctc	aaa	cca	ggc	750
Tyr	Asp	Asn	Glu	Leu	Trp	Ala	Pro	Ala	Ser	Glu	Gly	Leu	Lys	Pro	Gly	
		185						190					195			
cct	gag	gat	ggg	ccg	ggc	aag	gag	gaa	gct	ccg	gag	ctg	gac	gag	gcc	798
Pro	Glu	Asp	Gly	Pro	Gly	Lys	Glu	Glu	Ala	Pro	Glu	Leu	Asp	Glu	Ala	
		200				205						210				
gaa	ttg	gac	tac	ctc	atg	gat	gtg	ctg	gtg	ggc	aca	cag	gca	ctg	gag	846
Glu	Leu	Asp	Tyr	Leu	Met	Asp	Val	Leu	Val	Gly	Thr	Gln	Ala	Leu	Glu	
	215					220				225						
cga	ccg	ccg	ggg	cca	ggg	cgc	tgagccctcg	tgctggaatg	gttgtctggt							897
Arg	Pro	Pro	Gly	Pro	Gly	Arg										
230					235											
atctgaactg	agcctgctgg	ctggaccaac	tgtcctcgaa	aagacacagc	tggcttcctc											957
agtacagaga	acagggcttg	ggccactttg	gagagacaga	atctagtcct	gggcaacttc											1017
acatccgtcc	tctgtctca	gggctggcag	ggggagcctg	gaattacccc	ctagtgatgg											1077
aatgacaggg	tctggtgggg	acttaattcc	ctggccctgg	ggcatagct	tgggctgttc											1137
cttctctgat	acgggaagag	acccaatca	gatttttcaa	attaaagcca	gtcctgggaa											1197
atctcaaaaa	aaaaaaaaaa	aa														1219

<210> 172
 <211> 1487
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..640

<400> 172	
gacgaaggac	tggaaggtgg
ggtgact	atg aaa ggc tta tat ttc caa cag agt tcc aca gat gaa gaa
	Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu
	1 5 10
ata aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat	157
Ile Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp	
	15 20 25 30
aac ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat	205
Asn Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn	
	35 40 45
aca aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt	253
Thr Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val	
	50 55 60
ggg aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca	301
Gly Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser	
	65 70 75
ttc ttt caa cca gat gat gaa gta gtt gga att ttg ccc ctg gac tct	349
Phe Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser	
	80 85 90
gaa gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg	397
Glu Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu	
	95 100 105 110
ggt cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att	445

Val	His	Lys	Pro	Glu	Lys	Val	Thr	Trp	Thr	Glu	Ala	Ala	Gly	Ser	Ile						
									115							120			125		
cgg	gat	gga	gtg	cgt	gcc	tat	aca	gct	ctg	cat	tat	ctt	tct	cat	ctc						
Arg	Asp	Gly	Val	Arg	Ala	Tyr	Thr	Ala	Leu	His	Tyr	Leu	Ser	His	Leu						
							130							135			140				
tct	cct	gga	aaa	tca	gtg	ctg	ata	atg	gat	gga	gca	agt	gca	ttt	gg.						
Ser	Pro	Gly	Lys	Ser	Val	Leu	Ile	Met	Asp	Gly	Ala	Ser	Ala	Phe	Gly						
								145							150			155			
aca	ata	gct	att	cag	tta	gca	cat	cat	aga	gga	gcc	aaa	gta	ttt	caa						
Thr	Ile	Ala	Ile	Gln	Leu	Ala	His	His	Arg	Gly	Ala	Lys	Val	Phe	Gln						
						160							165			170					
cag	cat	gca	gcc	ttg	aag	ata	agc	agt	gcc	ttg	aaa	gat	tca	gac	ctc						
Gln	His	Ala	Ala	Leu	Lys	Ile	Ser	Ser	Ala	Leu	Lys	Asp	Ser	Asp	Leu						
				175							180							185			190
cca tagccccgagt gattgatgta tctaattggga aagttcatgt tgctgaaagc															690						
Pro																					
tgtttgggaag		aaacagggtgg			cctggggagta			gatattgtcc			tagatgctgg			agtgagatta			750				
tatagtaaag		atgatgaacc			agctgtaaaa			ctacaactac			taccacataa			acatgatatc			810				
atcacacttc		ttgggtgttgg			aggccactgg			gtaacaacag			aagaaaacct			tcagttggat			870				
cctccagata		gccactgcct			tttccctcaag			ggagcaacgt			tagctttcct			gaatgatgaa			930				
gtttggaatt		tgtcaaatgt			acaacaggga			aaatatcttt			gtatcttaaa			ggatgtgatg			990				
gagaagttaa		caactgggtgt			tttcagacct			cagttggatg			aacccattcc			actgtatgag			1050				
gcaaaaagttt		ccatggaagc			tgttcagaaa			aatcaaggaa			gaaaaaagca			agttgttcaa			1110				
ttttaattttt		cttcttttctc			agacctcagt			cgatgaaca			tattccagta			tttgaagcca			1170				
gaattttctt		tggaatttgt			tgagaaaaaac			caaggaagat			aaaacaagtt			gcatttttta			1230				
gcacgtttct		ctgctaagac			aagatgctca			gttgacacat			ttgaaaagtgt			tttgaaaaaat			1290				
tcttgtgcac		atgatcaaga			taattctata			attaacatct			taaggggaatt			tttctaaaaa			1350				
ccttttctatt		gtttctatat			attttgcccc			tgctataaaa			ttcctttccat			gaagaaaact			1410				
cctgttttca		gcaaaaagtca			cactactctt			gataaaagct			gttgaggccc			tttgctaagc			1470				
aaaaaaaaaaa		aaaaaaaaa														1487					

```
<220>
<221> CDS
<222> 132..1298
```

				50				55				60				
ctg	acc	ttg	gaa	ggg	gtg	gcc	cgg	tac	atg	cag	agc	gaa	cgc	tgt	cgc	362
Leu	Thr	Leu	Glu	Gly	Val	Ala	Arg	Tyr	Met	Gln	Ser	Glu	Arg	Cys	Arg	
			65					70				75				
aga	gtc	atc	tgt	ttg	gtg	gga	gct	gga	atc	tcc	aca	tcc	gca	ggc	atc	410
Arg	Val	Ile	Cys	Leu	Val	Gly	Ala	Gly	Ile	Ser	Thr	Ser	Ala	Gly	Ile	
		80						85				90				
ccc	gac	ttt	cgc	tct	cca	tcc	acc	ggc	ctc	tat	gac	aac	cta	gag	aag	458
Pro	Asp	Phe	Arg	Ser	Pro	Ser	Thr	Gly	Leu	Tyr	Asp	Asn	Leu	Glu	Lys	
	95					100				105						
tac	cat	ctt	ccc	tac	cca	gag	gcc	atc	ttt	gag	atc	agc	tat	ttc	àag	506
Tyr	His	Leu	Pro	Tyr	Pro	Glu	Ala	Ile	Phe	Glu	Ile	Ser	Tyr	Phe	Lys	
110					115					120					125	
aaa	cat	ccg	gaa	ccc	ttc	ttc	gcc	ctc	gcc	aag	gaa	ctc	tat	cct	ggg	554
Lys	His	Pro	Glu	Pro	Phe	Phe	Ala	Leu	Ala	Lys	Glu	Leu	Tyr	Pro	Gly	
				130				135						140		
cag	ttc	aag	cca	acc	atc	tgt	cac	tac	ttc	atg	cgc	ctg	ctg	aag	gac	602
Gln	Phe	Lys	Pro	Thr	Ile	Cys	His	Tyr	Phe	Met	Arg	Leu	Leu	Lys	Asp	
			145					150				155				
aag	ggg	cta	ctc	ctg	cgc	tgc	tac	acg	cag	aac	ata	gat	acc	ctg	gag	650
Lys	Gly	Leu	Leu	Leu	Arg	Cys	Tyr	Thr	Gln	Asn	Ile	Asp	Thr	Leu	Glu	
		160					165					170				
cga	ata	gcc	ggg	ctg	gaa	cag	gag	gac	ttg	gtg	gag	gcg	cac	ggc	acc	698
Arg	Ile	Ala	Gly	Leu	Glu	Gln	Glu	Asp	Leu	Val	Glu	Ala	His	Gly	Thr	
	175					180					185					
ttc	tac	aca	tca	cac	tgc	gtc	agc	gcc	agc	tgc	cgg	cac	gaa	tac	ccg	746
Phe	Tyr	Thr	Ser	His	Cys	Val	Ser	Ala	Ser	Cys	Arg	His	Glu	Tyr	Pro	
190					195					200					205	
cta	agc	tgg	atg	aaa	gag	aag	atc	ttc	tct	gag	gtg	acg	ccc	aag	tgt	794
Leu	Ser	Trp	Met	Lys	Glu	Lys	Ile	Phe	Ser	Glu	Val	Thr	Pro	Lys	Cys	
				210				215					220			
gaa	gac	tgt	cag	agc	ctg	gtg	aag	cct	gat	atc	gtc	ttt	ttt	ggg	gag	842
Glu	Asp	Cys	Gln	Ser	Leu	Val	Lys	Pro	Asp	Ile	Val	Phe	Phe	Gly	Glu	
			225					230				235				
agc	ctc	cca	gcg	cgt	ttc	ttc	tcc	tgt	atg	cag	tca	gac	ttc	ctg	aag	890
Ser	Leu	Pro	Ala	Arg	Phe	Phe	Ser	Cys	Met	Gln	Ser	Asp	Phe	Leu	Lys	
		240				245				250						
gtg	gac	ctc	ctc	ctg	gtc	atg	ggg	acc	tcc	ttg	cag	gtg	cag	ccc	ttt	938
Val	Asp	Leu	Leu	Leu	Val	Met	Gly	Thr	Ser	Leu	Gln	Val	Gln	Pro	Phe	
	255					260				265						
gcc	tcc	ctc	atc	agc	aag	gca	ccc	ctc	tcc	acc	cct	cgc	ctg	ctc	atc	986
Ala	Ser	Leu	Ile	Ser	Lys	Ala	Pro	Leu	Ser	Thr	Pro	Arg	Leu	Leu	Ile	
270					275				280						285	
aac	aag	gag	aaa	gct	ggc	cag	tcg	gac	cct	ttc	ctg	ggg	atg	att	atg	1034
Asn	Lys	Glu	Lys	Ala	Gly	Gln	Ser	Asp	Pro	Phe	Leu	Gly	Met	Ile	Met	
			290					295					300			
ggc	ctc	gga	gga	ggc	atg	gac	ttt	gac	tcc	aag	aag	gcc	tac	agg	gac	1082
Gly	Leu	Gly	Gly	Gly	Met	Asp	Phe	Asp	Ser	Lys	Lys	Ala	Tyr	Arg	Asp	
		305					310					315				
gtg	gcc	tgg	ctg	ggg	gaa	tgc	gac	cag	ggc	tgc	ctg	gcc	ctt	gct	gag	1130
Val	Ala	Trp	Leu	Gly	Glu	Cys	Asp	Gln	Gly	Cys	Leu	Ala	Leu	Ala	Glu	
		320				325					330					
ctc	ctt	gga	tgg	aag	aag	gag	ctg	gag	gac	ctt	gtc	cgg	agg	gag	cac	1178
Leu	Leu	Gly	Trp	Lys	Lys	Glu	Leu	Glu	Asp	Leu	Val	Arg	Arg	Glu	His	

335	340	345	
gcc agc ata gat gcc cag tgc ggg gcg ggg gtc ccc aac ccc agc act			1226
Ala Ser Ile Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr			
350	355	360	365
tca gct tcc ccc aag aag tcc ccg cca cct gcc aag gac gag gcc agg			1274
Ser Ala Ser Pro Lys Lys Ser Pro Pro Ala Lys Asp Glu Ala Arg			
370	375	380	
aca aca gag agg gag aaa ccc cag tgacagctgc atctcccagg cgggatgccg			1328
Thr Thr Glu Arg Glu Lys Pro Gln			
385			
agctcctcag ggacagctga gcccacaaccg ggccctggccc cctctttaacc agcagttctt			1388
gtctggggag ctccagaacat ccccgaatct cttacagctc cctccccaaa actgggggtcc			1448
cagcaaccct ggcccccaac cccagcaaat ctctaaccac tcctagaggc caaggcttaa			1508
acaggcatct ctaccagccc cactgtctct aaccactcct gggctaagga gtaacctccc			1568
tcctctctaa ctgccccac ggggccaggg ctaccccaga actttttaact cttccaggac			1628
aggagcttc gggccccac tctgtctcct gcccccgagg gcctgtggct aagtaaacca			1688
tacctaacct acccagtggt ggggtgtgggc ctctgaatct aaccacacc cagcgtaggg			1748
ggagtctgag ccgggagggc tcccaggtct ctgccttcag ctcccaaagt ggggtgggtggg			1808
cccccttcac gtgggaccca cttcccatgc tggatgggca gaagacattg cttattggag			1868
acaaattaaa aacaaaaaca actaacaagg aaaaaaaaaa aaaaaaa			1915

<210> 174
 <211> 1990
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 259..1701

<400> 174	
ttagaacatc ytaatcaaaa aattttggtg cgagagaaac aataggacgg aaacgccgag	60
gaaccgggct gaggcggcag cttcctaggt gacagacagg tacactgtat gctagccctg	120
tatctgtctg agcagtggaa tgtgccagga aagaaggagc aaccactgac tgatgaacct	180
ttgccagtct cccttccaag agggatgccg gaggcttctg taagctcctc agatgtcact	240
ggtatctagg caacaggg atg agc ctg aac ctc cct gag gcc agc tta ctt	291
Met Ser Leu Asn Leu Pro Glu Ala Ser Leu Leu	
1 5 10	
agc aga gca tcc tgg cca gaa caa gcc aag gag cca aga cga gag gga	339
Ser Arg Ala Ser Trp Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly	
15 20 25	
cac acg gac aaa caa cag aca gaa gac gta ctg gcc gct gga ctc cgc	387
His Thr Asp Lys Gln Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg	
30 35 40	
tgc ctc ccc cat ctc ccc gcc atc tgc gcc cgg agg atg agc cca gcc	435
Cys Leu Pro His Leu Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala	
45 50 55	
ttc agg gcc atg gat gtg gag ccc cgc gca aaa ggc gtc ctt ctg gag	483
Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu	
60 65 70 75	
ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc ttc aat	531
Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg Phe Asn	
80 85 90	
gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag ttc tac	579

Glu	Thr	Thr	Leu	Cys	Lys	Pro	Leu	Val	Pro	Arg	Glu	His	Gln	Phe	Tyr	
			95					100					105			
gag	acc	ctc	cct	gct	gag	atg	cgc	aaa	ttc	act	ccc	cag	tac	aaa	ggg	627
Glu	Thr	Leu	Pro	Ala	Glu	Met	Arg	Lys	Phe	Thr	Pro	Gln	Tyr	Lys	Gly	
		110					115					120				
gtg	gta	tct	gtg	cgc	ttt	gaa	gaa	gat	gaa	gac	agg	aac	ttg	tgt	cta	675
Val	Val	Ser	Val	Arg	Phe	Glu	Glu	Asp	Glu	Asp	Arg	Asn	Leu	Cys	Leu	
	125					130					135					
ata	gca	tat	cca	ttg	aaa	ggg	gac	cat	gga	att	gtg	gac	att	gta	gat	723
Ile	Ala	Tyr	Pro	Leu	Lys	Gly	Asp	His	Gly	Ile	Val	Asp	Ile	Val	Asp	
140					145				150						155	
aat	tca	gac	tgt	gaa	cca	aaa	agt	aag	ctc	cta	agg	tgg	aca	aca	aac	771
Asn	Ser	Asp	Cys	Glu	Pro	Lys	Ser	Lys	Leu	Leu	Arg	Trp	Thr	Thr	Asn	
			160					165						170		
aaa	aaa	cat	cat	gtc	tta	gaa	aca	gaa	aag	acc	cct	aag	gac	tgg	gtg	819
Lys	Lys	His	His	Val	Leu	Glu	Thr	Glu	Lys	Thr	Pro	Lys	Asp	Trp	Val	
		175					180					185				
cg	cag	cac	cg	aaa	gag	gag	aaa	atg	aag	agc	cat	aag	tta	gaa	gaa	867
Arg	Gln	His	Arg	Lys	Glu	Glu	Lys	Met	Lys	Ser	His	Lys	Leu	Glu	Glu	
	190					195						200				
gaa	ttt	gag	tgg	cta	aag	aaa	tct	gaa	gtc	ttg	tac	tac	act	gta	gag	915
Glu	Phe	Glu	Trp	Leu	Lys	Lys	Ser	Glu	Val	Leu	Tyr	Tyr	Thr	Val	Glu	
	205					210				215						
aag	aag	ggg	aat	ata	agt	tcc	cag	ctt	aaa	cac	tat	aac	cct	tgg	agc	963
Lys	Lys	Gly	Asn	Ile	Ser	Ser	Gln	Leu	Lys	His	Tyr	Asn	Pro	Trp	Ser	
220				225					230					235		
atg	aaa	tgt	cac	cag	caa	cag	tta	cag	aga	atg	aag	gag	aat	gca	aag	1011
Met	Lys	Cys	His	Gln	Gln	Gln	Leu	Gln	Arg	Met	Lys	Glu	Asn	Ala	Lys	
			240					245						250		
cat	cg	aac	cag	tac	aaa	ttt	atc	tta	ctg	gaa	aac	ctg	act	tcc	cg	1059
His	Arg	Asn	Gln	Tyr	Lys	Phe	Ile	Leu	Leu	Glu	Asn	Leu	Thr	Ser	Arg	
		255					260						265			
tat	gag	gtg	cct	tgt	gtc	ctt	gac	ctc	aag	atg	ggc	aca	cga	caa	cat	1107
Tyr	Glu	Val	Pro	Cys	Val	Leu	Asp	Leu	Lys	Met	Gly	Thr	Arg	Gln	His	
	270					275						280				
ggg	gat	gat	gct	tca	gag	gag	aag	gca	gcc	aac	cag	atc	cga	aaa	tgt	1155
Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln	Ile	Arg	Lys	Cys	
	285				290						295					
cag	cag	agc	aca	tct	gca	gtc	att	ggg	gtg	cg	gtg	tgt	ggc	atg	cag	1203
Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val	Cys	Gly	Met	Gln	
300				305					310					315		
gtg	tac	caa	gca	ggc	agt	ggg	cag	ctc	atg	ttc	atg	aac	aag	tac	cat	1251
Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met	Asn	Lys	Tyr	His	
			320					325						330		
gga	cg	aag	cta	tcg	gtg	cag	ggc	ttc	aag	gag	gca	ctt	ttc	cag	ttc	1299
Gly	Arg	Lys	Leu	Ser	Val	Gln	Gly	Phe	Lys	Glu	Ala	Leu	Phe	Gln	Phe	
		335					340						345			
ttc	cac	aat	ggg	cg	tac	ctg	cg	cg	gaa	ctc	ctg	ggc	cct	gtg	ctc	1347
Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu	Gly	Pro	Val	Leu	
		350				355						360				
aag	aag	ctg	act	gag	ctc	aag	gca	gtg	ttg	gag	cga	cag	gag	tcc	tac	1395
Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg	Gln	Glu	Ser	Tyr	
	365				370				375							
cg	ttc	tac	tca	agc	tcc	ctg	ctg	gtc	att	tat	gat	ggc	aag	gag	cg	1443

Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp	Gly	Lys	Glu	Arg	
380					385					390					395	
ccc	gaa	gtg	gtc	ctg	gac	tca	gat	gct	gag	gat	ttg	gag	gac	ctg	tca	1491
Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu	Glu	Asp	Leu	Ser	
				400					405					410		
gag	gaa	tca	gct	gat	gag	tct	gct	ggg	gcc	tat	gcc	tac	aaa	ccc	atc	1539
Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala	Tyr	Lys	Pro	Ile	
			415					420					425			
ggc	gcc	agc	tct	gta	gat	gtg	cgc	atg	atc	gac	ttt	gca	cac	acc	acc	1587
Gly	Ala	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe	Ala	His	Thr	Thr		
		430				435					440					
tgc	agg	ctg	tat	ggc	gag	gac	acc	gtg	gtg	cat	gag	ggc	cag	gat	gct	1635
Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu	Gly	Gln	Asp	Ala	
	445				450					455						
ggc	tat	atc	ttc	ggg	ctc	cag	agc	ctg	ata	gac	att	gtc	aca	gag	ata	1683
Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu	Ile	Asp	Ile	Val	Thr	Glu	Ile	
460					465				470					475		
agt	gag	gag	agt	ggg	gag	tgagcttgct	agctgctcca	gtacttgaga								1731
Ser	Glu	Glu	Ser	Gly	Glu											
				480												
gcgactctgt	gtcccaggma	cagctgtgct	gcgtcagggg	ggaagccagt	atggccaggt											1791
ggtggctcct	gcagcctgga	gctgatgtgc	agtggcctct	gtgagcccca	gcctgagcca											1851
gtcccagctg	tgcttgaggt	ctttatttat	tttaactatt	tcttcaacat	tccacatttg											1911
atgatgatac	ctctttcttc	cctgagtgtg	tatgtttctaa	tacaaatctt	tttgtttatt											1971
ataaaaaaaaa	aaaaaaaaa															1990

<210> 175
 <211> 1971
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 213..1274

<400> 175	
ttcagcccca gccagatccc gcgtcaacgg acgcggaacg gcggaccccg taccctggca	60
gcatcgagac accggcgggg gaaggcaagg tccctggact ggtcatatac ctcttggtggc	120
cctggcagaa tcaagatgag gccctgtcat gcctccccag tgaggcctac agtctgagca	180
gacagcatgg cctgccactg gcagtgaaca cc atg tct gca gga ggt ggc cgg	233
	Met Ser Ala Gly Gly Gly Arg
	1 5
gcc ttt gct tgg caa gtg ttc ccc ccc atg ccc act tgc cgg gtc tat	281
Ala Phe Ala Trp Gln Val Phe Pro Pro Met Pro Thr Cys Arg Val Tyr	
	10 15 20
ggc aca gtg gca cac caa gat ggg cac ctg ctg gtg ttg ggg ggt tgt	329
Gly Thr Val Ala His Gln Asp Gly His Leu Leu Val Leu Gly Gly Cys	
	25 30 35
ggc cgg gct gga ctg ccc ctg gac act gct gag aca ctg gac atg gcc	377
Gly Arg Ala Gly Leu Pro Leu Asp Thr Ala Glu Thr Leu Asp Met Ala	
40 45 50 55	
tcg cac aca tgg ctg gca ctg gca ccc ctg ccc act gcc cgg gct ggt	425
Ser His Thr Trp Leu Ala Leu Ala Pro Leu Pro Thr Ala Arg Ala Gly	
	60 65 70

gca gct gcg gta gtt ctg ggc aag cag gtg cta gtg gtg ggt ggt gtg	473
Ala Ala Ala Val Val Leu Gly Lys Gln Val Leu Val Val Gly Gly Val	
75 80 85	
gat gag gtc cag agc ccg gta gct gct gta gag gcc ttc ctg atg gat	521
Asp Glu Val Gln Ser Pro Val Ala Ala Val Glu Ala Phe Leu Met Asp	
90 95 100	
gag ggc cgc tgg gag cgt cgg gcc acc ctc cct caa gca gcc atg ggg	569
Glu Gly Arg Trp Glu Arg Arg Ala Thr Leu Pro Gln Ala Ala Met Gly	
105 110 115	
gtt gca act gtg gag aga gat ggt atg gtg tat gct ctg ggg gga atg	617
Val Ala Thr Val Glu Arg Asp Gly Met Val Tyr Ala Leu Gly Gly Met	
120 125 130 135	
ggc cct gac acg gcc ccc cag gcc cag gta cgt gtg tat gag ccc cgt	665
Gly Pro Asp Thr Ala Pro Gln Ala Gln Val Arg Val Tyr Glu Pro Arg	
140 145 150	
cgg gac tgc tgg ctt tcg cta ccc tcc atg ccc aca ccc tgc tat ggg	713
Arg Asp Cys Trp Leu Ser Leu Pro Ser Met Pro Thr Pro Cys Tyr Gly	
155 160 165	
gcc tcc acc ttc ctg cac ggg aac aag atc tat gtc ctg ggg gcc cgc	761
Ala Ser Thr Phe Leu His Gly Asn Lys Ile Tyr Val Leu Gly Gly Arg	
170 175 180	
cag ggc aag ctc ccg gtg act gct ttt gaa gcc ttt gat ctg gag gcc	809
Gln Gly Lys Leu Pro Val Thr Ala Phe Glu Ala Phe Asp Leu Glu Ala	
185 190 195	
cgt aca tgg acc cgg cat cca agc cta ccc agc cgt cgg gcc ttt gct	857
Arg Thr Trp Thr Arg His Pro Ser Leu Pro Ser Arg Arg Ala Phe Ala	
200 205 210 215	
ggc tgc gcc atg gct gaa ggc agc gtc ttt agc ctg ggt gcc ctg cag	905
Gly Cys Ala Met Ala Glu Gly Ser Val Phe Ser Leu Gly Gly Leu Gln	
220 225 230	
cag cct ggg ccc cac aac ttc tac tct cgc cca cac ttt gtc aac act	953
Gln Pro Gly Pro His Asn Phe Tyr Ser Arg Pro His Phe Val Asn Thr	
235 240 245	
gtg gag atg ttt gac ctg gag cat ggg tcc tgg acc aaa ttg ccc cgc	1001
Val Glu Met Phe Asp Leu Glu His Gly Ser Trp Thr Lys Leu Pro Arg	
250 255 260	
agc ctg cgc atg agg gat aag agg gca gac ttt gtg gtt ggg tcc ctt	1049
Ser Leu Arg Met Arg Asp Lys Arg Ala Asp Phe Val Val Gly Ser Leu	
265 270 275	
ggg ggc cac att gtg gcc att ggg ggc ctt gga aac cag cca tgt cct	1097
Gly Gly His Ile Val Ala Ile Gly Gly Leu Gly Asn Gln Pro Cys Pro	
280 285 290 295	
ttg ggc tct gtg gag agc ttt agc ctt gca cgg cgg cgc tgg gag gca	1145
Leu Gly Ser Val Glu Ser Phe Ser Leu Ala Arg Arg Arg Trp Glu Ala	
300 305 310	
ttg cct gcc atg ccc act gcc cgc tgc tcc tgc tct agt ctg cag gct	1193
Leu Pro Ala Met Pro Thr Ala Arg Cys Ser Cys Ser Ser Leu Gln Ala	
315 320 325	
ggg ccc cgg ctg ttt gtt att ggg ggt gtg gcc cag gcc ccc agt caa	1241
Gly Pro Arg Leu Phe Val Ile Gly Gly Val Ala Gln Gly Pro Ser Gln	
330 335 340	
gcc gtg gag gca ctg tgt ctg cgt gat ggg gtc tgaaggcttg gtgggagctg	1294
Ala Val Glu Ala Leu Cys Leu Arg Asp Gly Val	
345 350	

tccactggag	cagctcattg	ccagaggcag	ctatttctat	ggctcctttt	gctgctgagg	1354
acactcactg	tggctctgtg	ggatgagaga	ggcatggggg	tgagcacttg	aaacactgcc	1414
ttggggcctt	gggttagggg	agcctttgtc	tttagtgag	gacacacata	tgcttacacc	1474
tacctttatc	accattcggt	catgaatcat	gcctagctcc	atccttgccc	tgggacctac	1534
taggccttcc	atccaactgg	gaaatgggga	gaagcaaagc	tggcctcatg	ctcttcaggg	1594
tcagttccta	tctggagttg	accaggccta	ccccagttgc	cattcctgaa	aaatctcagc	1654
tgccaggctg	ccttttaggg	ccctgtagac	ccaggagagt	tgagaggggtg	ggggacacag	1714
agagaataga	gaggatgtgg	gaactgccag	agggccggag	cgcaggagtt	caagtggagg	1774
aatgctggct	ttgagccctc	tacactgctg	gttgtagtac	cttggaacaag	tcacttcacc	1834
tctctgtgcc	tcagcatctc	catctataaa	tggggatctc	tgaaaccttc	ctaccctacc	1894
tacctcacag	ggctgtttgtg	aggacccagg	gagtttggat	gtggaagtaa	aagtgctgcc	1954
aaaaaaaaaa	aaaaaaaa					1971

<210> 176
 <211> 1613
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..127

<400> 176						
gacgaaggac	tggaaggtgg	cggtggtgaa	ggtgcaggcc	gttggggcgg	ctcagaggca	60
ggtgact atg	aaa ggc tta tat	ttc caa cag agt	tcc aca gat	gaa gaa		109
Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu						
1	5	10				
ata aca ttt gta ttt caa	taaaaggaag	atcttctctgt	tacagaggat			157
Ile Thr Phe Val Phe Gln						
15	20					
aactttgtga	aacttcaagt	taaagcttgt	gctctgagcc	agataaatac	aaagcttctg	217
gcagaaatga	agatgaaaaa	ggattttat	ctgtttggga	gagaaattgc	tggaattgta	277
ttagatgttg	gaagcaagg	atcattcttt	caaccagatg	atgaagtagt	tggaattttg	337
cccctggact	ctgaagaccc	tggactttgt	gaagttgtta	gagtacatga	gcattacttg	397
gttcataaac	cagaaaagg	cacatggacg	gaagcagcag	gaagcattcg	ggatggagtg	457
cgtgcctata	cagctctgca	ttatctttct	catctctctc	ctggaaaatc	agtgtctgata	517
atggatggag	caagtgcatt	tgggtacaata	gctattcagt	tagcacatca	tagaggagcc	577
aaagtgattt	caacagcatg	cagccttgaa	gataagcagt	gccttgaaag	attcagacct	637
cccatagccc	gagtgtttga	tgtatctaata	gggaaagtcc	atgttgctga	aagctgtttg	697
gaagaaacag	gtggcctggg	agtagatatt	gtcctagatg	ctggagttag	attatatagt	757
aaagatgatg	aaccagctgt	aaaactacaa	ctactaccac	ataaacatga	tatcatcaca	817
cttcttggtg	ttggaggcca	ctgggtaaca	acagaagaaa	accttcagtt	ggatcctcca	877
gatagccact	gccttttcc	caagggagca	acgttagctt	tcctgaatga	tgaagtttgg	937
aattttgtcaa	atgtacaaca	gggaamaata	tctttgtatc	ttaaaggatg	tgatggagaa	997
gttatcaact	ggtgttttca	gacctcagtt	ggatgaaccc	attccactgt	atgaggcaaa	1057
agtttccatg	gaagctgttc	agaaaaatca	aggaagaaaa	aagcaagttg	ttcaatttta	1117
atcttcttct	ttctcagacc	tcagtcggat	gaacatatct	cagtatttga	agccagaatt	1177
ttctttggaa	attgttgaga	aaaaccaagg	aagataaaac	aagttgcatt	tttaagcacg	1237
tttctctgct	aagacaagat	gctcagttga	cacatttgaa	aagtgtttga	aaaattcttg	1297
tgcaaatgat	caagataatt	ctataattaa	catcttaagg	gaatttttct	aaaaaccttt	1357
tcattgtttc	tatatatttt	gccccgtgta	taaaattcct	tccatgaaga	aaactgctgc	1417
tttcagcaaa	agtcacacta	ctcttgataa	aagctgtttg	aggcctttgc	taagctatca	1477
aagtaacgta	ttaattttgt	atcaactccg	ttctcaacac	cttccttaag	tctttgctgt	1537
cataatttaa	gcatttgagt	atattttgaa	gtcttaaaag	acttagccca	taggcactca	1597

aaaaaaaaaa aaaaaa

1613

<210> 177
<211> 1361
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 65..1024

<400> 177
gaaggactgg aaggtggcgg tgggtgaaggt gcaggccggt ggggcggctc agaggcaggt 60
gact atg aaa ggc tta tat ttc caa cag agt tcc aca gat gaa gaa ata 109
Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile
1 5 10 15
aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat aac 157
Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn
20 25 30
ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat aca 205
Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn Thr
35 40 45
aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt ggg 253
Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val Gly
50 55 60
aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca ttc 301
Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser Phe
65 70 75
ttt caa cca gat gat gaa gta gtt gga att ttg ccc ctg gac tct gaa 349
Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser Glu
80 85 90 95
gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg gtt 397
Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu Val
100 105 110
cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att cgg 445
His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile Arg
115 120 125
gat gga gtg cgt gcc tat aca gct ctg cat tat ctt tct cat ctc tct 493
Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu Ser
130 135 140
cct gga aaa tca gtg ctg ata atg gat gga gca agt gca ttt ggt aca 541
Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly Thr
145 150 155
ata gct att cag tta gca cat cat aga gga gcc aaa gtg att tca aca 589
Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Ile Ser Thr
160 165 170 175
gca tgc agc ctt gaa gat aag cag tgc ctt gaa aga ttc aga cct ccc 637
Ala Cys Ser Leu Glu Asp Lys Gln Cys Leu Glu Arg Phe Arg Pro Pro
180 185 190
ata gcc cga gtg att gat gta tct aat ggg aaa gtt cat gtt gct gaa 685
Ile Ala Arg Val Ile Asp Val Ser Asn Gly Lys Val His Val Ala Glu
195 200 205
agc tgt ttg gaa gaa aca ggt ggc ctg gga gta gat att gtc cta gat 733
Ser Cys Leu Glu Glu Thr Gly Gly Leu Gly Val Asp Ile Val Leu Asp

210	215	220	
gct gga gtg aga tta tat agt aaa gat gat gaa cca gct gta aaa cta			781
Ala Gly Val Arg Leu Tyr Ser Lys Asp Asp Glu Pro Ala Val Lys Leu			
225	230	235	
caa cta cta cca cat aaa cat gat atc atc aca ctt ctt ggt gtt gga			829
Gln Leu Leu Pro His Lys His Asp Ile Ile Thr Leu Leu Gly Val Gly			
240	245	250	255
ggc cac tgg gta aca aca gaa gaa aac ctt cag ttg gat cct cca gat			877
Gly His Trp Val Thr Thr Glu Glu Asn Leu Gln Leu Asp Pro Pro Asp			
260	265	270	
agc cac tgc ctt ttc ctc aag gga gca acg tta gct ttc ctg aat gat			925
Ser His Cys Leu Phe Leu Lys Gly Ala Thr Leu Ala Phe Leu Asn Asp			
275	280	285	
gaa gtt tgg aat ttg tca aat gta caa cag gga aaa tat ctt tat ctt			973
Glu Val Trp Asn Leu Ser Asn Val Gln Gln Gly Lys Tyr Leu Tyr Leu			
290	295	300	
aaa gga tgt gat gga gaa gtt atc aac tgg tgt ttt cag acc tca gtc			1021
Lys Gly Cys Asp Gly Glu Val Ile Asn Trp Cys Phe Gln Thr Ser Val			
305	310	315	
gga tgaacatatt ccagtatttg aagccagaat tttctttgga aattggtgag			1074
Gly			
320			
aaaaaccaag gaagataaaa caagttgcat ttttaagcac gtttctctgc taagacaaga			1134
tgctcagttg acacatttga aaagtgtttg aaaaattctg gcttctaate ctgcctctgt			1194
tcccttttct ctccttgaaa gtccagcaca ccattcttgt ccttccccag tttcctcgcc			1254
ctccaccctt ccagcttcat gctcagtggt gtgcttaata aaatggacat atttttctct			1314
aaaaaaaaaa aaaaaakaaa aaaaaaaaaat aaaaaaaaaa aaaaaaaa			1361

<210> 178
 <211> 1113
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 109..585

<400> 178	
gcgggaccgg acttccggct ggtctgtggg gtttcggggt cggggtttcc tgggtggcgct	60
caggggcagg caacagagtg gcggccgcta cggccctgga acggggcc atg gag aag	117
	Met Glu Lys
	1
ctg cgg cga gtc ctg agc ggc cag gac gac gag gag cag ggc ctg act	165
Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln Gly Leu Thr	
5	10
gcg cag gtc ctg gat gcc tca tcc ctt agt ttc aac acc aga ttg aaa	213
Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr Arg Leu Lys	
20	25
tggtttt gcc atc tgc ttc gta tgt ggc gtt ttc ttt tct att ctt gga	261
Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser Ile Leu Gly	
	40
act gga ttg ctg tgg ctt ccg ggc ggc ata aag ctt ttt gca gtg ttt	309
Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe Ala Val Phe	
	55
	60
	65

tat acc ctc ggc aat ctt gct gcg tta gcc agt aca tgc ttt tta atg	357
Tyr Thr Leu Gly Asn Leu Ala Ala Leu Ala Ser Thr Cys Phe Leu Met	
70 75 80	
gga cct gtg aag caa ctg aag aaa atg ttt gaa gca aca aga ttg ctt	405
Gly Pro Val Lys Gln Leu Lys Lys Met Phe Glu Ala Thr Arg Leu Leu	
85 90 95	
gca aca att gtt atg ctt ttg tgt ttc ata ttt acc ctg tgt gct gct	453
Ala Thr Ile Val Met Leu Leu Cys Phe Ile Phe Thr Leu Cys Ala Ala	
100 105 110 115	
ctt tgg tgg cat aag aag gga ctg gct gtg tta ttc tgc ata ttg cag	501
Leu Trp Trp His Lys Lys Gly Leu Ala Val Leu Phe Cys Ile Leu Gln	
120 125 130	
ttc ttg tca atg acc tgg tat agc ctg tcg tac atc cca tat gca agg	549
Phe Leu Ser Met Thr Trp Tyr Ser Leu Ser Tyr Ile Pro Tyr Ala Arg	
135 140 145	
gat gca gtt att aaa tgc tgt tct tct ctc cta agt tgaaaatcag	595
Asp Ala Val Ile Lys Cys Cys Ser Ser Leu Leu Ser	
150 155	
aaacattgtg gaaaagagca cttgaatgta tgggtactcta tgtttggtga agtttgcttt	655
tccccataaa acactccagg aacaactgac gtgacagttg aagaccgttt tgtactaagt	715
ctcattttgt atactggtaa aaactacatg cttgattaaa ccattaaatg cttgtaactt	775
taaattcatt atgtgtcatt aatatacttt tccaaagata agattttttaa tcaactgccag	835
ttgtaaatta tttttagcca atttttaaat cttttcaaag cagctttgaa atgtgaatat	895
ttaaaggtag acctcgtgct gcaagataat taaacttttt tgctttttaa aaatgtctgc	955
attttttaaga ttttttttac tttaaatgtg aaactttatt taagctagaa amattgctta	1015
ttatatgtaa taaaaataat atataaatct ttacaatktt tgaaataaac ccatccttgg	1075
aaaaataaaa aaaaaaaaaa agaaaaaaaa aaaaaaaa	1113

<210> 179
 <211> 1960
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..577

<400> 179	
atcggccaac ggacgcgagg cgcgcgcc atg gaa cag cgg tta gct gag ttt	52
Met Glu Gln Arg Leu Ala Glu Phe	
1 5	
cgg gcg gcg cgg aaa cgg gcg ggt ctg gcg gcc caa ccc cct gct gcc	100
Arg Ala Ala Arg Lys Arg Ala Gly Leu Ala Ala Gln Pro Pro Ala Ala	
10 15 20	
agt cag ggc gca caa acc cca gga gag aag gcg gaa gca gca gcg act	148
Ser Gln Gly Ala Gln Thr Pro Gly Glu Lys Ala Glu Ala Ala Ala Thr	
25 30 35 40	
cta aag gca gcc cca ggc tgg cta aag cgg ttc ctg gta tgg aaa cct	196
Leu Lys Ala Ala Pro Gly Trp Leu Lys Arg Phe Leu Val Trp Lys Pro	
45 50 55	
agg ccc gcg agt gcc cgg gcc cag ccc ggc cta gtt cag gaa gcg gct	244
Arg Pro Ala Ser Ala Arg Ala Gln Pro Gly Leu Val Gln Glu Ala Ala	
60 65 70	
cag ccc cag ggc agc aca tca gag aca cca tgg aac aca gcc att cct	292

Gln	Pro	Gln	Gly	Ser	Thr	Ser	Glu	Thr	Pro	Trp	Asn	Thr	Ala	Ile	Pro		
		75					80					85					
ctg	ccg	tcg	tgc	tgg	gac	cag	tct	ttc	ctg	acc	aat	atc	acc	ttc	ttg	340	
Leu	Pro	Ser	Cys	Trp	Asp	Gln	Ser	Phe	Leu	Thr	Asn	Ile	Thr	Phe	Leu		
		90					95				100						
aag	gtt	ctt	ctc	tgg	ttg	gtc	ctg	ctg	gga	ctg	ttt	gtg	gaa	ctg	gaa	388	
Lys	Val	Leu	Leu	Trp	Leu	Val	Leu	Leu	Gly	Leu	Phe	Val	Glu	Leu	Glu		
105						110				115					120		
ttt	ggc	ctg	gca	tat	ttt	gtc	ctg	tcc	ttg	ttc	tat	tgg	atg	tac	gtc	436	
Phe	Gly	Leu	Ala	Tyr	Phe	Val	Leu	Ser	Leu	Phe	Tyr	Trp	Met	Tyr	Val		
				125					130					135			
ggg	aca	cga	ggc	cct	gaa	gag	aag	aaa	gag	gga	gag	aag	agc	gcc	tac	484	
Gly	Thr	Arg	Gly	Pro	Glu	Glu	Lys	Lys	Glu	Gly	Glu	Lys	Ser	Ala	Tyr		
			140					145						150			
tct	gtg	ttc	aat	cca	ggc	tgt	gaa	gcc	atc	cag	ggc	acc	ctg	act	gca	532	
Ser	Val	Phe	Asn	Pro	Gly	Cys	Glu	Ala	Ile	Gln	Gly	Thr	Leu	Thr	Ala		
		155					160						165				
gag	cag	ttg	gag	cgc	gag	tta	cag	ttg	aga	ccc	ctg	gca	ggg	aga		577	
Glu	Gln	Leu	Glu	Arg	Glu	Leu	Gln	Leu	Arg	Pro	Leu	Ala	Gly	Arg			
		170					175				180						
tagg	acccag	ctgtgctg	ctc	atgcag	ctaa	cctctgat	gt	gg	tcttctc	accattg	gct					637	
atgg	atttga	tttcaggt	gt	ataggact	aa	gggcagct	tg	cggg	ttagct	ctgtgact	gc					697	
atag	tttttc	taccttct	ttt	ccctgat	ctt	ttgctgcc	at	ttgatc	tttg	atagtttt	tg					757	
tgaa	actctc	taaaata	cat	tactgt	ggg	tccgacg	caa	ttata	aaaaa	ttatgt	actc					817	
aaga	aggag	acctgtt	gt	ttcattt	ctc	atctgtt	tg	gagat	gattt	tagagc	acta					877	
gaa	aggcact	ggggag	attc	tcagct	taaa	acatccag	ca	gtttg	aa	tgattag	gta					937	
catc	agggt	gcattgt	caa	tgttct	cttt	aagtctt	ttta	acattt	atag	caattt	tttt					997	
tttccc	ggag	agtttag	gtt	gcaag	ttttg	ggtttct	tgt	ttgttt	ttgt	tttgc	ttcct					1057	
gcttta	atttc	tttaatt	tttc	agtcatt	act	ggtattg	aaa	aataaaa	atat	ctttaaa	aca					1117	
tctcct	cttc	agaaat	agg	ccctctt	cat	tgcccat	cac	catctt	ccac	tctcct	atta					1177	
ttttg	ccact	actcag	taaa	ggaagg	tagg	aagagac	aaa	cgccta	aagt	caggtg	tggg					1237	
gaggg	atttc	acaagt	ggtt	attaac	ggcc	agttcag	caa	gaagt	gttga	gtgtgt	tacaa					1297	
agggg	agggc	tggaag	tgtt	aactcc	agac	ccgttg	gctg	cttgag	tgtt	ttcttat	att					1357	
ctaa	agcagc	agtc	cccta	ac	cttttt	ggca	ccagg	gacca	gtttt	gtgga	acacag	tttt				1417	
tccat	ggacg	gggtg	gtggt	ggagg	atgaa	acttcc	ac	cagat	catca	ggcatt	tagag					1477	
tctcata	agg	agcacg	caac	ctagat	ccct	cgc	atgcgc	ca	gttcaca	aata	cggttc	taag				1537	
ggctt	tagag	taagcag	ctt	tttcac	ctgt	gggcct	ctg	tgagaa	attc	tgtaa	attgt					1597	
gataat	cagg	ctggat	tttta	atgctg	cttt	tccagt	tacaa	tgtaga	gtt	tgggtt	catt					1657	
aaaatt	taggc	aaactccc	at	tgggtt	taggg	cttctct	cat	tccatt	tttgt	ggcta	ac	ctt				1717	
actgtg	tttc	agccctt	gct	gaaaatt	ctt	ctgat	atgtg	ttgcc	cttcc	tcacag	ccct					1777	
ttggc	cattg	ggagttt	ggc	tgccct	cag	agccat	ccg	tcaag	cagat	ggtctg	ttct					1837	
atctc	acaga	aaagtct	tttt	cttccat	gag	ttctgt	ctga	actga	acatg	taaaaa	agtat					1897	
gggaa	acaga	tgaatcc	ccta	ttaa	acatga	agtttt	gatt	gtattc	aaaaa	aaaaaaaa						1957	
aaa																1960	

<210> 180
 <211> 1443
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 23..451

<400> 180
accggcgggc ggggcgggta ag atg gcg gcc ccg cgg cga ggg aga gga tcc 52
Met Ala Ala Pro Arg Arg Gly Arg Gly Ser
1 5 10
tcc aca gtg ctc tct tca gtt ccc ctt caa atg ctg ttt tat ctc agc 100
Ser Thr Val Leu Ser Ser Val Pro Leu Gln Met Leu Phe Tyr Leu Ser
15 20 25
gga acg tac tac gcc ctg tat ttc ctc gcc acg ctc ctg atg atc acg 148
Gly Thr Tyr Tyr Ala Leu Tyr Phe Leu Ala Thr Leu Leu Met Ile Thr
30 35 40
tat aaa agt cag gtg ttc agc tat cct cac cgc tac ctg gtc ctc gat 196
Tyr Lys Ser Gln Val Phe Ser Tyr Pro His Arg Tyr Leu Val Leu Asp
45 50 55
ctt gct ctg ctg ttt ctg atg ggg att cta gaa gca gtt cgg tta tac 244
Leu Ala Leu Leu Phe Leu Met Gly Ile Leu Glu Ala Val Arg Leu Tyr
60 65 70
ctg ggc acc agg ggc aac ctg aca gag gct gag agg ccg ctg gcc gcc 292
Leu Gly Thr Arg Gly Asn Leu Thr Glu Ala Glu Arg Pro Leu Ala Ala
75 80 85 90
agc ctg gcc ctc acg gct ggc acc gcc ctc ctc tct gcc cac ttc ctg 340
Ser Leu Ala Leu Thr Ala Gly Thr Ala Leu Leu Ser Ala His Phe Leu
95 100 105
ctt tgg cag gcc cta gtg ttg tgg gcg gac tgg gcc ctc agc gcc acg 388
Leu Trp Gln Ala Leu Val Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr
110 115 120
ctc ctg gcc ctt cac ggc ctg gag gcc gtc ctg cag gtg gtt gcc atc 436
Leu Leu Ala Leu His Gly Leu Glu Ala Val Leu Gln Val Val Ala Ile
125 130 135
gcg gcc ttc acc agg tagctacgga caccgggat accccacact ggggcctcc 491
Ala Ala Phe Thr Arg
140
tcctgggcct gaccagtcct ccagctgtca cctccccatt cctggacagg aagggcactt 551
ttcctagtga ctggccatag atggtttttg atggttccat ctgttctggc aggagtggga 611
gcaggagcca gggcagaaca aactgctgga ggccctggtg ttgggaacag ctgcggggag 671
ggtagggacc agacagaact gccttcaaga tgagtccag gagcgcacac tcagccctgt 731
cagtggggtc tggcttttagc agccaggcct ccacagaccc catggggccc ccagggccga 791
gagggaggac agagcccttc agaacagagg cctcatctca ctgcatcccc catcaccccc 851
tagttcccca atggctcctaa tttgtgttct gagatccag tttactctgt ggccaggccc 911
cacctgtgtt tccaagtcgg gctggagacg caggatgggg taggccttgt gctctgagca 971
acccagctc tgccctcacag gcaggcaggc ccggtgcaag agtggactct gggttcctaa 1031
agcaataaat gcaaacaagc caacagctct gctgcctagc aatttccatc ttagccacac 1091
ttctcccttc aggggcttcg gaggagaggc cagggctaag gccggggatg atactgcagg 1151
agagagagca gcggagggcc acattcggag cctccgtcca ctccagtttt atcagctttt 1211
gcttttgcac ggagtgtctaa acaaattcta gctctgtgtt tttttcccat tcccagattt 1271
actatcagtt ctcccttaaaa agtatctaag ctgttacagt agctttccct tcaattgatt 1331
ctattgtgtg ttttctatgt ttggaataat tacacccaaa tatctagata ttttctcttc 1391
accgcatttt gtaaataaag agatgtgtat gcctcaaaaa aaaaaaaaaa aa 1443

<210> 181
<211> 605
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
 <222> 232..450

<400> 181
 caaatacaaaa tgcccacaaga agactgagga taggagaaag aatatctcta cctgtgaaac 60
 attgttagac tgccctggcta ggagttcatt gttgttttct gaaggacgta accaaccact 120
 ccaaaactta caggcttaaa acaacaaaca tgtatcattt cttatgattc tgtgggttgg 180
 ctgggtggtt cttctagctg aggcaggatg gtctaggata gctacatcca c atg tct 237
 Met Ser
 1
 ggg gtc cca gct gag atg act ggg gct gtt gag gcc ttt ctc cct gtg 285
 Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu Pro Val
 5 10 15
 gtg tca tcc tcc aga agg ctg ccc aga ttt gtc cat atg gta gca gga 333
 Val Ser Ser Ser Arg Arg Leu Pro Arg Phe Val His Met Val Ala Gly
 20 25 30
 gtt tcc tcg aag caa gag agg gca aga tcc aac aca gaa gca ctt ttc 381
 Val Ser Ser Lys Gln Glu Arg Ala Arg Ser Asn Thr Glu Ala Leu Phe
 35 40 45 50
 aag ctc tgt ttc cat cac att tgc caa tgt ctc act gat gaa cac aag 429
 Lys Leu Cys Phe His His Ile Cys Gln Cys Leu Thr Asp Glu His Lys
 55 60 65
 ttc cat ggc caa gtc cag ttt taagaaatgg agaaataggg cttggctcag 480
 Phe His Gly Gln Val Gln Phe
 70
 tggctcatgt ctgtaatccc agcacttttg gaggccaagg catgcggatc atttgaggtc 540
 aggagttcca gaccagcctg gccaacatgg tgaaaaccca tctctaccaa aaaaaaaaaa 600
 aaaaa 605

<210> 182
 <211> 1724
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 758..1183

<400> 182
 aactaaagcc gggagtcagg tgaacgggca gaagcagggc catgcccaag ccacccccaa 60
 gatccccctg aacctgcacc tccatcacga cccattcagg agcctccagg agcccagaca 120
 ccagcccccc accatggtaa gtccttcaag ggtgggatct ggaagaggaa agaggaggga 180
 caccagccag gtggaggtgt cctaaaaatg accatcagaa attgggggtga ggggaggggc 240
 atggtggact tctgtggggg tggggtgtct ctcagtgcag ctcaggtgcc tccagcatcc 300
 cttaccaggg agcaagctcc catctgtagg tgggtgggat gccagggtgg tatccctgga 360
 tccaaggata gggcaggacc tggaagacag aaggtggccc agggagaatc acagagtctg 420
 cagggacaag gacatagcct cctttgcttg caaattaagg gagcccttcc ccagtcacgc 480
 ccagtctctc gtctccctgt gtagccttgg gctagtccact tcccctctct tggccccggt 540
 tcccacagat gtcatatttg gaaatccgtc tagatgcgga agttgtctct caggggtctt 600
 tcagttgcaa cattctcaag gtctgtgggt tctgccacag agtcctcggc tgagatggga 660
 agctatgtct aacaagcgat ggggtggatt gacgccctcc ctgtgccggt gacgggcggt 720
 atggctgcag cagaggcagg agaggctgaa tacgtcc atg cca ccc ttt ggt ggg 775
 Met Pro Pro Phe Gly Gly
 1 5

cat ccc tta tcc caa gag gag gat ggc agc cag agg tgt tgc tgc ctg	823
His Pro Leu Ser Gln Glu Glu Asp Gly Ser Gln Arg Cys Cys Cys Leu	
10 15 20	
tca agt ctg agg tct gtc gat gat agc aac ggg gag act gtc gtg atc	871
Ser Ser Leu Arg Ser Val Asp Asp Ser Asn Gly Glu Thr Val Val Ile	
25 30 35	
atg gcg cta ttc cta gca gta tcg tac cac cat aag acg caa agt aag	919
Met Ala Leu Phe Leu Ala Val Ser Tyr His His Lys Thr Gln Ser Lys	
40 45 50	
agg tgg cca ggg ctg acc cca ccc cac agc tct ctg ctg tgt aga cca	967
Arg Trp Pro Gly Leu Thr Pro Pro His Ser Ser Leu Leu Cys Arg Pro	
55 60 65 70	
ctt cag ctt tca ttt ctc gtc att cag tca gtg agg atg aga gca tgt	1015
Leu Gln Leu Ser Phe Leu Val Ile Gln Ser Val Arg Met Arg Ala Cys	
75 80 85	
ggc tgt gac agc ggc cac tgc agg att ctt ggc agg tac agc tta cta	1063
Gly Cys Asp Ser Gly His Cys Arg Ile Leu Gly Arg Tyr Ser Leu Leu	
90 95 100	
ggg tgg agt cag gga cat agg gca aga ggc aga ggt ggt gtt agt ctg	1111
Gly Trp Ser Gln Gly His Arg Ala Arg Gly Arg Gly Gly Val Ser Leu	
105 110 115	
aga gac aac acc ttc ttt cag gaa gcc agt gag ggc cag gga cag tgg	1159
Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser Glu Gly Gln Gly Gln Trp	
120 125 130	
ctc atg cct gta atc cca gca ttt taggaggctg agacaggtag atcacttgag	1213
Leu Met Pro Val Ile Pro Ala Phe	
135 140	
gtcaggtggt cgagaccagc ctggccaacg tggtgaaacc tcgtctctac taaaaaatac	1273
aaaaaattaa ctgggcgtgg tggcacacgc ctgtaatccc agctacatat gaggctgagg	1333
caagagaata acttgaaccc aggaggcgga ggggtgcagtg agctgagatc ctgccgctgc	1393
actccagcct ggggtgacaga gcacactccg tctcaaaaaa ggaaagctga tgagaaattg	1453
ggcatcccgg aattcacacc caaacatca gctggagctc tgagactgtt ggggtgggaa	1513
ttcttccaag atgagaagca agccaggag gctcaggtcc tgggatgggc agggctttga	1573
tcaaaagaac acaggaagtg atttgctact tgaaagaaag gcaaccctc cccaaggaag	1633
ccctctgaaa atgcttagtc aacagtcggc ttggcagaca aggtctggga ggggccaccc	1693
gtatcgcaga ggacaaaaaa aaaaaaaaaa a	1724

<210> 183

<211> 1686

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 486..932

<400> 183

cggctcactg cagcctcttc ctcccagtct caagtgatcc tcctgtctca gcctcctgag	60
tggctgggat tacaggtgtg caccactacc acttggtctaa tttttatact tttagtagag	120
atgggggttt accatgttgg ccaggctggc cttgaactcc tgacctcagg tgatccgccc	180
gcctcggcct cccaaagtgc tggggttaca ggcattgagcc accgcacccg gcccccttc	240
ttcgtcttag tcaatcctat cccacctctt ctccaccag tccccctacc tgatgggtcc	300
aacacttcat catccaccac ctccctggagg gggatcccg aggtgctccg ctggggactc	360
tgctcattct ggggggtgcag ttgacggctg gtcgtgatct ttcccgtaat ctgtccctc	420

```

ttacggaacc tagtctccgt tctgtccatg gccttcttct ggacactgct aggatccaga 480
agagt atg tta tca att ctc aag cct agg aga agt cag gag tgg aga aca 530
Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr
1 5 10 15
gct ctg aga aga tac tgt tgt cca act gat ctc cag gca cca cgg agt 578
Ala Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser
20 25 30
ccg gtc cct cca atc agg aag gtc gga atc tct gat gtc atc gtt cat 626
Pro Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His
35 40 45
gcc aac ctg gca acc agt ttg aaa aaa aac aca tgt aac tgc cag gct 674
Ala Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala
50 55 60
gat ctc ttg tcc tgg aga tcc tgg gtg aat ggt atc tcc tgc cac tgt 722
Asp Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys
65 70 75
ccc aac ctc aga cca ttg tcc aaa agc atc ttc agg gac tcc aca tcc 770
Pro Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser
80 85 90 95
ctc tgt tcc ctg tcc cag cag agg ctg tgt cct ctc cac tca aag cct 818
Leu Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro
100 105 110
gaa gca tgt tgg ggt ctc ttt gtc tct gta cat gcc cat ttc aga gtc 866
Glu Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val
115 120 125
cag gct ggt ggg aga ggg aac aga gtg gga aag aaa act agg gta agc 914
Gln Ala Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser
130 135 140
aga aac gat gaa acc tta taagagtgag attatcatgt gcaagagtga 962
Arg Asn Asp Glu Thr Leu
145
gattatcatg tacaagagat cccaggaaat actgactttg atgaaaaagt cacatcagag 1022
cactcagttt tggcagagct ttttctgccg aatggttact cacattcact gtccgagatt 1082
ctatactggg ggtacacacg tcctctgccc taaggcaatt ttgagtccaa gagacatttt 1142
gaggcctaaa aatcatagga aactgcccct gagctcacac atatttccaa tgggtgtcccc 1202
aatttcaggg aatccatgga ttacctaagc cagcccctcc agttcggcta agaaactcta 1262
gtctatatgt caagttttgt atcatatgta ttgctctgaa ctcagaaatt tcccttccat 1322
ttatggattc tatgaataaa atatcacatg tacaaaaaga ctaagtcaaa aaatttcagc 1382
tgtgcacagt ggctcatgct tgtaatcca gcaatttggg tggccgaggg gggaggattg 1442
cctgaggcca gcagttcaag accagtatgg gcaacatggc aagagcccat ctctaaaaaa 1502
acaaaaccaa accaaattgg ccaggtgtgg tggctggcac ctgtgttcca actacttggg 1562
agactcatgt gacaggaaga tcacttgagc ccgggggtta gaggctgcag tgagctatga 1622
tcttgccact gcactccagc ctgggtgaca gagcgagaca ccgtcgcaaa aaaaaaaaaa 1682
aaaa 1686

```

<210> 184
<211> 463
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..304

<400> 184
cttttaacag ctgaggtctc tctttaattc tcttaaatac catttctccc tcaaaaaaga 60
ccattagatc atttcacaa atg tat ctg cca cca aac agg tca gag ctt tgc 112
Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys
1 5 10
aac ttt gct ttg tct ctt aac ctc tat ggc aaa ggg ttt ttt agc ctg 160
Asn Phe Ala Leu Ser Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu
15 20 25
gtg gaa aag cat aac agc agg gat tta gaa gat aga gct agt tct ggc 208
Val Glu Lys His Asn Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly
30 35 40
cca tca ctt tca tct cca tca cac ccg gac tgg ggt tat ata gtt ctg 256
Pro Ser Leu Ser Ser Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu
45 50 55
att tta gtg gca acc ctg ggg gaa ctt gat acc cag gta ggt ggt cac 304
Ile Leu Val Ala Thr Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His
60 65 70 75
tgatcagtag ttgggagagg taggaattgg tgagtacagg taattagagg aaagtcttgt 364
gtcctgtttc ccccttttta attttatccc ttgctagaat taagatacta tatgcctcac 424
ttatcaatta cagtctaaat ccaaaagaaa aaaaaaaaaa 463

<210> 185
<211> 773
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 188..691

<400> 185
agttgctgggt tgcaggagtt caggaaagga ggtgggacta gagtcaacct ggaatagctc 60
tacagtaaca atggcagcct ttttgttgct gggacatcca tacaggcaac ttagctgggtg 120
aaaggactct ggattgggtg gcagtctgct ttttttttcc caaggtgatc actttactgt 180
agaagaa atg agg tta aca gaa aag agt gag gga gaa caa caa ctc aag 229
Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys
1 5 10
ccc aac aac tct aat gca ccc aat gaa gat caa gaa gaa gaa atc caa 277
Pro Asn Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln
15 20 25 30
cag tca gaa cag cat act cca gca agg cag cga aca caa aga gca gac 325
Gln Ser Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp
35 40 45
aca cag cca tcc aga tgt cga ttg cct tca cgt agg aca cct aca aca 373
Thr Gln Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr
50 55 60
tcc agc gac aga acg atc aac ctt ctt gaa gtc ctt ccg tgg cct act 421
Ser Ser Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr
65 70 75
gag tgg att ttc aac ccc tat cga ttg cct gct ctt ttt gag ctt tat 469
Glu Trp Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr
80 85 90
cct gaa ttt ctt ctg gtg ttt aaa gaa gcc ttc cat gac ata tcc cat 517
Pro Glu Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His

95		100		105		110	
tgt ctg aaa gcc cag atg gaa aag atc gga ctg ccc atc ata ctc cac							565
Cys Leu Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His							
	115		120		125		
ctc ttc gca ctc tcc acc ctc tac ttc tac aag ttt ttc ctt cct aca							613
Leu Phe Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr							
	130		135		140		
att ctt tcc ctt tct ttc ttt att ctt ctt gta ctt ctg ctt ctg ctt							661
Ile Leu Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu							
	145		150		155		
ttt att att gtc ttc att ctg atc ttc ttc tgattctttt gtttcaataa							711
Phe Ile Ile Val Phe Ile Leu Ile Phe Phe							
	160		165				
acagcaatga gcatgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa							771
aa							773

<210> 186
 <211> 753
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..573

<400> 186	
actttttcagg ggacattcag aggcattcagc cccttctctcc tcaccagctc ccagagttcc	60
catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc	114
	Met Pro Arg Ser Ser Arg Ser
	1 5
cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga	162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg	
	10 15 20
ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag	210
Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu	
	25 30 35
gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac	258
Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn	
	40 45 50 55
aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc	306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser	
	60 65 70
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt	354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val	
	75 80 85
ctg ttt aac acg tgc aga gac aga gtt tca cca tgt tgc cca ggc tgg	402
Leu Phe Asn Thr Cys Arg Asp Arg Val Ser Pro Cys Cys Pro Gly Trp	
	90 95 100
tct caa act cca gtg atc ctc cca cct cag cct tcc gaa gtg ctg gga	450
Ser Gln Thr Pro Val Ile Leu Pro Pro Gln Pro Ser Glu Val Leu Gly	
	105 110 115
tta cag atg caa gct gct gtg cca gaa gct cat gga gaa gac agg cat	498
Leu Gln Met Gln Ala Val Pro Glu Ala His Gly Glu Asp Arg His	
	120 125 130 135

tct gct cct ctg tgc ttt cgg tgt gtc cca ggg ccc tgc cca gtc cca	546
Ser Ala Pro Leu Cys Phe Arg Cys Val Pro Gly Pro Cys Pro Val Pro	
140 145 150	
ggg gga ggt atc cct ggg ccc tgg cac tgattatagg acactgggca	593
Gly Gly Gly Ile Pro Gly Pro Trp His	
155 160	
agacactgca ctgccacgtg actcagtttc cccatctgcc tgatgggtgt tgctgtgaga	653
attatgaaat gaaatgatga ccatgaaaat attgtagaag ccaagaaatg cttcagaagt	713
tataaagctc tccccaaacc gtgttaaaaa aaaaaaaaaa	753

<210> 187
 <211> 754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 181..462

<400> 187	
atcctatcaa aagttacggt gaagtcaggg tgggtggcga gtccctgcaa ggtcgcccct	60
ctgtgccaac acagcctgat ggcttcttgt ttcaggaaac atccagaatt acaactggcc	120
attgagttat tacatatcaa ttgaacaagg tagtttttaa atgaaagaaa atcttgcaac	180
atg aat aaa gag ata gac tct ttg aat ctg gca tac agc ttt ccc ttc	228
Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe	
1 5 10 15	
ctt ctt cct gct ttc ctg gac aca ccg tgg aca gac cca ttt ccc tct	276
Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser	
20 25 30	
gga ttc atg gta agg tcc cga gtg ctt ctg ata cag ctg ctg agc aga	324
Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg	
35 40 45	
ccc cgc tca tct cag gag tcc cga gga cac tcg ctt ccc tgc agc ccg	372
Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro	
50 55 60	
tcc gcc ctg cat aag cct ggg ggc atc tgc cct gca gca ctg ggg agg	420
Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg	
65 70 75 80	
agc cac ctg ctt gtc tgg gaa cag cca agc ctg cgt gac agc	462
Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser	
85 90	
tgaggattct tgtggattgt tctttctgta actggacagc acatccggaa ttccttgcca	522
tagctctgtg ccttgctggg gtctgaggtt cacaggtcag atgctgctgt ctggctcttc	582
ccaattgcgg cgtgaattcc ttcatactca ccagtagctt cttgctctcc ccaaggagg	642
cacgtgctta gtagggagag aggcctacca aggttgccat ctgccatggg ctcaattgtg	702
tccccaaccc ccctgcaaat tatatatattga agtccccaaa aaaaaaaaaa aa	754

<210> 188
 <211> 998
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 6..290

<220>

<221> misc_feature

<222> 871

<223> n=a, g, c or t

<400> 188

```
gattc atg aag gcc tcg ggt cct gac ctc tct gat gga ctc cac tgc ccc      50
      Met Lys Ala Ser Gly Pro Asp Leu Ser Asp Gly Leu His Cys Pro
        1           5           10           15
agt cta att aga cat tta aga acc ttc tct gca gct gct gcc tta gcc      98
Ser Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala
              20           25           30
cca aga tac cca acc aga ctt ccc agt tca ctg ctt cta tgg cac ctc      146
Pro Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu
              35           40           45
tgc cag tgc ctc cat ctc ctc tat gca gtt tct acc tca tgc aac agc      194
Cys Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser
              50           55           60
cat ggg aag aga tcg gct gcc tgg gca atg acc aga aca gaa gac aca      242
His Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr
              65           70           75
gat gcg cta aca gat tcc ttc gat gac agt ttc atc agt tct gca gat      290
Asp Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp
              80           85           90           95
taagacttt caccagaaaa aaaaattacc tgattttgcc ctgaggcagc cagggaggggc      350
tttgtccttg acaatcccac tgacttattt aacaggtagc tcaaaaccca acaaaaaactg      410
gaggaggctg ctccactgca gggatggttt caattcggtg actggagtat tgtactctcc      470
ttgcaccctg gctcatcccc acaaaagacc tttcaaagaa aacacttaat tacctccttg      530
cacaagccct gtaagcccta aggtgaaaag aaactcagca gacaagggtcc acagagaagg      590
agaaggcaca attcagtagg gacctacgct cagcaccagg ataaagaaac tgtccattcc      650
tgccacctcc taggaagcta aaagaattaa ggggaggccg ggcacggtgg ctcacgcctg      710
taatcccagc actttgggag gccgaggcgg gtggatcatg aggtcaggag atcgagacca      770
tcctggctaa catggtgaaa ccccatctct actaaaaata caaaaaatta gccgggcgctg      830
gtggcgggcg ccctgtagtc ccagctactc gggaggctga nggcaggaga atggtgtgaa      890
cctgggaggc ggagcttgca gtgagccgag attgcgccct gctccactcc agcctgagcg      950
acagagcgag actccgtctc aaaaaaaaaa argaaaaaaaa aaaaaaaaaa      998
```

<210> 189

<211> 605

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 115..411

<400> 189

```
aagaaagggg tgaggcctaa gggacaatca' ggatgttttt cagagagaag tgtggatgct      60
ggacaggaag aaccacagat accagatacg ggtactgttg taactctgtt ctcc atg      117
                                   Met
                                   1
aaa aaa aag gaa gaa aca aca ctt tca gag atg gag cct gtt gag cca      165
```


Lys	Lys	Lys	Glu	Glu	Thr	Thr	Leu	Ser	Glu	Met	Glu	Pro	Val	Glu	Pro	
			5					10					15			
cag	tac	caa	cta	gtc	aat	gct	gaa	tcg	act	tct	ccc	ttt	cta	cat	tgc	213
Gln	Tyr	Gln	Leu	Val	Asn	Ala	Glu	Ser	Thr	Ser	Pro	Phe	Leu	His	Cys	
			20					25				30				
ctg	aga	gaa	gtc	att	ggg	gaa	tac	tct	gta	cac	gaa	ttt	tca	ctg	ttg	261
Leu	Arg	Glu	Val	Ile	Gly	Glu	Tyr	Ser	Val	His	Glu	Phe	Ser	Leu	Leu	
			35				40				45					
ggg	aaa	aca	gag	agt	caa	ggg	att	gga	ttg	tgg	att	gca	ttg	gtg	ggt	309
Gly	Lys	Thr	Glu	Ser	Gln	Gly	Ile	Gly	Leu	Trp	Ile	Ala	Leu	Val	Val	
						55				60					65	
ttc	ctc	agt	ttc	ctc	atc	ttc	tcc	aca	agt	ttc	tac	ata	tcg	aat	gca	357
Phe	Leu	Ser	Phe	Leu	Ile	Phe	Ser	Thr	Ser	Phe	Tyr	Ile	Ser	Asn	Ala	
						70				75				80		
gag	cag	ccc	ttc	ttc	aaa	gaa	cct	cct	acg	gaa	gct	gct	aag	gaa	ctc	405
Glu	Gln	Pro	Phe	Phe	Lys	Glu	Pro	Pro	Thr	Glu	Ala	Ala	Lys	Glu	Leu	
						85				90				95		
agt	ctg	tagctctg	cg	tg	gagccat	g	tg	taa	ac	act	ga	act	gag	ac	ctg	461
Ser	Leu															
ctactac	cta	agggccc	att	ttc	atct	gat	at	cat	cccc	agaa	acaa	ac	tc	at	gat	521
ttccat	gttt	tttttag	att	ag	ata	cat	gg	aga	atttt	cc	ttcc	cttag	aatt	aaaa	atc	581
ctgcatt	cta	aaaaaaaa	aaa													605

<210> 190
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 3..368

<400> 190	
ag atc cga gcg acc atg gtg gcc cgg gtg tgg tcg ctg atg agg ttc	47
Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe	
1 5 10 15	
ctc atc aag gga agt gtg gct ggg ggc gcc gtc tac ctg gtg tac gac	95
Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp	
20 25 30	
cag gag ctg ctg ggg ccc agc gac aag agc cag gca gcc cta cag aag	143
Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys	
35 40 45	
gct ggg gag gtg gtc ccc ccc gcc atg tac cag ttc agc cag tac gtg	191
Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val	
50 55 60	
tgt cag cag aca ggc ctg cag ata ccc cag ctc cca gcc cct cca aag	239
Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys	
65 70 75	
att tac ttt ccc atc cgt gac tcc tgg aat gca ggc atc atg acg gtg	287
Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val	
80 85 90 95	
atg tca gct ctg tcg gtg gcc ccc tcc aag gcc cgc gag tac tcc aag	335
Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys	
100 105 110	

gag ggc tgg gag tat gtg aag gcg cgc acc aag tagcgagtca gcagggggccg	388
Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys	
115 120	
cctgcccccg ccagaacggg cagggctgcc actgacctga agactccgga ctggggacccc	448
actccgaggg cagctcccg ccttgccggc ccaataaagg acttcagaag tgaaaaaaaa	508
ataaaaaaaaa aaaaaaaaa	526

<210> 191
 <211> 910
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 174..527

<400> 191	
attttcctgt taggccaaga gagaagagga tccttcctca gagcctccag cctcccttga	60
tcccttgctt gtgggcatat gtgggtcata tttccctccc atcaccctct gcacgccacc	120
cccatcaccg ccacagaccc ccagcccttc agttgccctg cacctccttg gtg atg	176
Met	
1	

cag ccg tcc ttg tta agg tca tac agg ttg aag gcc caa tta agc ctg	224
Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser Leu	
5 10 15	
tca tct aca gtt ccc cga aga atc acg gac aaa cca gcc aca aag tcc	272
Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys Ser	
20 25 30	
tgg gaa gga ggc agg agg gag ctg tgt cct cgg gta ctc ttc acc caa	320
Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr Gln	
35 40 45	
ctc ctt ctc tgg gtt tgg cct gga gat cct ggc cct gaa ctc cag gaa	368
Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln Glu	
50 55 60 65	
aca ggc ttc cct ggc cca cct cgc cca gct cac ctc aaa act gac cga	416
Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp Arg	
70 75 80	
gcc atc atg gtt ggt gtc aaa ggc att gaa gag aaa agt ggc ata ggt	464
Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile Gly	
85 90 95	
gct gga gtc tgc agg gtg agt gtg gag aag ttg gct tcc aca cag gag	512
Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln Glu	
100 105 110	
agg act tcc tcc ctc taaggagctc cccatacccc ccatcacctt ggcattccca	567
Arg Thr Ser Ser Leu	
115	
gctcctccag aatccctccc tccctcagcc tagagaagga caactgcttc ccttggggcc	627
ttgtcccctc acctccttga ggaaagaact gggagtaa atgcttgaag ttctcctcat	687
tgacaattcc gctgggacat tcttgggaagg agagggcacc aggctgaggg cagagacaaa	747
atcccccttc gttcaccgcc cccaccctcc atggcccaag actcccaggg agggggataa	807
tcttcaagcc tccagaggac tcaccacgtg gctcatgtga tgggagggaa gacttctttc	867
ccagtgcaca aataaaaaaac atggaacgaa aaaaaaaaaaaa aaa	910

<210> 192

<211> 668
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 57..203

<400> 192
 tcctgtcgac gtgttcttcc ggtggcggag cggcggatta gccttcgcgg ggcaaa atg 59
 Met
 1
 gag ctc gag gcc atg agc aga tat acc agc cca gtg aac cca cct gtc 107
 Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro Val
 5 10 15
 ttc ccc cat ctg acc gtg gtg ctt ttg gcc att ggc atg ttc ttc acc 155
 Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr
 20 25 30
 gcc tgg ttc ttc gtg tat cct ttc act gag cag cca gag gac cag cat 203
 Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln His
 35 40 45
 tagtgatgtg ggaagctcag ggagaaacca cgctaggtac atggaccccg ccggttttgt 263
 acattggatt ggggctgaga gaagattgcc gtgggctggg ctctctgcac tccacagtcc 323
 accccttcgc tttgccttaa ctgctgtgcc cagttacgag gtcacctcta ccaagtacac 383
 tcgtgatatc tataaagagc tcctcatctc attagtggcc tcactcttca tgggctttgg 443
 agtcctcttc ctgctgctct gggttggcat ctacgtgtga gcaccaagg gtaacaacca 503
 gatggcttca ctgaaacctg cttttgtaaa ttactttttt ttactgttgc tggaagtgtc 563
 ccacctgctg ctcataataa atgcagatgt atagcaaaaa aaaaaaaaaa aaaaaaaaaa 623
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 668

<210> 193
 <211> 637
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..334

<400> 193
 agttatgaag ttctaaaagc aagtcttaat caggaagtgt ccttgatcac caacggctcg 60
 cccagggc atg ctg gct ctc ttc cac ttc cac ctt cca cca tgg gat gac 109
 Met Leu Ala Leu Phe His Phe His Leu Pro Pro Trp Asp Asp
 1 5 10
 gca gta aga agg cca tca gta gat gcc agt ccc tca acc ttg aac ttt 157
 Ala Val Arg Arg Pro Ser Val Asp Ala Ser Pro Ser Thr Leu Asn Phe
 15 20 25 30
 cca gac gca gaa ctt tat gcc tcc att ttc ctc tgc tgc atg gcc cca 205
 Pro Asp Ala Glu Leu Tyr Ala Ser Ile Phe Leu Cys Cys Met Ala Pro
 35 40 45
 gga gag att tta att agc ttt cta acc ttg gtc cag att gca cat gca 253
 Gly Glu Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala
 50 55 60
 aat ggt aga gga tgc aac acc ccc gct tgt gga gct gcc gct tgt gtc 301

Asn	Gly	Arg	Gly	Cys	Asn	Thr	Pro	Ala	Cys	Gly	Ala	Ala	Ala	Cys	Val	
	65					70					75					
tgg	cat	gaa	aat	tca	caa	gaa	gag	agg	aaa	tac	tgaggagaaaa	atggcagatt				354
Trp	His	Glu	Asn	Ser	Gln	Glu	Arg	Lys	Tyr							
	80					85										
gtgtttgctg	aatttgattg	acgaagaagt	caccatgaaa	atcacagtga	accatttgga											414
aagcaaaactg	ccaaaaaaat	aatagttagt	catgctctca	ggctggttgt	tttggctggt											474
gtgggtttct	tgcatattcca	gatgattgca	aagagctggt	tctcaatttc	tgcaacaagt											534
gccagctgaa	attttggtac	cagtttcatt	aaatatgtat	aacaaaakaa	aaaaaaaaaa											594
aaaaaaaaaa	aaaaaaaaaa	aaaaaaagaa	aaaaaaaaaa	aaa												637

<210> 194
 <211> 706
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 183..443

<400> 194																
agaagttctc	agaggggtgag	ggtcccacat	ctcctgcagg	acaggcccta	gctaccgagt											60
cacagaaacc	cagggccgaa	gcaaagtccc	aatcccagag	aggctggggc	acacctacaa											120
ctgaaaggag	gcttagaaaat	ccttcagaga	ccaccctatc	ggttctcctc	cacctggaca											180
gg atg agc	cag caa cac	aga agg aag	agg cct tcc	tcc gaa aga	aaa											227
Met Ser Gln	Gln His Arg	Arg Lys Arg	Pro Ser Ser	Glu Arg Lys												
1	5	10	15													
agc aca aga	aag atg gac	aca tgg cag	agt ctt aaa	gtc aaa gaa	gta											275
Ser Thr Arg	Lys Met Asp	Thr Trp Gln	Ser Leu Lys	Val Lys Glu	Val											
	20	25	30													
ttc tgt aag	cat aat tct	tcc tat gaa	tgc ctt ctc	tat aaa gag	gtt											323
Phe Cys Lys	His Asn Ser	Ser Tyr Glu	Cys Leu Leu	Tyr Lys Glu	Val											
	35	40	45													
gaa gca aga	cag gtt tct	aag aca gcc	acc gat ggg	tcc tac ctc	ctc											371
Glu Ala Arg	Gln Val Ser	Lys Thr Ala	Thr Asp Gly	Ser Tyr Leu	Leu											
	50	55	60													
gta ttc aca	tcc tat gta	atc tcc tcc	cca gtg tgg	act gga cct	ggt											419
Val Phe Thr	Ser Tyr Val	Ile Ser Ser	Pro Val Trp	Thr Gly Pro	Gly											
	65	70	75													
gac ttg ctt	cca gtg aat	aga ata tag	caaaaagt	gattgatgtc	acctccaaga											473
Asp Leu Leu	Pro Val Asn	Arg Ile														
80	85															
ttcagctata	gaagactatg	actatgactt	tcctcttggc	tagcattctc	gctaaccctt											533
cctgcttgct	tgtactgagc	tgccctatga	agaggcccat	gtagggtggc	ctgggtgggg											593
gtgatctgtg	gccaacagcc	agcaaggaac	taaactctgt	ttacaaccac	atgagcttgg											653
aaggagatcc	ttccccagta	aagccaggag	atgaatacaa	aaaaaaaaaa	aaa											706

<210> 195
 <211> 670
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 94..228

<400> 195

```
acttttcagg ggacattcag aggcattcagc cccttcctcc tcaccagctc ccagagttcc 60
catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc 114
                               Met Pro Arg Ser Ser Arg Ser
                               1       5
cct ggg gac cca ggc gcc cta ctc gaa gat ggc cca caa tcc cag acc 162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Gly Pro Gln Ser Gln Thr
      10       15       20
ccg gag gat tgc cca gcg agg ccg gaa cac cag cag gat ggc aga gga 210
Pro Glu Asp Cys Pro Ala Arg Pro Glu His Gln Gln Asp Gly Arg Gly
      25       30       35
cac ctc ccc aaa cat gaa tgacaacatc ctgttgctg tccgcaacaa 258
His Leu Pro Lys His Glu
40       45
tgaccaagcc ctaggcctga ctcagtgcac gctgggatgt gtgtcctggt tcacctgttt 318
tgcctgctcc ctgagaactc aggcccagca gggtctgttt aacacgtgca gatgcaagct 378
gctgtgccag aagctcatgg agaagacagg cattctgctc ctctgtgctt tcggtgtgtc 438
ccagggccct gccagtcctc aggtggaagg tatccctggg ccctggcact gattatagga 498
cactgggcaa gacactgcac cgccacgtga ctcagtttcc ccctctgcct gatgggtgtt 558
gctgtgagaa ttatgaaatg aaatgatgac catgaaaata ttgtagaagc caagaaatgc 618
ttcagaagtt ataaagctct ccccaaaccg tggttatgaaa aaaaaaaaaa aa 670
```

<210> 196

<211> 510

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 133..327

<400> 196

```
aacctcaagg agccctgttg tgctaccgac tgcagagctc atggacatcc atcaggaagc 60
ctccaatacc caaaccaggg gtagttgcct aatccatata catgtggata gctctttact 120
taggaaacct tg atg gct tat ttg gat gac aaa ggt tcc ctt ttg gcg ata 171
                               Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile
                               1       5       10
cat agc cat gcg aga caa cat agc cat gaa aca aac caa gtc cac cag 219
His Ser His Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln
      15       20       25
tgg ctt cct agg aac aca ttt gct ttc ctg ata aaa gag gac aga tgc 267
Trp Leu Pro Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys
      30       35       40       45
agt tgc aga agt acc tgt gcc tct ttt tct tct tct tct tct tct 315
Ser Cys Arg Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser
      50       55       60
ttt tta atc tct taaatgcaga tataagaact ggtactgaag cagccatctt 367
Phe Leu Ile Ser
      65
gtgaccataa ggaagaagcc aagaacatca gaaccagtgg cctagccatt gcacagtcac 427
ctaaacacac ctctggactt gttattatgt aaaaaaaaaa aaacacctgc tcttggttatt 487
tgcaatccaa aaaaaaaaaa aaa 510
```

<210> 197
 <211> 500
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..357

```

<400> 197
atagaatata cacaaaagga a atg aga aag aaa tgt aaa tgc ttc act ata      51
                        Met Arg Lys Lys Cys Lys Cys Phe Thr Ile
                        1      5      10
aaa aaa aca aat aca tac gaa gaa agt aat gca gga aat gaa gga caa      99
Lys Lys Thr Asn Thr Tyr Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln
                        15      20      25
aaa gaa gct ata agc att tgt att tgc aga aga gat ggt tta ctt cct      147
Lys Glu Ala Ile Ser Ile Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro
                        30      35      40
ctg tgg gta acc agg tta tca gat ttg gtg ttt tcc aaa gaa aag gca      195
Leu Trp Val Thr Arg Leu Ser Asp Leu Val Phe Ser Lys Glu Lys Ala
                        45      50      55
cat ggc atg att cca ctt ctt ggc tcc cat agg gaa aag aag aca agt      243
His Gly Met Ile Pro Leu Leu Gly Ser His Arg Glu Lys Lys Thr Ser
                        60      65      70
aaa gag atg aag act tct tcc agg aac ctg agg tac ttc att gtc tgc      291
Lys Glu Met Lys Thr Ser Ser Arg Asn Leu Arg Tyr Phe Ile Val Cys
75      80      85      90
aga gat gcc tca tcc tac acc cct cag tca ctc ata tct gga tac att      339
Arg Asp Ala Ser Ser Tyr Thr Pro Gln Ser Leu Ile Ser Gly Tyr Ile
                        95      100      105
gga cct tgt caa cat caa taatggacat acctctgata tttgaactct      387
Gly Pro Cys Gln His Gln
                        110
gaatctcact ctgtgaccac aactttgtat ctttctaagt ctttaatctt caacctcaca      447
gaactcttca taccctaaaa tatagtattt tcacctggaa aaaaaaaaaa aaa      500

```

<210> 198
 <211> 667
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 4..333

```

<400> 198
aaa atg gtg ttt gga gcc atg gtc ctt ctt gtg gga ctt gaa gaa ctg      48
      Met Val Phe Gly Ala Met Val Leu Leu Val Gly Leu Glu Glu Leu
      1      5      10      15
acc aat atc cgc aac gtg gag aga ctg aag aag gac ttg agg gcc agt      96
Thr Asn Ile Arg Asn Val Glu Arg Leu Lys Lys Asp Leu Arg Ala Ser
                        20      25      30

```

tat tgc ctc atc gac agc ttc ctg ggg gac tcg gag ctc atc ggg gac	144
Tyr Cys Leu Ile Asp Ser Phe Leu Gly Asp Ser Glu Leu Ile Gly Asp	
35 40 45	
ctg acc cag tgt gtg gac tgc gtg att cct cca gag ggg tcc ctc ttg	192
Leu Thr Gln Cys Val Asp Cys Val Ile Pro Pro Glu Gly Ser Leu Leu	
50 55 60	
cag atc tct agc tac ctc tac tta aat act gct ctt gtg gac ttg cct	240
Gln Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro	
65 70 75	
ggg gtg gcg gcc tcc cag gca tgt gac tct cag cag gtg act tgg ctt	288
Gly Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Gln Val Thr Trp Leu	
80 85 90 95	
ctc tac gtt gct aat ggt gcc tac tcg gca tgt aac agg cct gga	333
Leu Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly	
100 105 110	
tgaacggtag ctgctgcggt tacattatta gcttcagttt gcccgccag gctagatggt	393
taatcagatt tcacagactt cacagtgtga gttggggatg tgacttcgta tgaaagtgaa	453
ggaactcagg ctcagagagg gtgagacgta ggagcatggc cactgcgcga gctcggggct	513
ggctgtgggt ttctcccat tccctgccc tctgggaagt cgctgccacc ccctacgctt	573
gtctgtgac tcccagtcct cctaaccctc cagaatgtaa acagcagcag atgaacaaaa	633
ataaaaaatac aaaaggccga aaaaaaaaaa aaaa	667

<210> 199
 <211> 514
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..363

<400> 199	
acg agt tct tcc ggg gcg gag gtc acc atg gca gct gcc ttg gct cgg	48
Thr Ser Ser Ser Gly Ala Glu Val Thr Met Ala Ala Ala Leu Ala Arg	
1 5 10 15	
ctt ggt ctg cgg cct gtc aaa cag gtt cgg gtt cag ttc tgt ccc ttc	96
Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe	
20 25 30	
gag aaa aac gtg gaa tcg acg agg acc ttc ctg cag acg gtg agc agt	144
Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser	
35 40 45	
gag aag gtc cgc tcc act aat ctc aac tgc tca gtg att gcg gac gtg	192
Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val	
50 55 60	
agg cat gac ggc tcc gag ccc tgc gtg gac gtg ctg ttc gga gac ggg	240
Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly	
65 70 75 80	
cat cgc ctg att atg cgc ggc gct cat ctc acc gct ctg gaa atg ctc	288
His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu	
85 90 95	
acc gcc ttc gcc tcc cac atc cgg gcc agg gac gcg gcg ggc agc ggg	336
Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly	
100 105 110	
gac aag ccg ggc gct gat act ggt cgc tgacagcgcc aaagagacca	383

Asp Lys Pro Gly Ala Asp Thr Gly Arg
 115 120
 acaagatgat ttgcgtggac taggacactt aacctaagaa gagtttcact taatcattca 443
 aatcactatc tgaagggtca cggagcgcaa aataaaagttt aaaaccctgc taccaaaaaa 503
 aaaaaaaaaa a 514

 <210> 200
 <211> 462
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 41..337

 <400> 200
 cttcaccacc aaaactctcc actccaccag cacagccaaa atg ctc gca cgt gct 55
 Met Leu Ala Arg Ala
 1 5
 act ttc cgc gcc gcc tcg gcc cca act ctc gtc gcc cgc cgc ggc ttc 103
 Thr Phe Arg Ala Ala Ser Ala Pro Thr Leu Val Ala Arg Arg Gly Phe
 10 15 20
 cag tcg acc cgc gcg caa atg gcc agc cca tac cac tac ccc gag ggt 151
 Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr His Tyr Pro Glu Gly
 25 30 35
 cct cgc agc aac ttg cca ttc gac ccg ctg aag aag ggc ttt gct ttc 199
 Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys Lys Gly Phe Ala Phe
 40 45 50
 aag tac tgg ggc ttt atg ggc acc gga ttc gcc ctt ccc ttc ctc ctt 247
 Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala Leu Pro Phe Leu Leu
 55 60 65
 gct gtc tgg caa aca gaa caa gcc gta aat gcg ctg aga cac ggc gtg 295
 Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala Leu Arg His Gly Val
 70 75 80 85
 gac atg cgt atc ggg atc ccg ggg aac acg gca ttt gta gat 337
 Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala Phe Val Asp
 90 95
 taggtggagg gcccgcatatc ggctatacta gacatcacag catcaatttc attgtctgtc 397
 cccaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 457
 aaaaaa 462

 <210> 201
 <211> 551
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 1..549

 <400> 201
 aga gag gga gcc cga gcc agg cca tct cca acc atg tcc gac gag gcc 48
 Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
 1 5 10 15

tcg gcc atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttc	96
Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe	
20 25 30	
cca ctc ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag	144
Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu	
35 40 45	
ccg ggc tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc	192
Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys	
50 55 60	
cat cgc acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta	240
His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu	
65 70 75 80	
act tct tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg	288
Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu	
85 90 95	
ttt tca tct gtg tct gtt gga gat caa gat gat tgc tat tcc ctg tta	336
Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu	
100 105 110	
gat gat cag gac ttc act tct ttt gat tta ttt cct gag ggg agt gtc	384
Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val	
115 120 125	
tgc agt gat gtc tct tct tct att agc act tac tgg gat tgg tca gat	432
Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp	
130 135 140	
agc gag ttt gaa tgg cag tta cca ggc agt gac att gcc agt ggg agt	480
Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser	
145 150 155 160	
gat gta ctt tct gat gtc ata ccc agt att cca agt tca cct tgc ctg	528
Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu	
165 170 175	
ctt cct aaa aaa aaa aaa aa	551
Leu Pro Lys Lys Lys Lys Lys	
180	

<210> 202
 <211> 550
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..315

<220>
 <221> misc_feature
 <222> 483
 <223> n=a, g, c or t

<400> 202	
agagaggggag cccgagccag gccatctcca acc atg tcc gac gag gcc tcg gcc	54
Met Ser Asp Glu Ala Ser Ala	
1 5	
atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttc cca ctc	102
Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe Pro Leu	

	10		15		20	
ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag ccg ggc						150
Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu Pro Gly						
25		30		35		
tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc cat cgc						198
Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys His Arg						
40		45		50		55
acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta act tct						246
Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu Thr Ser						
	60		65		70	
tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg ttt tca						294
Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu Phe Ser						
	75		80		85	
tct gtc tgt tgg aga tca aga tgattgctat tccctgtag atgatcagga						345
Ser Val Cys Trp Arg Ser Arg						
90						
cttcacttct ttgatttat ttcctgaggg gagtgtctgc agtgatgtct cttcttctat						405
tagcacttac tgggattggg cagatagcga gtttgaatgg cagttaccag gcagtgcacat						465
tgccagtggg agtgatgnta ctttctgatg tcataccag tattccaagt tcaccttgcc						525
tgcttcctaa aaaaaaaaaa aaaaa						550

<210> 203
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..315

<400> 203	
atc ggg ccg cga gcg ccc tcc ccg tgc ttt tcc gtg aga gac gta gag	48
Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu	
1	5
ctg agc gac cca gcc cgc gag cga ggt gag atg ccg gtg gcc gtg ggt	96
Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly	
	20
ccc tac gga cag tcc cag cca agc tgc ttc gac cgt gtc aaa atg ggc	144
Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly	
	35
ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc ggg gcg ctc ttc ggc	192
Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly	
	50
acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc	240
Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly	
	65
ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc	288
Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe	
	85
atg gcc att ggg atg ggc atc cga tgc taaccatggt tgccaactac	335
Met Ala Ile Gly Met Gly Ile Arg Cys	
	100
atctgtccct tcccatcaat cccagcccat gtactaataa aagaaagtct ttgagcaaaa	395
aaaaaaaaaa aaa	408

<210> 204
 <211> 665
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..582

```

<400> 204
actttttcagg ggacattcag aggcattcagc cccttcctcc tcaccagctc ccagagttcc      60
catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc      114
                               Met Pro Arg Ser Ser Arg Ser
                               1           5

cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga      162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg
          10           15           20

ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag      210
Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu
          25           30           35

gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac      258
Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn
          40           45           50           55

aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc      306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser
          60           65           70

tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt      354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val
          75           80           85

ctg ttt aac acg tgc aga tgc aag ctg ctg tgc cag aag ctc atg gag      402
Leu Phe Asn Thr Cys Arg Cys Lys Leu Leu Cys Gln Lys Leu Met Glu
          90           95          100

aag aca ggc att ctg ctc ctc tgt gct ttc ggt gtg tcc cag ggc cct      450
Lys Thr Gly Ile Leu Leu Leu Cys Ala Phe Gly Val Ser Gln Gly Pro
          105          110          115

gcc cag tcc cag gtg gag gta tcc ctg ggc cct ggc act gat tat agg      498
Ala Gln Ser Gln Val Glu Val Ser Leu Gly Pro Gly Thr Asp Tyr Arg
          120          125          130          135

aca ctg ggc aag aca ctg cac tgc cac gtg act cag ttt ccc cat ctg      546
Thr Leu Gly Lys Thr Leu His Cys His Val Thr Gln Phe Pro His Leu
          140          145          150

cct gat ggg tgt tgc tgt gag aat tat gaa atg aaa tgatgaccat      592
Pro Asp Gly Cys Cys Cys Glu Asn Tyr Glu Met Lys
          155          160

gaaaatattg tagaagccaa gaaatgcttc agaagttata aagctctccc caaaccgcaa      652
aaaaaaaaaa aaa      665
  
```

<210> 205
 <211> 1008
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 540..923

```

<400> 205
atttaggtga gctgccacgt ccggaggagg gcagcaagaa tgaaagacct ctagttttcc      60
agactcccgg agccctggtc tctacaccac atggacgtta tccacctcct ctgtgtcctc      120
ccaaggcagc atttcagaag gtgatccacg gcaaagccgt cccttcaaat ccgtctttgt      180
gccactgcc atagtcaacc ccgtgagaag cacagccggc cctgggactt taggacaagg      240
gtctcttcgg aaagggcgga gcagcatgag aaagagtaag tgggtggcaga gagatggatc      300
cctgcagaga cccctccagt ccgggatccc cactctcgtg gtaggctccc tcagacgcag      360
ccccaccatg gtccttcggc ctcagcagtt ccaattctac cagccacagg ggatcacctc      420
ctccccctca gccgtggtgg tggagatggg gtccaagcct gccctcacgg gggagcccgc      480
cctcacgtgc atcagcaggg gcagtgaggg ggatccactc cgcgccagc tccctcatt      539
atg gaa gac aaa gaa atc ccc atc aag agt gag cct ctg cca aaa ccg      587
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro
  1             5             10            15
ccc gca tct gcc cca cca tcc atc ctg gtg aaa cca gaa aac tca aga      635
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg
             20             25             30
aat gga atc gaa aag caa gtc aaa acc gtg aga ttt cag aat tac agc      683
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser
             35             40             45
cct cct ccc acc aaa cat tac acc tcc cat ccc acc tcc gga aag cct      731
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro
             50             55             60
gaa cag cca gcc acc ctc aag gcg tcc cag cct gaa gca gcg tcc ttg      779
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu
             65             70             75             80
ggc cca gag atg acc gtc cta ttt gcc cac cga agt ggc tgc cac tcc      827
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
             85             90             95
gga cag cag aca gac ctc cgg aga aag tca gct ctt gcc aag gcc aca      875
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
             100            105            110
acc ctg gtg tcc act gcc tca ggc acg cag acc gtg ttt ccc agc aaa      923
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
             115            120            125
tgaacctacg ggtggctttt cctagacccc aaagaggtga attgcattta aatacagtct      983
gcctycactg aaaaaaaaaa aaaaaa
                                1008

```

<210> 206
<211> 455
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..364

```

<400> 206
tggacaaatg gacctgcggt aggagagagg gacaacagta ggagcaggca gatcttgctg      60
tttcaaccaa aacctc atg ctg acc aga gtt gag gaa cag aag aag atg gtg      112
Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val
  1             5             10

```

aag gcc tgc agg tat agg tgt tca gca tgt cat ctg aaa tat tcc cca	160
Lys Ala Cys Arg Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro	
15 20 25	
cag agg caa aaa gaa agg aaa tta tct ctg aaa agg ggg agg aca agt	208
Gln Arg Gln Lys Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser	
30 35 40	
cag cag aat atg tca atg ttt tgg ttg aag aag ctg ctt gaa tct ggg	256
Gln Gln Asn Met Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly	
45 50 55 60	
ctt ttc tgt gcc atg tgt tct ccc agg gcc agc aca aag aag ggc ttt	304
Leu Phe Cys Ala Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe	
65 70 75	
tgg tgc agg ccc aag acc acc ata atc atc att gat tat tcc tct cca	352
Trp Cys Arg Pro Lys Thr Thr Ile Ile Ile Ile Asp Tyr Ser Ser Pro	
80 85 90	
cgc cag tgt ctc taaataaaact ttctcttctt tctctgaaaa aaaaaaaaaa	404
Arg Gln Cys Leu	
95	
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaagaaaa aaaaaaaaaa a	455

<210> 207
 <211> 749
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..544

<400> 207	
ctttttacgac gcgccggaag gcaacggcaa gggccgcagc cagcaccggg cggagagggc	60
tacc atg ggg aaa atc gcg ctg caa ctc aaa gcc acg ctg gag aac atc	109
Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile	
1 5 10 15	
acc aac ctc cgg ccc gtg ggc gag gac ttc cgg tgg tac ctg aag atg	157
Thr Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met	
20 25 30	
aaa tgt ggc aac tgt ggt gag att tcg gac aag tgg cag tac atc cgg	205
Lys Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg	
35 40 45	
ctg atg gac agt gtg gca ctg aag ggg ggc cgt ggc agt gct tcc atg	253
Leu Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met	
50 55 60	
gtc cag aag tgc aag ctg tgt gca aga gaa aat tcc atc gag att tta	301
Val Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu	
65 70 75	
agc agc acc atc aag cct tac aat gct gaa gac aat gag aac ttc aag	349
Ser Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys	
80 85 90 95	
aca ata gtg gag ttt gag tgc cgg ggc ctt gaa cca gtt gat ttc cag	397
Thr Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln	
100 105 110	
ccg cas gwg rtw ttg ctg ctg aag gtg tgg agt cag gga cag cct tca	445
Pro Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser	

	115	120	125	
gtg aca tta atc tgc agg aga agg act ggg act gac tat gat gaa aag				493
Val Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys				
	130	135	140	
gcc cag gag tct gtg gga atc tat gag gtc acc cac cag ttt gtg aag				541
Ala Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys				
	145	150	155	
tgc tgatccctct tccttcccag ttgcccttaa gaactgagaa aggacaaagt				594
Cys				
160				
actctaagca gcagagccca cagaggctcg ttcccttgac ccttgtctcc tgggtggctat				654
acgaaacctt cacaatctgc atgctggact ttattacagc ttccaagcc ccatcaataa				714
agcccctgtt cagctacaa aaaaaaaaaa aaaaa				749
<210>	208			
<211>	594			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	117..467			
<400>	208			
aaatgtagcc tgggtggtgtt cccaggagga aaagaacgag agactggtgg cagcacaccc				60
tgggcccccc actccccgcc gcaagtcctg aggatggcca gcagagaaac aagaaa atg				119
			Met	
			1	
gac tcc ctg gct gct gga gag ttg aat gcc agc cac cag cca tgg gtg				167
Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp Val				
	5	10	15	
cca gag ttt gta gcc tat tgg agg aaa aca cac caa gat cac ctc tgc				215
Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu Cys				
	20	25	30	
agc ctg cac agc cgg gcc ttt gga ctc ctg gat gct aga gtg acc tgg				263
Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr Trp				
	35	40	45	
gcg ctg agg agg gcc ccc gag cca gta cca gga aag gat aga ctc ctg				311
Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu Leu				
	50	55	60	65
ctt gca gca ttc cca gca gag gca tgc cct gtg gac acc gcg tct gtg				359
Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser Val				
	70	75	80	
tct gta tat ggc aga gct ccc aga tat atg cac aag gga gtg aaa aaa				407
Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys Lys				
	85	90	95	
tgt gtt tgc acc cca gtc tct aaa aat tca aca gcc tgg tta ctt ctg				455
Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu Leu				
	100	105	110	
ggg ggt ata tgc taggtggctt taatacgtgt tatttgc tca tctgtatttc				507
Gly Gly Ile Ser				
	115			
ttactctttg cacaattaaa ccatgttcct ttacttatg tacattttta ataaaagaaa				567
gttgtaacg aaaaaaaaaa aaaaaaa				594

<210> 209
 <211> 2098
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 893..1897

<400> 209
 accagggtcct ccgtggtgca cctgaaatgg tcaacagaag tcttgtgaca cgtggaatca 60
 tttcagagtc accccttctg cctcctgctc aagcaacaga cctgccgata acccccgtcg 120
 ggcccgcggt tctcagggtc ttctaatcc cctgggcttt ccggcttgct gtgtgcctgg 180
 agtcaggccg ccgtgcggca ggctgttaac cttagcctcg ggagagtgg atggagccac 240
 cttctcatgg aacgatactc gccttccctc atctccattg ttttatggct tcacacggac 300
 cgtggctttc tgcattggaag cttggtggcc aggggtgctgt cactttggga agcagccaga 360
 gaaccacagg atgcgtgaat cggctctcct gtcttcatgg gcattctccg ccagggtggt 420
 gtcttgtgct gtgattagtg ggtcactggc aagtgtctga atgaagtgg gggtccgggtg 480
 gcaacagtga cggggaaggg ctatgggtcc gcctcaatgt catctgcccc atccctgggc 540
 ctccaggaat ccagggtctc agccctgct ttagaaggaa gtcctgacgg ccacgctgga 600
 tctggaggac gtccggagct acaggggcga gatttcatct cgaaacctgg cggccagcag 660
 ggcgagcccc taccacagag tgaagggtga ctttgccctc tcgtgccacg aggacttgct 720
 ggcacccatc tctgagccca tcgagtggaa ataccacagc cctgaggagg agataagcct 780
 tggacctgcc tgctggctct gggatttttt aagacgaagt caacaggcag gggttttctg 840
 gcccttgagt ggcggggtgg acagcgcagc caccgcctgc ctcattctact cc atg tgc 898

Met Cys

1

tgc	cag	gtc	tgc	gag	gcc	gtg	agg	agt	gga	aat	gag	gaa	gtg	ctg	gct	946
Cys	Gln	Val	Cys	Glu	Ala	Val	Arg	Ser	Gly	Asn	Glu	Glu	Val	Leu	Ala	
	5						10					15				
gat	gtc	cgc	acc	atc	gtg	aac	cag	atc	agc	tac	acc	ccc	cag	gat	ccc	994
Asp	Val	Arg	Thr	Ile	Val	Asn	Gln	Ile	Ser	Tyr	Thr	Pro	Gln	Asp	Pro	
	20					25					30					
cga	gac	ctc	tgt	gga	cgc	ata	ctg	acc	acc	tgc	tac	atg	gcc	agc	aag	1042
Arg	Asp	Leu	Cys	Gly	Arg	Ile	Leu	Thr	Thr	Cys	Tyr	Met	Ala	Ser	Lys	
	35				40					45					50	
aac	tcc	tcc	cag	gag	acg	tgc	acc	cgg	gcc	aga	gag	ttg	gcc	cag	cag	1090
Asn	Ser	Ser	Gln	Glu	Thr	Cys	Thr	Arg	Ala	Arg	Glu	Leu	Ala	Gln	Gln	
			55						60					65		
att	gga	agc	cac	cac	atc	agt	ctc	aac	atc	gat	cca	gcc	gtg	aag	gcc	1138
Ile	Gly	Ser	His	His	Ile	Ser	Leu	Asn	Ile	Asp	Pro	Ala	Val	Lys	Ala	
			70					75					80			
gtc	atg	ggc	atc	ttc	agc	ctg	gtg	acg	ggg	aag	agc	cct	ctg	ttt	gca	1186
Val	Met	Gly	Ile	Phe	Ser	Leu	Val	Thr	Gly	Lys	Ser	Pro	Leu	Phe	Ala	
	85					90						95				
gct	cat	gga	gga	agc	agc	agg	gaa	aac	ctg	gcg	ctg	caa	aat	gtg	cag	1234
Ala	His	Gly	Gly	Ser	Ser	Arg	Glu	Asn	Leu	Ala	Leu	Gln	Asn	Val	Gln	
	100					105					110					
gct	cga	ata	cgg	atg	gtc	ctc	gcc	tat	ctg	ttt	gct	cag	ttg	agc	ctc	1282
Ala	Arg	Ile	Arg	Met	Val	Leu	Ala	Tyr	Leu	Phe	Ala	Gln	Leu	Ser	Leu	
	115				120					125					130	
tgg	tct	cgg	ggg	gtc	cac	ggg	ggg	ctc	ctc	gtg	ctg	gga	tcc	gcc	aac	1330
Trp	Ser	Arg	Gly	Val	His	Gly	Gly	Leu	Leu	Val	Leu	Gly	Ser	Ala	Asn	

	135	140	145	
gtg gat gag agt ctc ctg ggc tac ctg acc aag tac gac tgc tcc agt				1378
Val Asp Glu Ser Leu Leu Gly Tyr Leu Thr Lys Tyr Asp Cys Ser Ser				
	150	155	160	
gcg gac atc aac ccc ata ggc ggg atc agc aag acg gac ctc agg gcc				1426
Ala Asp Ile Asn Pro Ile Gly Gly Ile Ser Lys Thr Asp Leu Arg Ala				
	165	170	175	
ttc gtc cag ttc tgc atc cag cgc ttc cag ctt cct gcc ctg cag agc				1474
Phe Val Gln Phe Cys Ile Gln Arg Phe Gln Leu Pro Ala Leu Gln Ser				
	180	185	190	
atc ctg ttg gcg ccg gcc acc gca gag ctg gag ccc ttg gct gat gga				1522
Ile Leu Leu Ala Pro Ala Thr Ala Glu Leu Glu Pro Leu Ala Asp Gly				
	195	200	205	210
cag gtg tcc cag acc gac gag gaa gat atg ggg atg aca tat gcg gag				1570
Gln Val Ser Gln Thr Asp Glu Glu Asp Met Gly Met Thr Tyr Ala Glu				
	215	220	225	
ctc tcg gtc tat ggg aaa ctc agg aag gtg gcc aag atg ggg ccc tac				1618
Leu Ser Val Tyr Gly Lys Leu Arg Lys Val Ala Lys Met Gly Pro Tyr				
	230	235	240	
agc atg ttc tgc aaa ctc ctc ggc atg tgg aga cac atc tgc acc ccg				1666
Ser Met Phe Cys Lys Leu Leu Gly Met Trp Arg His Ile Cys Thr Pro				
	245	250	255	
aga cag gtc gct gac aaa gtg aag cgg ttt ttc tcc aag tac tcc atg				1714
Arg Gln Val Ala Asp Lys Val Lys Arg Phe Phe Ser Lys Tyr Ser Met				
	260	265	270	
aac aga cac aag atg acc acg ctc aca ccc gcg tac cac gcc gag aac				1762
Asn Arg His Lys Met Thr Thr Leu Thr Pro Ala Tyr His Ala Glu Asn				
	275	280	285	290
tac agc cct gag gac aac agg ttt gat ctg cga cca ttt ctg tac aac				1810
Tyr Ser Pro Glu Asp Asn Arg Phe Asp Leu Arg Pro Phe Leu Tyr Asn				
	295	300	305	
aca agc tgg cct tgg cag ttt cgg tgc ata gaa aat cag gtg cta cag				1858
Thr Ser Trp Pro Trp Gln Phe Arg Cys Ile Glu Asn Gln Val Leu Gln				
	310	315	320	
ctc gag agg gca gag cca cag tcc ctg gac ggc gtg gac tgaggccggt				1907
Leu Glu Arg Ala Glu Pro Gln Ser Leu Asp Gly Val Asp				
	325	330	335	
tccttcctgaggaggcctcctg tcctcggggga cccagcacc tcctcctcag cattgctgga				1967
gccaagggta ggagccctac actaggagcc caggatggga cggcgcatca gccgagaggg				2027
aggggaacttt tcagtcaaat tcctcaaaaa gaggctggaa taaagcctgg gctcaaaaaa				2087
aaaaaaaaa a				2098

<210> 210
 <211> 428
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 85..342

<400> 210
 acactggtac agtcacctag cccatcagtt ccttcgtcga cagcgccggg gacatccaga 60
 ctacaattta cagttcctct atcc atg tgc tgg gtt ata aat cat gcc atc 111

	Met	Cys	Trp	Val	Ile	Asn	His	Ala	Ile	
	1				5					
ctc cct aga atg aga atg cac agc aag cgg cag aca atc acc cgg cat										159
Leu Pro Arg Met Arg Met His Ser Lys Arg Gln Thr Ile Thr Arg His										
10 15 20 25										
tcg gca tct ctt tct ttt cac gcg ctc cct cgc tcc gcc ttt ctc cag										207
Ser Ala Ser Leu Ser Phe His Ala Leu Pro Arg Ser Ala Phe Leu Gln										
30 35 40										
ctc tgc ctt ctc agg cag ata cat cag ata cct tgt tta tcc atc ttc										255
Leu Cys Leu Leu Arg Gln Ile His Gln Ile Pro Cys Leu Ser Ile Phe										
45 50 55										
agc tcc act ctg agg gcg cag acg cac gat tcc ggg atc ggg tgc acc										303
Ser Ser Thr Leu Arg Ala Gln Thr His Asp Ser Gly Ile Gly Cys Thr										
60 65 70										
acg gcg aas cca ggc ggg aga cgg cag gag cag ctc agg taaccagggg										352
Thr Ala Xaa Pro Gly Gly Arg Arg Gln Glu Gln Leu Arg										
75 80 85										
aagcttgctg gcccacggag atgcagccgt ggagctgtga ggaaagacgg tctggcttca										412
aaaaaaaaaaaa aaaaaa										428
<210> 211										
<211> 769										
<212> DNA										
<213> Homo sapiens										
<220>										
<221> CDS										
<222> 155..433										
<400> 211										
atttttcccc ccttgctcgg gatggtgccca caggaggctg tgcggggcccc gctccgcttc										60
gaatggtgga tgctgtgggg caccacctcc ttgaggacca aggcactcca gctgccagga										120
atttggtctgc taacctcaca cagctgagcc ttcc atg aaa att gct ctc tgc caa										175
	Met	Lys	Ile	Ala	Leu	Cys	Gln			
	1						5			
aga gaa ctt cct agt cca agg tca tgt cta ctc tcc aga gat gtg act										223
Arg Glu Leu Pro Ser Pro Arg Ser Cys Leu Leu Ser Arg Asp Val Thr										
10 15 20										
gga gtg att tgc acc cgg atg cct aga ctc gcc atc tgc tca aag act										271
Gly Val Ile Cys Thr Arg Met Pro Arg Leu Ala Ile Cys Ser Lys Thr										
25 30 35										
gct cag aaa gcc ctc cca tgc att ccc ctg ctg cat acc agc cca ctc										319
Ala Gln Lys Ala Leu Pro Cys Ile Pro Leu Leu His Thr Ser Pro Leu										
40 45 50 55										
tgc ctg cag ctg ctg tct gca gga ctt cat atc tat gcc aca ctg tgt										367
Cys Leu Gln Leu Leu Ser Ala Gly Leu His Ile Tyr Ala Thr Leu Cys										
60 65 70										
aaa agc tgt gct tca aga aat cac aaa aac att ttc ctg cac cta cta										415
Lys Ser Cys Ala Ser Arg Asn His Lys Asn Ile Phe Leu His Leu Leu										
75 80 85										
cac agc ctg agt gcg gca taagttgacc ttgcttgcta agaaatgggg										463
His Ser Leu Ser Ala Ala										
90										
caagaaatgc ttttttgtat gtgtcatgtc tgtttgtttt tcaattaaga gaggaaagca										523

ttaggcagat	ggaatgtaca	tgtgaggatg	aggagacaga	aaacaagtag	ccctttccat	583
caagatagag	ggttttctgg	ggttgctggc	tattgaatgt	cactcctgat	ttctctttcc	643
aaggcactgt	accaccagcc	tactgagatt	gtgtgggagc	tttcatgggg	gttgtatttc	703
actgatgaaa	ataaatTTTT	tgcataatgt	gaaaaaaaaa	aaaaaaaaaga	aaaaaaaaaa	763
aaaaaa						769

<210> 212
 <211> 914
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..386

<400> 212						
ctttttaggg	agtccaaggt	acagtcgccg	cgtgcggagc	ttgttactgg	ttacttggcc	60
tc atg gcg gtc cga gct tcg ttc gag aac aac tgt gag atc ggc tgc						107
Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys						
1	5	10	15			
ttt gcc aag ctc acc aac acc tac tgt ctg gta gcg atc gga ggc tca						155
Phe Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser						
	20	25	30			
gag aac ttc tac agt gtg ttc gag ggc gag ctc tcc gat acc atc ccc						203
Glu Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro						
	35	40	45			
gtg gtg cac gcg tct atc gcc ggc tgc cgc atc atc ggg cgc atg tgt						251
Val Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys						
	50	55	60			
gtg gga gac aga aga aat tct ggc aga tgt gct caa ggt gga agt ctt						299
Val Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu						
	65	70	75			
cag aca gac agt ggc cga cca ggt gct agt agg aag cta ctg tgt ctt						347
Gln Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu						
	80	85	90	95		
cag caa tca ggg agg gct ggt gca tcc caa gac ttc aat tgaagaccag						396
Gln Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn						
	100	105				
gatgagctgt	cctctcttct	tcaagtcctc	cttgtggcgg	ggactgtgaa	ccgaggcagt	456
gaggtgattg	ctgctgggat	ggtggtgaat	gactggtgtg	ccttctgtgg	cctggacaca	516
accagcacag	agctgtcagt	ggtggagagt	gtcttcaagc	tgaatgaagc	ccagcctagc	576
accattgccca	ccagcatgcg	ggattccctc	attgacagcc	tcacctgagt	caccttccaa	636
gttgttccat	gggtcctctg	ctctggactg	tggccaacct	tctccacatt	ccgccaatc	696
tgtacctgat	gctggcaggg	aggtggcaga	gagctcactg	ggactgaggg	gctgggcacc	756
caaccctttt	ccacctgtgc	ttatcgcttg	gatctatcat	tactgcaaaa	acctgctctg	816
ttgtgctggc	tggcaggccc	tgtggctgct	ggctgagggg	tctgctgtcc	tgtgccaccc	876
cattaaagtg	cagttccctc	caaaaaaaaa	aaaaaaaaa			914

<210> 213
 <211> 1489
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 460..1290

<400> 213

```

cttctttccc tctccgtttt ggtgggctgg ttgaagatga aatccactga ggaggggaagt    60
ccagcaccct gtgtgccagt ccagaactgg cccatctgta gacccctga aaatcatatg    120
ggcttgatt  tggatattct caacagaaag ggtaaaggc tgatgggtacc taaagcctgg    180
tacttgaatt ttgatcaaga taagctgcct taagttctct tcattacaca aatgatccta    240
gataattgat agatcctgtg gttcaactgg atttctagat agaagctgga ttcattgtgat    300
gccagaggag taaaatttca agagactgaa accagatctg agtttcgctg ttccagtctg    360
gacctctttg gtgctgtaaa tcctggatat actgtagatg agtactgcgt ttttctttta    420
tggactctct tcagcttctg gagacctcac tatcctatt atg tct ttg tgt gaa    474
                                Met Ser Leu Cys Glu
                                1           5

gac atg ctg ctt tgt aat tat cga aag tgt cgc atc aaa ctc tct ggc    522
Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg Ile Lys Leu Ser Gly
                                10           15           20

tat gca tgg gtc act gcc tgc tct cac atc ttc tgt gat cag cat ggc    570
Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe Cys Asp Gln His Gly
                                25           30           35

agt ggt gag ttt agt cgc tca cca gct atc tgt cct gcc tgc aac agt    618
Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys Pro Ala Cys Asn Ser
                                40           45           50

acc ctt tct gga aag cta gat att gtc cgc aca gaa ctc agt cca tca    666
Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr Glu Leu Ser Pro Ser
                                55           60           65

gag gaa tat aaa gct atg gta ttg gca gga ctg cga cca gag atc gtg    714
Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu Arg Pro Glu Ile Val
70                                75                                80                                85

ttg gac att agc tcc cga gcg ctg gcc ttc tgg aca tat cag gta cat    762
Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp Thr Tyr Gln Val His
                                90           95           100

cag gaa cgt ctc tat caa gaa tac aat ttc agc aag gct gag ggc cat    810
Gln Glu Arg Leu Tyr Gln Glu Tyr Asn Phe Ser Lys Ala Glu Gly His
                                105          110          115

ctg aaa cag atg gag aag ata tat act cag caa ata caa agc aag gat    858
Leu Lys Gln Met Glu Lys Ile Tyr Thr Gln Gln Ile Gln Ser Lys Asp
                                120          125          130

gta gaa ttg acc tct atg aaa ggg gag gtt acc tcc atg aag aaa gta    906
Val Glu Leu Thr Ser Met Lys Gly Glu Val Thr Ser Met Lys Lys Val
                                135          140          145

cta gaa gaa tac aag aaa aag ttc agt gac atc tct gag aaa ctt atg    954
Leu Glu Glu Tyr Lys Lys Lys Phe Ser Asp Ile Ser Glu Lys Leu Met
150                                155                                160                                165

gag cgc aat cgt cag tat caa aag ctc caa ggc ctc tat gat agc ctt    1002
Glu Arg Asn Arg Gln Tyr Gln Lys Leu Gln Gly Leu Tyr Asp Ser Leu
                                170          175          180

agg cta cga aac atc act att gct aac cat gaa ggc acc ctt gaa cca    1050
Arg Leu Arg Asn Ile Thr Ile Ala Asn His Glu Gly Thr Leu Glu Pro
                                185          190          195

tcc atg att gca cag tct ggt gtt ctt ggc ttc cca tta ggt aac aac    1098
Ser Met Ile Ala Gln Ser Gly Val Leu Gly Phe Pro Leu Gly Asn Asn
                                200          205          210

tcc aag ttt cct ttg gat aat aca cct gtt cga aat cgg ggc gat gga    1146

```


[illegible]

```
<210> 215
<211> 1412
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 34..1143
```

<400> 215																	
atgcggtgaa	gggcgagcgg	cgcggcggct	gcg	atg	agt	gcc	tct	gcg	gcc	acc							54
				Met	Ser	Ala	Ser	Ala	Ala	Thr							
				1				5									
ggg	gtc	ttc	gtg	ctg	tcc	ctc	tcg	gcc	atc	ccg	gtc	acc	tat	gtc	ttc		102
Gly	Val	Phe	Val	Leu	Ser	Leu	Ser	Ala	Ile	Pro	Val	Thr	Tyr	Val	Phe		
		10						15						20			
aac	cac	ctg	gcg	gcc	cag	cat	gat	tcc	tgg	act	att	gta	ggg	gtt	gct		150
Asn	His	Leu	Ala	Ala	Gln	His	Asp	Ser	Trp	Thr	Ile	Val	Gly	Val	Ala		
		25				30					35						
gcc	ctc	atc	ctg	ttc	ctg	gta	gca	ctg	ctg	gct	cgt	gtc	ctc	gtc	aaa		198
Ala	Leu	Ile	Leu	Phe	Leu	Val	Ala	Leu	Leu	Ala	Arg	Val	Leu	Val	Lys		
40					45					50					55		
aga	aaa	cca	ccc	cgg	gac	cca	ctg	ttc	tat	gtg	tat	gca	gtt	ttt	gga		246
Arg	Lys	Pro	Pro	Arg	Asp	Pro	Leu	Phe	Tyr	Val	Tyr	Ala	Val	Phe	Gly		
				60				65						70			
ttt	acc	agc	gtg	gtg	aac	ctc	atc	ata	gga	ctg	gag	caa	gat	gga	atc		294
Phe	Thr	Ser	Val	Val	Asn	Leu	Ile	Ile	Gly	Leu	Glu	Gln	Asp	Gly	Ile		
			75				80						85				
att	gac	ggg	ttc	atg	aca	cac	tac	ttg	aga	gag	ggg	gaa	ccg	tat	ctg		342
Ile	Asp	Gly	Phe	Met	Thr	His	Tyr	Leu	Arg	Glu	Gly	Glu	Pro	Tyr	Leu		
		90					95					100					
aac	acc	gca	tat	ggg	cac	atg	atc	tgc	tac	tgg	gat	ggc	tct	gct	cat		390
Asn	Thr	Ala	Tyr	Gly	His	Met	Ile	Cys	Tyr	Trp	Asp	Gly	Ser	Ala	His		
		105				110					115						
tat	ctg	atg	tac	ctg	gtg	atg	gtg	gca	gcc	ata	gca	tgg	gag	gaa	act		438
Tyr	Leu	Met	Tyr	Leu	Val	Met	Val	Ala	Ala	Ile	Ala	Trp	Glu	Glu	Thr		
120					125					130					135		
tat	aga	acc	att	ggc	cta	tat	tgg	gtt	gga	tct	att	att	atg	agt	gtt		486
Tyr	Arg	Thr	Ile	Gly	Leu	Tyr	Trp	Val	Gly	Ser	Ile	Ile	Met	Ser	Val		
				140					145				150				
gtt	gtt	ttt	gtg	cca	gga	aac	att	gta	ggg	aag	tat	gga	aca	cga	att		534
Val	Val	Phe	Val	Pro	Gly	Asn	Ile	Val	Gly	Lys	Tyr	Gly	Thr				

tgc cct gct ttt ttc tta agc ata cca tat act tgt ctt cct gtc tgg	582
Cys Pro Ala Phe Phe Leu Ser Ile Pro Tyr Thr Cys Leu Pro Val Trp	
170 175 180	
gct ggt ttc aga atc tat aat cag cca tca gaa aat tat aat tac ccc	630
Ala Gly Phe Arg Ile Tyr Asn Gln Pro Ser Glu Asn Tyr Asn Tyr Pro	
185 190 195	
tca aag gtt att caa gaa gcc caa gcg aaa gac ctg ctg aga aga cca	678
Ser Lys Val Ile Gln Glu Ala Gln Ala Lys Asp Leu Leu Arg Arg Pro	
200 205 210 215	
ttt gat tta atg ttg gtt gtg tgt ctc ctc ctg gca act gga ttt tgc	726
Phe Asp Leu Met Leu Val Val Cys Leu Leu Ala Thr Gly Phe Cys	
220 225 230	
ctg ttc aga ggt ttg att gct ttg gat tgc cca tct gag ctc tgc cga	774
Leu Phe Arg Gly Leu Ile Ala Leu Asp Cys Pro Ser Glu Leu Cys Arg	
235 240 245	
tta tat acg caa ttt caa gag ccc tat cta aag gat cct gct gct tat	822
Leu Tyr Thr Gln Phe Gln Glu Pro Tyr Leu Lys Asp Pro Ala Ala Tyr	
250 255 260	
cct aaa att cag atg ctg gca tat atg ttc tat tct gtt cct tac ttt	870
Pro Lys Ile Gln Met Leu Ala Tyr Met Phe Tyr Ser Val Pro Tyr Phe	
265 270 275	
gtg act gca ctg tat ggc tta gtg gtt cct gga tgt tcc tgg atg cct	918
Val Thr Ala Leu Tyr Gly Leu Val Val Pro Gly Cys Ser Trp Met Pro	
280 285 290 295	
gac atc aca ttg ata cat gct gga ggt ctg gct cag gct cag ttt tct	966
Asp Ile Thr Leu Ile His Ala Gly Gly Leu Ala Gln Ala Gln Phe Ser	
300 305 310	
cac att ggt gca tct ctt cat gct aga act gct tat gtc tac aga gtc	1014
His Ile Gly Ala Ser Leu His Ala Arg Thr Ala Tyr Val Tyr Arg Val	
315 320 325	
cct gaa gaa gca aaa atc ctt ttt tta gca tta aac ata gca tat gga	1062
Pro Glu Glu Ala Lys Ile Leu Phe Leu Ala Leu Asn Ile Ala Tyr Gly	
330 335 340	
gtt ctt cct cag ctc ttg gcc tat cgt tgt atc tac aaa cca gag ttc	1110
Val Leu Pro Gln Leu Leu Ala Tyr Arg Cys Ile Tyr Lys Pro Glu Phe	
345 350 355	
ttc ata aaa aca aag gca gaa gaa aaa gtg gaa taaaaatatt acttcatggt	1163
Phe Ile Lys Thr Lys Ala Glu Glu Lys Val Glu	
360 365 370	
cctcctttct aaattactaa cttttgttat actggtactg atattttgtc ccatttcact	1223
ctcttctcat acgtgagtac ttaagaatat gtacattctt gctctgcact gtatgtgtga	1283
gctatatggt attgtgtaaa ttttttttga aggaaaatgg aaattcttga gaaacagttt	1343
gtttaaagaa atatattcaa aatcatttgt gaataaactt gatcatccat ctcaaaaaaa	1403
aaaaaaaa	1412

<210> 216
 <211> 1773
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 6..1184

<400> 216
ccaac atg acc tac agg tgg ggg aca ctg ctc atg aag aga aag ttt gag 50
Met Thr Tyr Arg Trp Gly Thr Leu Leu Met Lys Arg Lys Phe Glu
1 5 10 15
gag ccc cgg cca gga ttt cat ggt gtc ttg ggt atc aat tcc atc act 98
Glu Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr
20 25 30
ggg aag gag gag cct ctg tac ccc agc tac aag aga cag ttg cgc att 146
Gly Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile
35 40 45
tac ctg gtc tcc ctg cca ttc gtg tgc ctc tgc ctc tat ttc tca ctg 194
Tyr Leu Val Ser Leu Pro Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu
50 55 60
tat gtc atg atg att tac ttc gac atg gag gtt tgg gcc ttg ggt cta 242
Tyr Val Met Met Ile Tyr Phe Asp Met Glu Val Trp Ala Leu Gly Leu
65 70 75
cat gag aac agc ggg tct gag tgg acc agt gtc ctg ttg tat gtg ccc 290
His Glu Asn Ser Gly Ser Glu Trp Thr Ser Val Leu Leu Tyr Val Pro
80 85 90 95
agc atc atc tat gcc att gtg att gag atc atg aat cgt ctc tat cga 338
Ser Ile Ile Tyr Ala Ile Val Ile Glu Ile Met Asn Arg Leu Tyr Arg
100 105 110
tat gct gcc gag ttt tta act tca tgg gag aat cac aga ttg gaa tct 386
Tyr Ala Ala Glu Phe Leu Thr Ser Trp Glu Asn His Arg Leu Glu Ser
115 120 125
gcc tat cag aac cat cta att ctg aaa gtt tta gtg ttc aac ttc ctc 434
Ala Tyr Gln Asn His Leu Ile Leu Lys Val Leu Val Phe Asn Phe Leu
130 135 140
aat tgc ttt gcc tca ctc ttc tat att gcc ttt gtc ttg aaa gat atg 482
Asn Cys Phe Ala Ser Leu Phe Tyr Ile Ala Phe Val Leu Lys Asp Met
145 150 155
aag ctt ttg cgc cag agc ttg gcc act ctc cta att acc tcc cag atc 530
Lys Leu Leu Arg Gln Ser Leu Ala Thr Leu Leu Ile Thr Ser Gln Ile
160 165 170 175
ctc aac caa att atg gaa tct ttt ctt cct tat tgg ctc caa agg aag 578
Leu Asn Gln Ile Met Glu Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys
180 185 190
cat ggt gtg cgg gtg aag agg aag gtg cag gct tta aag gca gac att 626
His Gly Val Arg Val Lys Arg Lys Val Gln Ala Leu Lys Ala Asp Ile
195 200 205
gat gct aca tta tat gaa caa gtc atc ctg gaa aaa gaa atg gga act 674
Asp Ala Thr Leu Tyr Glu Gln Val Ile Leu Glu Lys Glu Met Gly Thr
210 215 220
tat ttg ggc acc ttt gat gat tac ttg gag tta ttc ctg cag ttt ggt 722
Tyr Leu Gly Thr Phe Asp Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly
225 230 235
tat gtg agc ctt ttc tcc tgt gtt tac cca tta gca gct gcc ttt gct 770
Tyr Val Ser Leu Phe Ser Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala
240 245 250 255
gtg tta aat aac ttc act gaa gta aat tca gat gcc tta aaa atg tgc 818
Val Leu Asn Asn Phe Thr Glu Val Asn Ser Asp Ala Leu Lys Met Cys
260 265 270
agg gtc ttc aaa cgt cca ttc tca gaa cct tca gcc aat att ggt gtg 866

Arg Val Phe Lys Arg Pro Phe Ser Glu Pro Ser Ala Asn Ile Gly Val	
275 280 285	
tgg cag ttg gct ttt gaa acg atg agt gtt ata tct gtg gtc act aac	914
Trp Gln Leu Ala Phe Glu Thr Met Ser Val Ile Ser Val Val Thr Asn	
290 295 300	
tgt gcg ctg att gga atg tca cca caa gtg aat gca gtc ttt cca gaa	962
Cys Ala Leu Ile Gly Met Ser Pro Gln Val Asn Ala Val Phe Pro Glu	
305 310 315	
tca aaa gca gac ctc att ttg att gta gta gca gtg gag cac gca ctc	1010
Ser Lys Ala Asp Leu Ile Leu Ile Val Val Ala Val Glu His Ala Leu	
320 325 330 335	
ctg gct tta aag ttt ata ctt gca ttt gcc ata cct gat aag cca cgg	1058
Leu Ala Leu Lys Phe Ile Leu Ala Phe Ala Ile Pro Asp Lys Pro Arg	
340 345 350	
cat atc cag atg aaa cta gcc aga ctg gaa ttt gag tct ttg gag gca	1106
His Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Ser Leu Glu Ala	
355 360 365	
ctc aag cag cag caa atg aag ctc gtg acc gag aac ctg aag gag gaa	1154
Leu Lys Gln Gln Gln Met Lys Leu Val Thr Glu Asn Leu Lys Glu Glu	
370 375 380	
cca atg gaa agc ggg aag gag aag gca acc tgagtgccca gcgtgcccag	1204
Pro Met Glu Ser Gly Lys Glu Lys Ala Thr	
385 390	
ctgccctgtt ggcagaggcc tgtgtctgtg ccacacctgc cacggtggca gggggggtac	1264
cgggggcagc atcgtggctc ctgaaccag acccaatgct tagccaaacg aagtggctcc	1324
catgtggcaa gcacccttct cagtttcgca gtggcttggc tcgggatcct tggcagttcc	1384
cccagcccca ccctgtctgc tccttcccag ttcttcccgc ggccccacac gctgctccag	1444
ctgccaactt tgctgcagag ccactgccgc ccttgagcct ctcaccatga gtgagccacc	1504
agctctccac gttccctca tagcagtgtc actcccaacc ccaccatggc ccagggaccc	1564
gtggacaggt tggggatggg gtgtgtgccc actgtgtctca tcacaggagc ctcagttgag	1624
agtgagcggg gtacagtaag gcagtgttc ccacactgga cctctttcct gggtctcttt	1684
tgcaatacat taacagaccc tttatcaaca taaacaatag taactgagct attaaaggca	1744
aaaaaaaaa taaaaaaaaa aaaaaaaaaa	1773

<210> 217
 <211> 1251
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..376

<400> 217	
tatccggtcc tcggctgcgg cgggcacc atg gtc ggt ggc gag gcg gct gcc	52
Met Val Gly Gly Glu Ala Ala Ala	
1 5	
gca gtg gag gag ctg gtt tcg ggg gtg cgg cag gcg gcc gac ttc gcg	100
Ala Val Glu Glu Leu Val Ser Gly Val Arg Gln Ala Ala Asp Phe Ala	
10 15 20	
gag cag ttc cgc tcc tac tca gag agc gag aag caa tgg aag gcc cgc	148
Glu Gln Phe Arg Ser Tyr Ser Glu Ser Glu Lys Gln Trp Lys Ala Arg	
25 30 35 40	
atg gaa ttc atc ctg cgc cac ctg ccc gac tac cgc gac ccg ccc gac	196

Met	Glu	Phe	Ile	Leu	Arg	His	Leu	Pro	Asp	Tyr	Arg	Asp	Pro	Pro	Asp		
				45					50					55			
ggc	agt	ggc	cgc	ctg	gac	cag	ctg	ctc	tcc	ctc	tcc	atg	gtc	tgg	gcc	244	
Gly	Ser	Gly	Arg	Leu	Asp	Gln	Leu	Leu	Ser	Leu	Ser	Met	Val	Trp	Ala		
			60					65					70				
aac	cat	ctc	ttc	cta	ggc	tgc	agt	tac	aat	aaa	gac	ctt	tta	gac	aag	292	
Asn	His	Leu	Phe	Leu	Gly	Cys	Ser	Tyr	Asn	Lys	Asp	Leu	Leu	Asp	Lys		
		75					80					85					
gtg	atg	gaa	atg	gcc	gat	ggg	att	gaa	gtg	gaa	gac	ctg	cca	caa	ttt	340	
Val	Met	Glu	Met	Ala	Asp	Gly	Ile	Glu	Val	Glu	Asp	Leu	Pro	Gln	Phe		
	90					95					100						
act	acc	aga	agt	gaa	tta	atg	aaa	aag	cat	caa	agc	taagccagaa				386	
Thr	Thr	Arg	Ser	Glu	Leu	Met	Lys	Lys	His	Gln	Ser						
	105				110				115								
gatttatcac	attttcatca	tcagctacag	gatttagaaag	gaggctggga	tgaatgtgac											446	
atagaccaca	gcagctctct	taagactcct	ggtattacca	acataaagag	gcagggtggaa											506	
tgagaaggac	tctgtctaga	ttggcttttt	taacattctc	attttcccag	gagttatcac											566	
tgtaaaagta	tgcattggata	tttatgtatt	tataaatcat	gcactctaag	atgagttcat											626	
caacattgta	aaagccctct	tttctgtttt	cagggtttttt	tttttcttat	cgacaagggtc											686	
tcactctgtc	gccagggcag	aatcacaaag	gtgcattatt	ggctcattgc	agcctcgaac											746	
tcctgggctc	atattttcag	ggttttttgt	tttttgtttt	gtttttttga	gacagagtct											806	
tgctctgttg	cccaggcagt	agtgcmagtg	gcgcgatata	ttttcagttt	ttaaactgca											866	
gaatttttgt	ttaaaatgcc	tttttggtgt	gggccacagt	ggccttatgc	ccataataat											926	
cccagcactt	tgggaggccg	aggtgagcag	atcacctgag	gttaggagtt	tgagaccagc											986	
ctggccaaca	cgatgaaacc	ccgtctctac	taaaaatata	aacaaaatta	gctggggcatg											1046	
gtggcggaca	tctgtaatcc	cagctactca	ggaggctgaa	gcagaagaac	tgcttgaacc											1106	
tgggaggtgg	aggttgacgt	gagccaagat	cgcaccattg	cactccatcc	tgggcgacaa											1166	
aaatgaaaca	ccgtctcaaa	aaaaaaaaataa	aaataataaa	ataaaaatgcc	tttttggtgt											1226	
tgatgtgaaa	aaaaaaaaaa	aaaaaa														1251	

<210> 218
 <211> 894
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..566

<400> 218																	
gcgcgccatc	ttggctccgg	atcgtgcgtg	aggcggcttc	gtgggcagcg	agagtcacag											60	
acaagacagc	aagcagg	atg gag cac tac	cgg aaa gct ggc tct gta gag													110	
		Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu															
	1		5		10												
ctc cca gcg cct tcc cca atg ccc cag cta cct cct gat acc ctt gag																158	
Leu Pro Ala Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu																	
	15		20		25												
atg cgg gtc cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct																206	
Met Arg Val Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala																	
	30		35		40												
ctg ggt cgg ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt																254	
Leu Gly Arg Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly																	
	45		50		55												
tct ggc agg gct gca gga aag gct gtc agc tgc gct gag att gtc aag																302	

Ser Gly Arg Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys	
60 65 70 75	
cgg cgg gtc cca ggc ctg cac cag ctc acc aag cta cgt ttc ctt cag	350
Arg Arg Val Pro Gly Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln	
80 85 90	
act gag gac agc tgg gtc cca gcc tca cct gac aca ggg cta gac ccc	398
Thr Glu Asp Ser Trp Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro	
95 100 105	
ctc aca gtg cgc cgc cat gtg cct gca gtg tgg gtg ctg ctc agc cgg	446
Leu Thr Val Arg Arg His Val Pro Ala Val Trp Val Leu Leu Ser Arg	
110 115 120	
gac ccc ctg gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc	494
Asp Pro Leu Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro	
125 130 135	
cct ggc ctg ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cga	542
Pro Gly Leu Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg	
140 145 150 155	
aga agg gct cga gac acc cga tcg tgaagacctg ctgagccagc ctgttctccg	596
Arg Arg Ala Arg Asp Thr Arg Ser	
160	
ggcctgaatg tctgggggtgc ttgtgccttt tctgagaagc gttgtgactg ctcaacatcc	656
ccatcaaggt ttgagtccac aaaagtggac ctccctatca tgcttcccct tccctctagc	716
atgtgggaag ggactgctgt gaagaatgac agatgtgggg cctctgccaa gttctgcatt	776
gctaaataag ggcttctctt gccttctacc tacagtgcatt ttgaactgcc ttctgaaaga	836
ggtccagggg gggatttagg aaataaaagtt tctacctatt taaaaaaaaa aaaaaaaa	894
<210> 219	
<211> 910	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 16..705	
<400> 219	
acatgagcca ccaaa atg gtg gtg ttc ggg tat gag gct ggg act aag cca	51
Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro	
1 5 10	
agg gat tca ggt gtg gtg ccg gtg gga act gag gaa gcg ccc aag gtt	99
Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val	
15 20 25	
ttc aag atg gca gca tct atg cat ggt cag ccc agt cct tct cta gaa	147
Phe Lys Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu	
30 35 40	
gat gca aaa ctc aga aga cca atg gtc ata gaa atc ata gaa aaa aat	195
Asp Ala Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn	
45 50 55 60	
ttt gac tat ctt aga aaa gaa atg aca caa aat ata tat caa atg gcg	243
Phe Asp Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala	
65 70 75	
aca ttt gga aca aca gct ggt ttc tct gga ata ttc tca aac ttc ctg	291
Thr Phe Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu	
80 85 90	

ttc aga cgc tgc ttc aag gtt aaa cat gat gct ttg aag aca tat gca	339
Phe Arg Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala	
95 100 105	
tca ttg gct aca ctt cca ttt ttg tct act gtt gtt act gac aag ctt	387
Ser Leu Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu	
110 115 120	
ttt gta att gat gct ttg tat tca gat aat ata agc aag gaa aac tgt	435
Phe Val Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys	
125 130 135 140	
gtt ttc aga agc tca ctg att ggc ata gtt tgt ggt gtt ttc tat ccc	483
Val Phe Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro	
145 150 155	
agt tct ttg gct ttt act aaa aat gga cgc ctg gca acc aag tat cat	531
Ser Ser Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His	
160 165 170	
acc gtt cca ctg cca cca aaa gga agg gtt tta atc cat tgg atg acg	579
Thr Val Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr	
175 180 185	
ctt tgt caa aca caa atg aaa tta atg gcg att cct cta gtc ttt cag	627
Leu Cys Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln	
190 195 200	
att atg ttt gga ata tta aat ggt cta tac cat tat gca gta ttt gaa	675
Ile Met Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu	
205 210 215 220	
gag aca ctt gag aaa act ata cat gaa gag taacacaaaaa aatgaatggt	725
Glu Thr Leu Glu Lys Thr Ile His Glu Glu	
225 230	
tgctaactta gcaaaatgaa gtttctataa agaggactca ggcattgctg aaagagttaa	785
aagtaactgt gaacaaataa tttgttctgt gccttttgcc tggatatatag caaataactca	845
aaaaatattc aataattcaa tcaataaata taagtttcat cttacaccaa aaaaaaaaaa	905
aaaaa	910

<210> 220

<211> 519

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 103..405

<400> 220

acttccggtg cgaaccgcct cggccggtcc ctgcgcggagc ttactgagcg cggccgcccga	60
gccagctcc gccgcgagc gcctgtgccg gcacgbhaca cc atg gag cgc ccg	114
Met Glu Arg Pro	

1

gat aag gcg gcg ctg aac gca ctg cag cct cct gag ttc aga aat gaa	162
Asp Lys Ala Ala Leu Asn Ala Leu Gln Pro Pro Glu Phe Arg Asn Glu	
5 10 15 20	

agc tca tta gca tct aca ctg aag acg ctc ctg ttc ttc aca gct tta	210
Ser Ser Leu Ala Ser Thr Leu Lys Thr Leu Leu Phe Phe Thr Ala Leu	
25 30 35	

atg atc act gtt cct att ggg tta tat ttc aca act aaa tct tac ata	258
Met Ile Thr Val Pro Ile Gly Leu Tyr Phe Thr Thr Lys Ser Tyr Ile	

	40	45	50	
ttt gaa ggc gcc ctt ggg atg tcc aat agg gac agc tat ttt tac gct				306
Phe Glu Gly Ala Leu Gly Met Ser Asn Arg Asp Ser Tyr Phe Tyr Ala				
	55	60	65	
gct att gtt gca gtg gtc gcc gtc cat gtg gtg ctg gcc ctc ttt gtg				354
Ala Ile Val Ala Val Val Ala Val His Val Val Leu Ala Leu Phe Val				
	70	75	80	
tat gtg gcc tgg aat gaa ggc tca cga cag tgb cgt gaa ggc aaa cag				402
Tyr Val Ala Trp Asn Glu Gly Ser Arg Gln Xaa Arg Glu Gly Lys Gln				
	85	90	95	100
gat taaagtgaac atcacctttt tatagcatta aattcatttt ttaaaatgat				455
Asp				
aatgctggag ggggccatct gattttgaata aagttgaaag aacatgtaaa aaaaaaaaaa				515
aaaa				519
<210>	221			
<211>	632			
<212>	DNA			
<213>	Homo sapiens			
<220>				
<221>	CDS			
<222>	72..350			
<400>	221			
agtgagaccg cgcggaaca gcttgccggt gcggtagtcc cgtgggcgct ccgctggctg				60
tgcaggcggc c atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca atg				110
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met				
	1	5	10	
ctg ggc gca ggg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg acc				158
Leu Gly Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr				
	15	20	25	
ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg cag				206
Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln				
	30	35	40	45
gac cca agg agc aga gag gag gcg gcc agg acc cag cag cta ttg ctg				254
Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu				
	50	55	60	
gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg agg				302
Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg				
	65	70	75	
aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc gcc ggg agg tca ccg				350
Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro				
	80	85	90	
tgagaccgga cttgcctccg tgggcgcggc accttggtt gggcgcagga atccgaggca				410
gcctttctcc ttcgtgggcc cagcggagag tccggaccga gataccatgc caggactctc				470
cggggtcctg tgagctgccg tcgggtgagc acgtttcccc caaaccctgg actgactgct				530
ttaaggtccg caaggcgggc cagggccgag acgcgagtcg gatgtggtga actgaaagaa				590
ccaataaaat catgttcctc cacccaaaaa aaaaaaaaaa aa				632
<210>	222			
<211>	652			
<212>	DNA			
<213>	Homo sapiens			

<222> 38..436

taggcctggt	gaagaccacc	tgggccgga	gaggaactgg	gggcaccctg	agctccagta	496
ccaccactca	caacaggcct	cccagtggca	gctcccagac	ctgggccctg	gccagggctc	556
tagggggcgg	cagtcttggg	gtgggccctg	ccaattggga	cgagtatccc	tgatttgtga	616
aaatgatgga	aaaacattca	aaaaaaaaa	aaaaaa			652

<213> Homo sapiens

<222> 38...322

										1				5					
atc	gtt	ctt	gcg	gac	tTG	aac	ttc	ccg	gcc	tcc	tcc	atc	tgc	cag	tgt				103
Ile	Val	Leu	Ala	Asp	Leu	Asn	Phe	Pro	Ala	Ser	Ser	Ile	Cys	Gln	Cys				
			10					15					20						

```

ggg ccc atg gag atc cgt gca gac ggc ctg ggc atc ccg cag ctc ctg      151
Gly Pro Met Glu Ile Arg Ala Asp Gly Leu Gly Ile Pro Gln Leu Leu
      25                      30                      35
gag gcc gtg cta gct gct gcc cct gga cac cta tgt gga gag tcc ggc      199
Glu Ala Val Leu Ala Ala Ala Pro Gly His Leu Cys Gly Glu Ser Gly
      40                      45                      50
tgc agt cat gga gct ggt gcc cag cga caa gga gag ggg cct gca gac      247
Cys Ser His Gly Ala Gly Ala Gln Arg Gln Gly Glu Gly Pro Ala Asp
55                      60                      65                      70
ccc agt gtg gac gga gta cga gtc cat cct acg cag ggc cgg ctg tgt      295
Pro Ser Val Asp Gly Val Arg Val His Pro Thr Gln Gly Arg Leu Cys
      75                      80                      85
gag agc cct ggc aaa gat aga gag gtt tgagttttat gaacgggcta      342
Glu Ser Pro Gly Lys Asp Arg Glu Val
      90                      95
agaaggtttt tgctgttgtg gcaacggggg agaaggccct ctacggaaac ctcatactca      402
ggaaggggggt gcttgccctc aaccccctgc ttagggcctg gtgaagacca cctggggccgg      462
aagaggaact gggggcaccc tgagctccag taccaccact cacaacaggc ctcccagtgg      522
cagctcccag acctggggccc tggccagggc tctagggggcc ggcagtcctg ggggtgggccc      582
tgccaattgg gacgagtatc cctgatttgt gaaaatgatg gaaaaacgtt caaaaaaaaaa      642
aaaaaaaaa      650

<210> 224
<211> 502
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 202..480

<400> 224
attctaaggc tacaggtcct ttggcaactg ctccccctct tccttctcct tttttttcaa      60
tctaatatgt gggacatacc aagtgatgag atcctttctg gcatacctaag aaaatgccaa      120
ctatagaaca acagatgtag tctccttatt aagtctgaag accaaacttc ttagtgcaaa      180
gcagtcaagt cttttctcaa c atg acc cca atc aag ctt ttg aac tta aca      231
      Met Thr Pro Ile Lys Leu Leu Asn Leu Thr
      1                      5                      10
tca aga tat aac ttc aga aga acg ttt gga ata gag ctc agt tca aac      279
Ser Arg Tyr Asn Phe Arg Arg Thr Phe Gly Ile Glu Leu Ser Ser Asn
      15                      20                      25
tct tcc tat tgc aaa cga gga aat ggc tac aga agc aga gtg ccc aaa      327
Ser Ser Tyr Cys Lys Arg Gly Asn Gly Tyr Arg Ser Arg Val Pro Lys
      30                      35                      40
gaa tgc gaa tgc aac tgg ctt cat ctt gaa agc gac act ctg aag aaa      375
Glu Cys Glu Cys Asn Trp Leu His Leu Glu Ser Asp Thr Leu Lys Lys
      45                      50                      55
tta ccc ata att tct ccc tct tgg aca tgc aga att atc ctg ttc ttg      423
Leu Pro Ile Ile Ser Pro Ser Trp Thr Cys Arg Ile Ile Leu Phe Leu
      60                      65                      70
tat ttt tct ggc cag ctt ctc caa ctt tcc ctt tct tgt ttg caa cta      471
Tyr Phe Ser Gly Gln Leu Leu Gln Leu Ser Leu Ser Cys Leu Gln Leu
      75                      80                      85                      90
att aaa ctt taaggataaa aaaaaaaaaa aa      502

```

Ile Lys Leu

<210> 225

<211> 1739

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 171..1670

<400> 225

```

actctggcct tgctgcttct ctccagctcc tgaacttttc tttcttccat catgctctga      60
gccattcctt tgaaaactaa aaggctccctg actcccagtc tgcagccatc ctgggcctgc      120
tgagctctga ttcaagtgcc tgcctctgcc ccttggtggg ctgaagcttc atg gag      176
                                     Met Glu
                                     1
gta tcc acc aac ccc tcc tcc aac atc gat cca ggc aac tat gtt gaa      224
Val Ser Thr Asn Pro Ser Ser Asn Ile Asp Pro Gly Asn Tyr Val Glu
      5      10      15
atg aat gat tca atc acc cac cta ccc tct aaa gtg gtg ata caa gat      272
Met Asn Asp Ser Ile Thr His Leu Pro Ser Lys Val Val Ile Gln Asp
      20      25      30
att act atg gag cta cac tgc cct ctg tgc aat gat tgg ttc cga gac      320
Ile Thr Met Glu Leu His Cys Pro Leu Cys Asn Asp Trp Phe Arg Asp
      35      40      45      50
cca ctg atg cta agc tgt ggc cac aac ttc tgt gaa gcc tgt atc caa      368
Pro Leu Met Leu Ser Cys Gly His Asn Phe Cys Glu Ala Cys Ile Gln
      55      60      65
gac ttt tgg agg ctg caa gca aag gaa aca ttc tgt cct gag tgt aag      416
Asp Phe Trp Arg Leu Gln Ala Lys Glu Thr Phe Cys Pro Glu Cys Lys
      70      75      80
atg cta tgt cag tat aac aac tgt aca ttc aac cct gta ctg gac aag      464
Met Leu Cys Gln Tyr Asn Asn Cys Thr Phe Asn Pro Val Leu Asp Lys
      85      90      95
ttg gta gag aag att aag aag tta ccc tta ctc aag ggc cat cca cag      512
Leu Val Glu Lys Ile Lys Lys Leu Pro Leu Leu Lys Gly His Pro Gln
      100      105      110
tgc cca gag cat gga gag aac ctg aaa ctg ttc agt aaa cca gat ggg      560
Cys Pro Glu His Gly Glu Asn Leu Lys Leu Phe Ser Lys Pro Asp Gly
      115      120      125      130
aaa ctg atc tgc ttt caa tgc aag gat gct cgg ttg tct gtg ggg cag      608
Lys Leu Ile Cys Phe Gln Cys Lys Asp Ala Arg Leu Ser Val Gly Gln
      135      140      145
tct aag gag ttc ctg caa atc tct gat gct gtc cat ttc ttc atg gag      656
Ser Lys Glu Phe Leu Gln Ile Ser Asp Ala Val His Phe Phe Met Glu
      150      155      160
gag ctt gcc atc caa cag ggt caa ctg gag aca act ctg aag gag ctt      704
Glu Leu Ala Ile Gln Gln Gly Gln Leu Glu Thr Thr Leu Lys Glu Leu
      165      170      175
cag acc ctg agg aac atg cag aag gaa gct att gct gct cac aag gaa      752
Gln Thr Leu Arg Asn Met Gln Lys Glu Ala Ile Ala Ala His Lys Glu
      180      185      190
aac aag cta cat ctg cag caa cat gtg tcc atg gag ttt cta aag ctg      800

```

Asn	Lys	Leu	His	Leu	Gln	Gln	His	Val	Ser	Met	Glu	Phe	Leu	Lys	Leu		
195					200					205					210		
cat	cag	ttc	ctg	cac	agc	aaa	gaa	aag	gac	att	tta	act	gag	ctc	cgg	848	
His	Gln	Phe	Leu	His	Ser	Lys	Glu	Lys	Asp	Ile	Leu	Thr	Glu	Leu	Arg		
				215					220					225			
gaa	gag	ggg	aaa	gcc	ttg	aat	gag	gag	atg	gag	ttg	aat	ctg	agc	cag	896	
Glu	Glu	Gly	Lys	Ala	Leu	Asn	Glu	Glu	Met	Glu	Leu	Asn	Leu	Ser	Gln		
			230					235					240				
ctt	cag	gag	caa	tgt	ctc	tta	gcc	aag	gat	atg	ttg	gtg	agc	att	cag	944	
Leu	Gln	Glu	Gln	Cys	Leu	Leu	Ala	Lys	Asp	Met	Leu	Val	Ser	Ile	Gln		
			245					250					255				
gca	aag	acg	gaa	caa	cag	aac	tcc	ttc	gac	ttt	ctc	aaa	gac	atc	aca	992	
Ala	Lys	Thr	Glu	Gln	Gln	Asn	Ser	Phe	Asp	Phe	Leu	Lys	Asp	Ile	Thr		
	260					265					270						
act	ctc	tta	cat	agc	ttg	gag	caa	gga	atg	aag	gtg	ctg	gca	acc	aga	1040	
Thr	Leu	Leu	His	Ser	Leu	Glu	Gln	Gly	Met	Lys	Val	Leu	Ala	Thr	Arg		
	275				280					285					290		
gag	ctt	att	tcc	aga	aag	ctg	aac	ctg	ggc	cag	tac	aaa	ggg	cct	atc	1088	
Glu	Leu	Ile	Ser	Arg	Lys	Leu	Asn	Leu	Gly	Gln	Tyr	Lys	Gly	Pro	Ile		
				295					300					305			
cag	tac	atg	gta	tgg	agg	gaa	atg	cag	gac	act	ctc	tgc	cca	ggc	ctg	1136	
Gln	Tyr	Met	Val	Trp	Arg	Glu	Met	Gln	Asp	Thr	Leu	Cys	Pro	Gly	Leu		
			310					315					320				
tct	cca	cta	act	ctg	gac	cct	aaa	aca	gct	cac	cca	aat	ctg	gtg	ctc	1184	
Ser	Pro	Leu	Thr	Leu	Asp	Pro	Lys	Thr	Ala	His	Pro	Asn	Leu	Val	Leu		
		325					330					335					
tcc	aaa	agc	caa	acc	agc	gtc	tgg	cat	ggg	gac	att	aag	aag	ata	atg	1232	
Ser	Lys	Ser	Gln	Thr	Ser	Val	Trp	His	Gly	Asp	Ile	Lys	Lys	Ile	Met		
	340					345					350						
cct	gat	gat	cct	gag	agg	ttt	gac	tca	agt	gtg	gct	gta	ctg	ggc	tca	1280	
Pro	Asp	Asp	Pro	Glu	Arg	Phe	Asp	Ser	Ser	Val	Ala	Val	Leu	Gly	Ser		
	355				360					365				370			
aga	ggc	ttc	acc	tct	gga	aag	tgg	tac	tgg	gaa	gta	gaa	gta	gca	aag	1328	
Arg	Gly	Phe	Thr	Ser	Gly	Lys	Trp	Tyr	Trp	Glu	Val	Glu	Val	Ala	Lys		
				375					380					385			
aag	aca	aaa	tgg	aca	gtt	gga	gtt	gtc	aga	gaa	tcc	atc	att	cgg	aag	1376	
Lys	Thr	Lys	Trp	Thr	Val	Gly	Val	Val	Arg	Glu	Ser	Ile	Ile	Arg	Lys		
			390					395					400				
ggc	agc	tgt	cct	cta	act	cct	gag	caa	gga	ttc	tgg	ctt	tta	aga	cta	1424	
Gly	Ser	Cys	Pro	Leu	Thr	Pro	Glu	Gln	Gly	Phe	Trp	Leu	Leu	Arg	Leu		
		405					410					415					
agg	aac	caa	act	gat	cta	aag	gct	ctg	gat	ttg	cct	tct	ttc	agt	ctg	1472	
Arg	Asn	Gln	Thr	Asp	Leu	Lys	Ala	Leu	Asp	Leu	Pro	Ser	Phe	Ser	Leu		
	420					425					430						
aca	ctg	act	aac	aac	ctc	gac	aag	gtg	ggc	ata	tac	ctg	gat	tat	gaa	1520	
Thr	Leu	Thr	Asn	Asn	Leu	Asp	Lys	Val	Gly	Ile	Tyr	Leu	Asp	Tyr	Glu		
	435				440					445				450			
gga	gga	cag	ttg	tcc	tac	aat	gct	aaa	acc	atg	act	cac	att	tac		1568	
Gly	Gly	Gln	Leu	Ser	Phe	Tyr	Asn	Ala	Lys	Thr	Met	Thr	His	Ile	Tyr		
				455					460					465			
acc	ttc	agt	aac	act	ttc	atg	gag	aaa	ctt	tat	ccc	tac	ttc	tgc	ccc	1616	
Thr	Phe	Ser	Asn	Thr	Phe	Met	Glu	Lys	Leu	Tyr	Pro	Tyr	Phe	Cys	Pro		
			470					475					480				
tgc	ctt	aat	gat	ggg	aga	gag	aat	aaa	gaa	cca	ttg	cac	atc	tta	cat	1664	

Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile Leu His
485 490 495
cca cag taatgagtca taatattata caaattcaga gtgttattaa agaggttttg 1720
Pro Gln
500
aaataaaaaa aaaaaaaaaa 1739

<210> 226
<211> 657
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 199..618

<400> 226
aactggatag agtactgccc ccttcagccc atggagaaaag gcaaatgcct ccttcagagt 60
ctacctaatag ctttctcaga taaataagca tgaagaaaag tcaaagtcca ttctagctct 120
aaaataagga atgaaatggt ttcctgatat gattttttgt tttcatctga taataatttt 180
atatatcaca gaaacagc atg gtt ctt act aaa cct ctt caa aga aat ggc 231
Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly
1 5 10
agc atg atg agc ttt gaa aat gtg aaa gaa aag agc aga gaa gga ggg 279
Ser Met Met Ser Phe Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly
15 20 25
ccc cat gca cac aca ccc gaa gaa gaa ttg tgt ttc gtg gta aca cac 327
Pro His Ala His Thr Pro Glu Glu Glu Leu Cys Phe Val Val Thr His
30 35 40
tac cct cag gtt cag acc aca ctc aac ctg ttt ttc cat ata ttc aag 375
Tyr Pro Gln Val Gln Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys
45 50 55
gtt ctt act caa cca ctt tcc ctt ctg tgg ggt tgt gat cag aag cct 423
Val Leu Thr Gln Pro Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro
60 65 70 75
cgt act gtt cct acc ctt gga aac ggc gca tgg gat acc tgc caa caa 471
Arg Thr Val Pro Thr Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln
80 85 90
cac ata cgc act tca tca tgg aca gca aac aca ctc gtc att caa aac 519
His Ile Arg Thr Ser Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn
95 100 105
cag cat tca cgg gaa agc act gtt tct gtt tgc ctt ttt atg tta atc 567
Gln His Ser Arg Glu Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile
110 115 120
cgc atg caa cat att ttg aaa aca gat aca ctt caa cag ttc aga ata 615
Arg Met Gln His Ile Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile
125 130 135
tgc tagtactaat aaaaccaaca tgttaaaaaa aaaaaaaaaa 657
Cys
140

<210> 227
<211> 888
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 182..481

<400> 227

```
atTTTgcctc tCagTgttca agcttgagcc cagcatcca actcctgaga tcttactggg      60
aagctgctga tcatcagttt caggaagtca gcatggatca gccttacgtt catggcctcc    120
aggccctatt ctctgcctc acagggaccg gccaggatct ctatccttac agcacgttgg      180
a atg tat atg ctC ctC tcc cca cat cgc ctt agg gag cag gca ggt gtc      229
  Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
      1           5           10          15
agg ggc agc ata agg acg gcc aac agg aca gaa gac ggg ttg aag atc      277
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
      20          25          30
cga gag gct gag tca ctt cca caa agt aac aca gct gat ttt aaa tgc      325
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
      35          40          45
ctg cat tca gca tcc ctg cag cag gct cca ggt gga att cta atg gga      373
Leu His Ser Ala Ser Leu Gln Gln Ala Pro Gly Gly Ile Leu Met Gly
      50          55          60
cca gcc tcc agt ccc tgg acc tta gcc gtg gaa gga gag aag agg aca      421
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
      65          70          75          80
tct gca cct cct ctC aga gaa agc ctg atg cct act aaa gga ctt ggg      469
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
      85          90          95
tgg tgg acg cag tgaccctcag tctggagctt gttcactgaa cattggagac      521
Trp Trp Thr Gln
      100
tatcatttgc gcagatggtc ttgggcctct atgagcagca ggctgcaccc cacagtgacc      581
tcctcattct actctgaggc atcttcatga aagcagatgt ccattgaaaa gcaccaagt      641
gcagtctcag ctgatgaact tcagaggcga ttgagacaaa ggctctcggg cccctctgcc      701
cttgatgggt gcctctggta tgcacttggc ctctgtgtct ttatttagac tggtcacttc      761
acaaccctac atgtacccc acccctaacc gtgcccactc tgggtcctcc cctcaactgc      821
ctgacttccc actttgagct cagcaaaggc aatagatgtt ttgtctgctt cgaaaaaaaa      881
aaaaaaaa
```

<210> 228

<211> 716

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 161..517

<400> 228

```
acctgtcatt atgcttacta acgttcggga cgtctcccgg gctgcttggg cgaggagagg      60
caggggtgtg tgaccccggt gggttactgtg ctgcgctaga gcacctaggg cctgctgaag    120
ccctccctcg cccgcgcctc tccttagtcc ttgagatgag atg gca agt tac agc      175
      Met Ala Ser Tyr Ser
              1              5
```

ggc ttc tcc ggc ctg ctg gag att cgc tac ggg cca gga cac cgc agc	223
Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly Pro Gly His Arg Ser	
10 15 20	
tgc ctt ccc caa ttc gct ttc ttt ccg cag ccg ccg ctg ccc cga ccc	271
Cys Leu Pro Gln Phe Ala Phe Phe Pro Gln Pro Pro Leu Pro Arg Pro	
25 30 35	
cgg atc tgc atg tgg gtg ctg gct gag ctg ctg gag cta ggg tgt cct	319
Arg Ile Cys Met Trp Val Leu Ala Glu Leu Leu Glu Leu Gly Cys Pro	
40 45 50	
gag cag agc ctg agg gac gcc atc acc ctg gac ctc ttc tgc cac gcg	367
Glu Gln Ser Leu Arg Asp Ala Ile Thr Leu Asp Leu Phe Cys His Ala	
55 60 65	
ctc att ttc tgc cgc cag cag ggc ttc tca ctg gag cag acg tca gcg	415
Leu Ile Phe Cys Arg Gln Gln Gly Phe Ser Leu Glu Gln Thr Ser Ala	
70 75 80 85	
gct tgt gcc ctg ctc cag gat ctt cac aag gct tgt att ggt gag agg	463
Ala Cys Ala Leu Leu Gln Asp Leu His Lys Ala Cys Ile Gly Glu Arg	
90 95 100	
ggg cag cta cca ggt ttg agc ccc agg gag aag agg aac cgg gcc tgg	511
Gly Gln Leu Pro Gly Leu Ser Pro Arg Glu Lys Arg Asn Arg Ala Trp	
105 110 115	
cac aag tgaccatggg aagcagaagc aggggatttc tgcctggaat atgtcattat	567
His Lys	
tagtagcatc atcacacaca agccatcagc tttccaatcc actgcttcct tatctagaaa	627
ttaaggatac agcacacatt ttacaggact gttctgagaa ataatatatg caaatatatg	687
catagtgcac aataaaaaaaaa aaaaaaaaaa	716

<210> 229
 <211> 654
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 86..505

<400> 229	
agttcgcggt gtcagcctcc gctccgagc ctcagttgtc ttctctgtga ggtgggaatg	60
ccggtgaatc ctgccgctgg cgtgg atg aga agt gaa tgc gtg ctc gga gct	112
Met Arg Ser Glu Cys Val Leu Gly Ala	
1 5	
gcg agt gac agc ggg cag gag gcg ccc agg gac act tgg ttt ctc cag	160
Ala Ser Asp Ser Gly Gln Glu Ala Pro Arg Asp Thr Trp Phe Leu Gln	
10 15 20 25	
ggc tgg aag gct tct aga agg ttc ctc atc aag gga agt gtg gct ggg	208
Gly Trp Lys Ala Ser Arg Arg Phe Leu Ile Lys Gly Ser Val Ala Gly	
30 35 40	
ggc gcc gtc tac ctg gtg tac gac cag gag ctg ctg ggg ccc agc gac	256
Gly Ala Val Tyr Leu Val Tyr Asp Gln Glu Leu Leu Gly Pro Ser Asp	
45 50 55	
aag agc cag gca gcc cta cag aag gct ggg gag gtg gtc ccc ccc gcc	304
Lys Ser Gln Ala Ala Leu Gln Lys Ala Gly Glu Val Val Pro Pro Ala	
60 65 70	
atg tac cag ttc agc cag tac gtg tgt cag cag aca ggc ctg cag ata	352

Met	Tyr	Gln	Phe	Ser	Gln	Tyr	Val	Cys	Gln	Gln	Thr	Gly	Leu	Gln	Ile		
75						80					85						
ccc	cag	ctc	cca	gcc	cct	cca	aag	att	tac	ttt	ccc	atc	cgt	gac	tcc	400	
Pro	Gln	Leu	Pro	Ala	Pro	Pro	Lys	Ile	Tyr	Phe	Pro	Ile	Arg	Asp	Ser		
90					95					100					105		
tgg	aat	gca	ggc	atc	atg	acg	gtg	atg	tca	gct	ctg	tcg	gtg	gcc	ccc	448	
Trp	Asn	Ala	Gly	Ile	Met	Thr	Val	Met	Ser	Ala	Leu	Ser	Val	Ala	Pro		
				110					115					120			
tcc	aag	gcc	cgc	gag	tac	tcc	aag	gag	ggc	tgg	gag	tat	gtg	aag	gcg	496	
Ser	Lys	Ala	Arg	Glu	Tyr	Ser	Lys	Glu	Gly	Trp	Glu	Tyr	Val	Lys	Ala		
			125				130						135				
cgc	acc	aag	tagcgagtca	gcagggggccg	cctgcccccg	ccagaacggg										545	
Arg	Thr	Lys															
		140															
cagggctgcc	actgacctga	agactccgga	ctgggacccc	actccgaggg	cagctccccg											605	
ccttgccggc	ccaataaagg	acttcagaag	tcaaaaaaaaa	aaaaaaaaa												654	
 <210> 230																	
<211> 635																	
<212> DNA																	
<213> Homo sapiens																	
 <220>																	
<221> CDS																	
<222> 56..382																	
 <400> 230																	
aattcgggtg	gagctgagcc	ggagacaggc	agttgtgaaa	aacttcagga	caaaa	atg										58	
						Met											
						1											
ttt	cat	tta	agg	act	tgt	gct	gct	aag	ttg	agg	cca	ttg	acg	gct	tcc	106	
Phe	His	Leu	Arg	Thr	Cys	Ala	Ala	Lys	Leu	Arg	Pro	Leu	Thr	Ala	Ser		
			5					10					15				
cag	act	ggt	aag	aca	ttt	tca	caa	aac	aga	cca	gca	gca	gct	agg	aca	154	
Gln	Thr	Val	Lys	Thr	Phe	Ser	Gln	Asn	Arg	Pro	Ala	Ala	Ala	Arg	Thr		
			20				25					30					
ttt	caa	cag	att	cgg	tgc	tat	tct	gca	cct	ggt	gct	gct	gag	ccc	ttt	202	
Phe	Gln	Gln	Ile	Arg	Cys	Tyr	Ser	Ala	Pro	Val	Ala	Ala	Glu	Pro	Phe		
			35			40					45						
ctc	agt	ggg	act	agt	tcg	aac	tat	gtg	gag	gag	atg	tac	tgt	gct	tgg	250	
Leu	Ser	Gly	Thr	Ser	Ser	Asn	Tyr	Val	Glu	Glu	Met	Tyr	Cys	Ala	Trp		
					55				60					65			
ctg	gaa	aac	ccc	aaa	agt	gta	cat	aag	aca	ggg	tcc	cac	tgt	tgt	cca	298	
Leu	Glu	Asn	Pro	Lys	Ser	Val	His	Lys	Thr	Gly	Ser	His	Cys	Cys	Pro		
				70				75					80				
ggc	tgg	agt	gca	gtg	gcg	gga	tct	cgg	ctt	gct	gca	acc	tcc	gac	tcc	346	
Gly	Trp	Ser	Ala	Val	Ala	Gly	Ser	Arg	Leu	Ala	Ala	Thr	Ser	Asp	Ser		
			85				90					95					
tgg	ggt	caa	gtg	att	ctt	atg	cct	cag	cct	ccc	gag	taactgggac				392	
Trp	Val	Gln	Val	Ile	Leu	Met	Pro	Gln	Pro	Pro	Glu						
		100					105										
tacaggtgca	cgtcaccacg	cctgactagt	ttttgtat	tttagtagaga	tgggatttta											452	
ctttgttggc	caggetgggc	ttgaaccct	ggcctcaagt	gatccaccca	ccttggcctc											512	
ccaaagtgct	gggattacag	gtatgatcaa	ccacgcctgg	ccatgtcatg	ccttgtgaca											572	

gaattcctttt attctgtttt gagccaataa atatttatag gtttcgaaaa aaaaaaaaaa 632
aaa 635

<210> 231
<211> 634
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 56..355

<400> 231
aattcgggtg gagctgagcc ggagacaggc agttgtgaaa aatttcagga caaaa atg 58
Met
1
ttt cat tta agg act tgt gct gct aag ttg agg cca ttg acg gct tcc 106
Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser
5 10 15
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca 154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr
20 25 30
ttt caa cag att cgt gct att ctg cac ctg ttg ctg ctg agc cct ttc 202
Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Ser Pro Phe
35 40 45
tca gtg gga cta gtt cga act atg tgg agg aga tgt act gtg ctt ggc 250
Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu Gly
50 55 60 65
tgg aaa acc cca aaa gtg tac ata aga cag ggt ccc act gtt gtc cag 298
Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val Gln
70 75 80
gct gga gtg cag tgg cgg gat ctg ggc ttg ctg caa cct ccg act cct 346
Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr Pro
85 90 95
ggg ttc aag tgattcttat gcctcagcct cccgagtaac tgggactaca 395
Gly Phe Lys
100
ggtgcacgtc accacgcctg actagttttt gtatttttag tagagatggg attttacttt 455
gttggccagg ctggtcttga acccctggcc tcaagtgatc caccacctt ggcctcccaa 515
agtgtggga ttacaggtat gatcaaccac gcctggccat gtcatgcctt gtgacagaat 575
tcctttattc tgttttgagc caataaatat ttatagggtt cgaaaaaaaa aaaaaaaaaa 634

<210> 232
<211> 583
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 76..498

<400> 232
aatatagcca gccgcggctg cccttgcgct tcccagagctg gcgggggtccg tgggtgcggga 60
tcgagattgc gggct atg gcg ccg aag gtt ttt cgt cag tac tgg gat atc 111

	Met	Ala	Pro	Lys	Val	Phe	Arg	Gln	Tyr	Trp	Asp	Ile	
	1				5					10			
ccc gat ggc acc gat tgc cac cgc aaa gcc tac agc acc acc agt att													159
Pro Asp Gly Thr Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile													
	15				20					25			
gcc agc gtc gct ggc ctg acc gcc gct gcc tac aga gtc aca ctc aat													207
Ala Ser Val Ala Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn													
	30				35					40			
cct ccg ggc acc ttc ctt gaa gga gtg gct aag gtt gga caa tac acg													255
Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr													
	45				50					55			60
ttc act gca gct gct gtc ggg gcc gtg ttt ggc ctc acc acc tgc atc													303
Phe Thr Ala Ala Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile													
	65				70					75			
agc gcc cat gtc cgc gag aag ccc gac gac ccc ctg aac tac ttc ctc													351
Ser Ala His Val Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu													
	80				85					90			
ggc ggc tgc gcc gga ggc ctg act ctg gga gca cgc acg cac aac tac													399
Gly Gly Cys Ala Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr													
	95				100					105			
ggg att ggc gcc gcc gcc tgc gtg tac ttt ggc ata gcg gcc tcc ctg													447
Gly Ile Gly Ala Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu													
	110				115					120			
gtc aag atg ggc cgg ctg gag ggc tgg gag gtg ttt gca aaa ccc aag													495
Val Lys Met Gly Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys													
	125				130					135			140
gtg tgagccctgt gcctgccggg acctccagcc tgcagaatgc gtccagaaat													548
Val													
aaattctgtg tctgtgtgaa aaaaaaaaaa aaaaa													583

<210> 233
 <211> 753
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 199..600

<400> 233	
atttttccga tgccaggcac cctcaaggca cagaggctgg ggctcatggt gggggcactt	60
ggcctctcca ggcctcgaag gcttctctgg gctgatgcga gctggggaac gggagggacg	120
gacgtgggag cgagaacgtc acaactggagg cagctggtgg cacgatgggg gacagagtga	180
aagagccttc gtgtcacc atg gcc aca cac ccc gat ggc ttc cgg ctt gag	231
Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu	
	1 5 10
gga ccc ctg gct gca gcc cac agc cct ggg cct tgc act gtg ctc tac	279
Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr	
	15 20 25
gaa ggc cct gtc cgt ggg ctc tgc ccy ttt gcc ccg cga aat tcc aac	327
Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn	
	30 35 40
acc atg gcg gcg gct gcc ctg gct gcc ccc agc ctg ggc ttc gat ggg	375
Thr Met Ala Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly	

45	50	55	
gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac atg cac gtg			423
Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp Met His Val			
60	65	70	75
gtg gat gta gag ctg agc gga ccc cgg ggc ccc act ggc cga agc ttt			471
Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe			
	80	85	90
gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc gcg gtc acc			519
Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr			
	95	100	105
ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg gcc tgc tgc			567
Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys			
	110	115	120
cag ctc ccc tcc agg ccg ggg atc cat ctc tgc tgagaagcct cctccctccc			620
Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys			
	125	130	
gagacaagat catctgcctg gcctctcacc accaccatcc caccctgcc ctgccccact			680
tccccagggt ctcccttctg actcagtaaa gatcaccgct gcctcccccc gcaaataaaa			740
aaaaaaaaaa aaa			753

<210> 234
 <211> 762
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 211..612

<400> 234	
atttccgatg ccaggcacc tcaaggcaca gaggctgggg ctcattgttg gggcacttgg	60
cctctccagg cctcgaaggc ttctcctggg ctgatgagag ctggggaacg ggaggacgg	120
acgtgggagc gagaacgtca cactggaggc agctggtggc acgatggggg acagagtga	180
aggtagcaag tcaagagcct tcgtgtcacc atg gcc aca cac ccc gat ggc ttc	234
Met Ala Thr His Pro Asp Gly Phe	
	1 5
cgg ctt gag gga ccc ctg gct gca gcg cac agc cct ggg cct tgc act	282
Arg Leu Glu Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr	
	10 15 20
gtg ctc tac gaa ggc cct gtc cgt ggg ctc tgc ccc ttt gcc ccg cga	330
Val Leu Tyr Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg	
	25 30 35 40
aat tcc aac acc atg tcg gcg gct gcc ctg gct gcc ccc agc ctg ggc	378
Asn Ser Asn Thr Met Ser Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly	
	45 50 55
ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac	426
Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp	
	60 65 70
atg cac gtg gtg gat gta gag ctg agc gga ccc cgg ggc ccc acg tgc	474
Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Cys	
	75 80 85
cga agc ttt gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc	522
Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly	
	90 95 100

gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg	570
Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu	
105 110 115 120	
gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat ctc tgc	612
Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys	
125 130	
tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc accaccatcc	672
cacccctgcc ctgccccact tccccagggt ctccctttctg actcagtaaa gatcaccgct	732
gcctcccccc gccaaaaaaaa aaaaaaaaaa	762

<210> 235

<211> 537

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<221> CDS

<222> 5..259

<400> 235

[illegible]

<210> 236

<211> 994

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 23...370

<400> 236

gattgctgtt tgctgtaaag tg atg ggg agg ccc tgg atg gtg atg ata ttg 52
Met Gly Arg Pro Trp Met Val Met Ile Leu
1 5 10
gag tca aaa tct gaa gaa aag atg tgg tat ggt gta ttc ctg tgg gca 100
Glu Ser Lys Ser Glu Glu Lys Met Trp Tyr Gly Val Phe Leu Trp Ala
15 20 25
ctg gtg tct tct ctc ttc ttt cat gtc cct gct gga tta ctg gcc ctc 148
Leu Val Ser Ser Leu Phe Phe His Val Pro Ala Gly Leu Leu Ala Leu
30 35 40
ttc acc ctc aga cat cac aaa tat ggt agg ttc atg tct gta agc atc 196
Phe Thr Leu Arg His His Lys Tyr Gly Arg Phe Met Ser Val Ser Ile
45 50 55
ctg ttg atg ggc atc gtg gga cca att act gct gga atc ttg aca agt 244
Leu Leu Met Gly Ile Val Gly Pro Ile Thr Ala Gly Ile Leu Thr Ser
60 65 70
gca gct att gct gga gtt tac cga gca gca ggg aag gaa atg ata cca 292
Ala Ala Ile Ala Gly Val Tyr Arg Ala Ala Gly Lys Glu Met Ile Pro
75 80 85 90
ttt gaa gcc ctc aca ctg ggc act gga cag aca ttt tgc gtc ttg gtg 340
Phe Glu Ala Leu Thr Leu Gly Thr Gly Gln Thr Phe Cys Val Leu Val
95 100 105
gtc tcc ttt tta cgg att tta gct act cta tagcatacat ccttatgctg 390
Val Ser Phe Leu Arg Ile Leu Ala Thr Leu
110 115
agatgttgaa cttaaacttt atggaatcct ccaaaagaat acattatgga gtgtagtggt 450
ttcttagttc ttcaaaggga agcaacttgg atgaacagga acatgaagga caacacatct 510
cagccttttc ttcatgttga agctcctaga attgaagact tatgtggact cctattgttc 570
tcaacccaaa caagtctttt ggctttcttt tttgtagata tttaatttaa gcagttttca 630
tgtgtacctt tacccaagcc aagtcaacag tgtctctggg gtggcctcct ttgcactgaa 690
atttacagta ttctgtgaga tgtcgcatat tttgaagaaa ccgtggaaga tactgggttta 750
tttcaaataa gcagagtatg ttgtattaaa atcttatcta atcttgatta aaatttgga 810
aactcttttc tttgctacat cttagtgaaca ataaatgcca aatagggtttt gggtgagtat 870
agttttgaaa acaaatttgg tgaaataaag caggaaaaaa aatttaagta taactcaagt 930
agtggctttg gttccactgt ttataaataa aaagtagata acaatggaaa aaaaaaaaaa 990
aaaa 994

<210> 237
<211> 662
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 41..352

<400> 237
tagctaaaaa ttgagggttc taaataactaa ggaagaaggg atg aat aga tat tgt 55
Met Asn Arg Tyr Cys
1 5
ggc aag ata ttt gtc tct gtc atg gtt aaa ttg caa aaa aat aaa ctt 103
Gly Lys Ile Phe Val Ser Val Met Val Lys Leu Gln Lys Asn Lys Leu
10 15 20
acc tcc ttc ccc agg cag cca ttg tta aca ttt ttt gaa tat cta gaa 151
Thr Ser Phe Pro Arg Gln Pro Leu Leu Thr Phe Phe Glu Tyr Leu Glu

	25		30		35	
aaa gtc ctt tgt tca gga tta ttt tcc cac tct gcc aag agt cac cat						199
Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser Ala Lys Ser His His						
	40		45		50	
gac ctg ctc aca cgc cac cct tat gaa act gcc gcg cca ctt ctc agc						247
Asp Leu Leu Thr Arg His Pro Tyr Glu Thr Ala Ala Pro Leu Leu Ser						
	55		60		65	
tcc cat ttg att ctc aca gaa gct cta cga aat ggg ttg ggc aaa tgt						295
Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn Gly Leu Gly Lys Cys						
	70		75		80	
cat gat cct cat ttc aca ggg gaa gaa act gag gcc cag agg ggg aaa						343
His Asp Pro His Phe Thr Gly Glu Glu Thr Glu Ala Gln Arg Gly Lys						
	90		95		100	
ctg act acc taaaattgcc atgtaggccg gcgcggtggc tcacgcctgt						392
Leu Thr Thr						
aatcccagca ctgtgggagg ccaaggcggg tggatcgca ggtcaggaga tcgagaccat						452
cctggctggc acttgaagcc ccgtctctac tagggataca aataattggc cgggtgtggt						512
ggcgggcgcc tgtgkwccca gctgttcggc aggctgagga gggcgaatgg tgtgagcctg						572
ggaggcggag cttgcggtgg gccgggattg cgccactgca ctccagcctg ggcgacagag						632
ccagattccg tccaaaaaaaa aaaaaaaaaa						662

<210> 238
 <211> 1829
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 3..1319

<400> 238	
at cta ggt gac cat gga tgg gag ctg agc ttg gag gag gac gca cag	47
Leu Gly Asp His Gly Trp Glu Leu Ser Leu Glu Glu Asp Ala Gln	
1 5 10 15	
ctg tgg ggt ggg gtg gtg aag agt tgt ttt gag gga aaa ggc cca caa	95
Leu Trp Gly Gly Val Val Lys Ser Cys Phe Glu Gly Lys Gly Pro Gln	
20 25 30	
aga gaa gcc caa cca gcc agc ccc cag gcc gcc ccg cca gga ccc acc	143
Arg Glu Ala Gln Pro Ala Ser Pro Gln Ala Ala Pro Pro Gly Pro Thr	
35 40 45	
aat gag gca cag atg gca gcc gct gcc gcc cta gcc cgg ctg gag cag	191
Asn Glu Ala Gln Met Ala Ala Ala Ala Leu Ala Arg Leu Glu Gln	
50 55 60	
aag cag tcc cgg gcc tgg ggc ccc aca tcg cag gac acc atc cga aac	239
Lys Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg Asn	
65 70 75	
cag gtg aga aag gaa ctt caa gcc gaa gcc acc gtc agc ggg agc ccc	287
Gln Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser Pro	
80 85 90 95	
gag gcc cca ggg acc aac gtg gta tct gag ccc aga gag gaa ggc tct	335
Glu Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly Ser	
100 105 110	
gcc cac ctg gct gtg cct ggc gtg tac ttc acc tgt ccg ctc act ggg	383
Ala His Leu Ala Val Pro Gly Val Tyr Phe Thr Cys Pro Leu Thr Gly	

gcc acc ctg agg aag gac cag cgg gac gcc tgc atc aag gag gcc att	115	120	125	431
Ala Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala Ile				
ctc ttg cac ttc tcc acc gac cca gtg gcc gcc tcc atc atg aag atc	130	135	140	479
Leu Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys Ile				
tac acg ttc aac aaa gac cag gac cgg gtg aag ctg ggt gtg gac acc	145	150	155	527
Tyr Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp Thr				
att gcc aag tac ctg gac aac atc cac ctg cac ccc gag gag gag aag	160	165	170	575
Ile Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu Lys				
tac cgg aag atc aag ctg cag aac aag gtg ttt cag gag cgc att aac	180	185	190	623
Tyr Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile Asn				
tgc ctg gaa ggg acc cac gag ttt ttt gag gcc att ggg ttc cag aag	195	200	205	671
Cys Leu Glu Gly Thr His Glu Phe Phe Glu Ala Ile Gly Phe Gln Lys				
gtg ttg ctt ccc gcc cag gat cag gag gac ccc gag gag ttc tac gtg	210	215	220	719
Val Leu Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr Val				
ctg agc gag acc acc ttg gcc cag ccc cag agc ctg gag agg cac aag	225	230	235	767
Leu Ser Glu Thr Thr Leu Ala Gln Pro Gln Ser Leu Glu Arg His Lys				
gaa cag ctg ctg gct gcg gag ccc gtg cgc gcc aag ctg gac agg cag	240	245	250	815
Glu Gln Leu Leu Ala Glu Pro Val Arg Ala Lys Leu Asp Arg Gln				
cgc cgc gtc ttc cag ccc tcg ccc ctg gcc tcg cag ttc gaa ctg cct	260	265	270	863
Arg Arg Val Phe Gln Pro Ser Pro Leu Ala Ser Gln Phe Glu Leu Pro				
ggg gac ttc ttc aac ctc aca gca gag gag atc aag cgg gag cag agg	275	280	285	911
Gly Asp Phe Phe Asn Leu Thr Ala Glu Glu Ile Lys Arg Glu Gln Arg				
ctc agg tcc gag gcg gtg gag cgg ctg agc gtg ctg cgg acc aag gcc	290	295	300	959
Leu Arg Ser Glu Ala Val Glu Arg Leu Ser Val Leu Arg Thr Lys Ala				
atg cgg gag aag gag gag cag cgg ggg ctg cgc aag tac aac tac acg	305	310	315	1007
Met Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr				
ctg ctg cgc gtg cgc ctc ccc gat ggc tgc ctc ctg cag ggc act ttc	320	325	330	1055
Leu Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe				
tac gct cgg gag cgg ctg ggg gcg gtg tac ggg ttc gtc cgg gag gcc	340	345	350	1103
Tyr Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala				
ctg cag agc gac tgg ctg cct ttt gag ctg ctg gcc tcg gga ggg cag	355	360	365	1151
Leu Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln				
aag ctg tcc gag gac gag aac ctg gcc ttg aac gag tgc ggg ctg gtg	370	375	380	1199
Lys Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val				
ccc tct gcc ctc ctg acc ttc tcg tgg gac atg gct gtg ctg gag gac	385	390	395	1247
Pro Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp				

400	405	410	415	
atc aag gcc gcg ggg gcc gag ccg gac tcc atc ctg aaa ccc gag ctc				1295
Ile Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu				
	420	425	430	
ctg tca gcc atc gag aag ctc ttg tgaaataaaa gcaggggttg cctcagccct				1349
Leu Ser Ala Ile Glu Lys Leu Leu				
	435			
gtgggtctgt ctcattgtct ccctgttcct ctccccgcca cccaggggcc tccaagccac				1409
ctctggaaat acttggtct gcccattggg cacgggaggg gcgccagccg tggagctgtg				1469
gaattgggcc ccgtggcaga gcccctatcc cttgggggct gtggggatgc gcccaagccc				1529
ccgagggaga ggcctgggga caccaacaaa tctaagccct ccctagctct tggtaactgt				1589
gtcatgaagc tgccggacag acacacgtgg catctccctg ggcaggagag caggcctgca				1649
gcatgggtcc cgttcccggtg tgccgtgggt ggcagtggct gcacctggca ctagggtgctg				1709
tctgtggatg tgggtgacaa cggcaggagg ggacgtggc cttcctgcac atagacctgc				1769
agttagtaaa tcataagccc aaataaacag gttgtttgaa tataaaaaaa aaaaaaaaaa				1829

<210> 239
 <211> 1083
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 421..768

<400> 239	
aaggatgtgc tctttcccaa ggagagggag ctctgttgcc tccttccac agaatcactc	60
tgtgcaaacc tcttcccctc cttggcccca gtctcccaa ttctaaaatc ggatactgga	120
taaaatgcc aaggaagacc tagggatgca ccaggaacca cgcgcctgaa tgccacaggt	180
ttgatattgat tcatgacct catctggaca caagctctaa aatacttgag ccttggcaga	240
aatggctgat agagtccaca gaacacgtg tcctcatctc agagaggaga actctgaacc	300
cagaggggaa ggatttacct gcagttgtat ggcaagccag aggtaggcgc tgcactggaa	360
cgcagcctaa ccagcctaaa gaaaccatgg gaggagaggc tcttaccctc tcctttgcag	420
atg tgg gcc cgg ctg cct cac act cca gag cag atg ggc cac agg ctt	468
Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu	
1 5 10 15	
ata ggt ccc aag gaa gct tca ctt cat gtg gta ccc agc tgg cca gcc	516
Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala	
20 25 30	
agg aag atg gag ggg ctt ctg gct ggc ctc tct tcc tct cct aga aag	564
Arg Lys Met Glu Gly Leu Leu Ala Gly Leu Ser Ser Ser Pro Arg Lys	
35 40 45	
tca tgc tgg ccc ttt tgg gtc cat ggg cca aag gtt cat gaa ggt ggc	612
Ser Cys Trp Pro Phe Trp Val His Gly Pro Lys Val His Glu Gly Gly	
50 55 60	
tct gcc tgt gag aca tca agc tcc tgg gtt gaa gga ctt gga tta aga	660
Ser Ala Cys Glu Thr Ser Ser Ser Trp Val Glu Gly Leu Gly Leu Arg	
65 70 75 80	
aga gtg aca tca gtg cac agt tta tgc caa ggg ctt ggg gcc tca gtc	708
Arg Val Thr Ser Val His Ser Leu Cys Gln Gly Leu Gly Ala Ser Val	
85 90 95	
cag ctt ctt cct gga cca cca cca aca aca acc agt gat aaa aat aat	756
Gln Leu Leu Pro Gly Pro Pro Pro Thr Thr Thr Ser Asp Lys Asn Asn	
100 105 110	

tat act agt ggc tgacatttat ggattcttcc tacacactag gctataccac 808
 Tyr Thr Ser Gly
 115
 agcgagtgcc tcgaaaggaa atatagtata gcactgtgcc gtccaacatg gcggccacta 868
 gccacatgca ctactgagca cttgaaatgt ggctagccca cattgagatg tgctgtaaata 928
 aaagaataga caccagattt ccaagactta gtacaaaaaa aagaatgtaa aattttctcat 988
 taacaatttt ttttcttaca tttattacat gttaacatga cgctatttgg agtttaaata 1048
 aatgcattat taaaattcaa aaaaaaaaaa aaaaa 1083

 <210> 240
 <211> 1831
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 78..590

 <400> 240
 aaggacttaa gcgccccgga gccgggaggc gaacttgga cccgctggcc tcgctcggtg 60
 cgcgccctccc tccccgc atg cag ccc gcc gag cgc tcg cgg gtc ccc agg 110
 Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg
 1 5 10
 atc gac ccg tac gga ttc gag cgg cct gag gac ttc gac gac gcc gcc 158
 Ile Asp Pro Tyr Gly Phe Glu Arg Pro Glu Asp Phe Asp Ala Ala
 15 20 25
 tac gag aag ttt ttc tcc agc tac ctg gtc acg ctc acc cgc agg gcg 206
 Tyr Glu Lys Phe Phe Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala
 30 35 40
 atc aaa tgg tcc cgg ctg ctg cag ggc ggg ggc gtc ccc agg agc cgg 254
 Ile Lys Trp Ser Arg Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg
 45 50 55
 aca gtg aag cgc tat gtc cgg aaa ggg gtc ccg ctg gag cac cgt gcc 302
 Thr Val Lys Arg Tyr Val Arg Lys Gly Val Pro Leu Glu His Arg Ala
 60 65 70 75
 cgc gtc tgg atg gtg ctg agt ggg gcc cag gcg cag atg gac cag aat 350
 Arg Val Trp Met Val Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn
 80 85 90
 ccc ggc tac tac cac cag ctt ctc cag gga gag aga aac ccc agg ctg 398
 Pro Gly Tyr Tyr His Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu
 95 100 105
 gag gac gcc atc agg aca gac ctg aac cgg acc ttc ccc gac aac gtg 446
 Glu Asp Ala Ile Arg Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val
 110 115 120
 aag ttc cgg aag acc acg gac ccc tgc tta cag agg acc ctg tac aat 494
 Lys Phe Arg Lys Thr Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn
 125 130 135
 gtg ctg ctg gca tat ggg cac cat aac cag gga gtg ggc tac tgc cag 542
 Val Leu Leu Ala Tyr Gly His His Asn Gln Gly Val Gly Tyr Cys Gln
 140 145 150 155
 gga atg aat ttt ata gca gga tat ctg att ctt ata aca aat aat gaa 590
 Gly Met Asn Phe Ile Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Glu
 160 165 170
 taagaatctt tttggctgtt agatgctctt gttggaagaa tactaccaga ttactacagc 650

```

ccggccatgc tgggcctgaa gaccgaccag gaggtcctcg gggagctggt gcgggcgaag 710
ctgccggctg tgggggccct gatggagcgt ctccgtgtgc tgtggacgct gctgggtgtcc 770
cgctggttca tctgcctgtt tgtggacatc ttgcccgagg agacagtgtc tcggatctgg 830
gactgtttgt ttaacgaagg ctccaagatt atcttccggt tggccctgac cttaattaag 890
cagcaccagg agttgatttt ggaagccacc agcgttccag acattttgca taagtttaag 950
cagataacca aagggagttt cgtgatggag tgtcacacgt ttatgcagggt gtgtggggct 1010
gcacgtggct cagtcctctc ccagggggcc ccgcctcacc tgcagcccgg gggctgtctc 1070
gaccaccggg aggatgcaca ggatggggcag cagtgggcat agggcacagg atgagcctcc 1130
agctctgtcc tgcactgtcc ccctgcgcct ggcttccgag ggctttcctg tctatggcgg 1190
ccctgtcttc ttggccctgg cactgcggac gctgtcctg gtcctaattg ctgtactcat 1250
ctgctgtgtg tggtgccaga agtgtggctt cccgaggccc ggcttcccca ctgggtcctg 1310
gacctggcgc aggccgtata gactcaggct ctgatgaggg cgttgtggga gctgtacctg 1370
acaggccttc tgaggaagcc aagacgccag gagaggctca ggcttgggag tcagtagttt 1430
cctaagaggg agtggaggct cggggccact ctgggtgcag catggcaaac gtgggcggta 1490
tttcagcagc tgggccttca tcaaagagaa gaccatgttg gccgggcgcg gtggctcacg 1550
cctgcagtcc cagcactttg ggaggccaag gcgtgtggat cacctgaggt caggagtcca 1610
agaccagcct ggccaacacg gtgaaacccc gtcttacta aaaaatacaa aaattagcca 1670
ggtgtggtgg ctacgcctta tgtagtccca gttactcggg aggctgaggc acgagaatca 1730
cttgaacctg ggaggcggag gttgcagtga gccgagatcg cgccactgca ctccagcctg 1790
ggcaacagag tgagactctg tctcaaaaaa aaaaaaaaaa a 1831

```

<210> 241
 <211> 1830
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..608

```

<400> 241
aaggacttaa gcgccccgga gccgggaggc gaacttggga cccgctggcc tcgctcgggtg 60
cgcgccctccc tccccgc atg cag ccc gcc gag cgc tcg cgg gtc ccc agg 110
          Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg
                1                5                10
atc gac ccg tac gga ttc gag cgg cct gag gac ttc gac gac gcc gcc 158
Ile Asp Pro Tyr Gly Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala
                15                20                25
tac gag aag ttt ttc tcc agc tac ctg gtc acg ctc acc cgc agg gcg 206
Tyr Glu Lys Phe Phe Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala
                30                35                40
atc aaa tgg tcc cgg ctg ctg cag ggc ggg ggc gtc ccc agg agc cgg 254
Ile Lys Trp Ser Arg Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg
                45                50                55
aca gtg aag cgc tat gtc cgg aaa ggg gtc ccg ctg gag cac cgt gcc 302
Thr Val Lys Arg Tyr Val Arg Lys Gly Val Pro Leu Glu His Arg Ala
                60                65                70                75
cgc gtc tgg atg gtg ctg agt ggg gcc cag gcg cag atg gac cag aat 350
Arg Val Trp Met Val Leu Ser Gly Ala Gln Ala Gln Met Asp Gln Asn
                80                85                90
ccc ggc tac tac cac cag ctt ctc cag gga gag aga aac ccc agg ctg 398
Pro Gly Tyr Tyr His Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu
                95                100                105
gag gac gcc atc agg aca gac ctg aac cgg acc ttc ccc gac aac gtg 446

```

Glu Asp Ala Ile Arg Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val	
110 115 120	
aag ttc cgg aag acc acg gac ccc tgc tta cag agg acc ctg tac aat	494
Lys Phe Arg Lys Thr Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn	
125 130 135	
gtg ctg ctg gca tat ggg cac cat aac cag gga gtg ggc tac tgc cag	542
Val Leu Leu Ala Tyr Gly His His Asn Gln Gly Val Gly Tyr Cys Gln	
140 145 150 155	
gga atg aat ttt ata gca gga tat ctg att ctt ata aca aat aat gat	590
Gly Met Asn Phe Ile Ala Gly Tyr Leu Ile Leu Ile Thr Asn Asn Asp	
160 165 170	
aag aat ctt ttt ggc tgt tagatgctct tgttgaaga atactaccag	638
Lys Asn Leu Phe Gly Cys	
175	
attactacag cccggccatg ctgggcctga agaccgacca ggaggctctc ggggagctgg	698
tgcgggcgaa gctgccggct gtgggggccc tgatggagcg tctcgggtgtg ctgtggacgc	758
tgtcgggtgtc ccgctgggttc atctgcctgt ttgtggacat cttgcccgtg gagacagtgc	818
ttcggatctg ggactgtttg tttaacgaag gctcgaagat tatcttccgg ttggccctga	878
ccttaattaa gcagcaccag gagttgattt tggaagccac cagcgttcca gacatttgcg	938
ataagtttaa gcagataaacc aaagggagtt tcgtgatgga gtgtcacacg tttatgcagg	998
tgtgtggggc tgcacgtggc tcagtcccct cccagggggc cccgcctcac ctgcagcccg	1058
ggggctgctc tgaccaccg gaggatgcac aggatgggca ccagtgggca tagggcacag	1118
gatgagcctc cagctctgtc ctgcatctgc cccctgcgcc tggcctccga gggctttcct	1178
gtctatggcg gccctgtctt cttggccctg gcaactgcgga cgctgctcct ggtcctaata	1238
gctgtactca tctgctgtgt gtggtgccag aagtgtggct tcccaggagg cggcctcccc	1298
actgggtcct ggacctggcg caggccgtat agactcaggt cctgatgagg gcgttgtggg	1358
agctgtacct gacaggcctt ctgaggaagc caagacgcca ggagaggctc aggcctggga	1418
gtcagtagtt tcctaagagg gagtggaggc tcggggccac tctgggtgca gcatggcaaa	1478
cgtgggcggg atttcagcag ctgggccttc atcaaagaga agaccatgtt ggccgggcgc	1538
ggtggctcac gcctgcagtc ccagcacttt gggaggccaa ggcgtgtgga tcacctgagg	1598
tcaggagttc aagaccagcc tggccaacac ggtgaaaccc cgtctctact aaaaaataca	1658
aaaattagcc aggtgtggtg gctcacgctt atgtagtccc agttactcgg gaggctgagg	1718
cacgagaatc acttgaacct gggaggcgga ggttgcaagt agccgagatc gcgccactgc	1778
actccagcct gggcaacaga gtgagactct gtctcaaaaa aaaaaaaaaa aa	1830

<210> 242
 <211> 508
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 242
 Met Asp Pro Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val Leu
 -25 -20 -15
 Leu Leu Leu Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro Pro
 -10 -5 1 5
 Pro Ala Leu Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His Gln Asp
 10 15 20
 Glu Phe Val Gln Thr Leu Lys Glu Trp Val Ala Ile Glu Ser Asp Ser
 25 30 35
 Val Gln Pro Val Pro Arg Phe Arg Gln Glu Leu Phe Arg Met Met Ala

470

475

480

<210> 243
 <211> 331
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 243

Met	Trp	Leu	Trp	Glu	Asp	Gln	Gly	Gly	Leu	Leu	Gly	Pro	Phe	Ser	Phe
-30						-25					-20				
Leu	Leu	Leu	Val	Leu	Leu	Leu	Val	Thr	Arg	Ser	Pro	Val	Asn	Ala	Cys
-15					-10					-5					1
Leu	Leu	Thr	Gly	Ser	Leu	Phe	Val	Leu	Leu	Arg	Val	Phe	Ser	Phe	Glu
		5						10					15		
Pro	Val	Pro	Ser	Cys	Arg	Ala	Leu	Gln	Val	Leu	Lys	Pro	Arg	Asp	Arg
	20						25					30			
Ile	Ser	Ala	Ile	Ala	His	Arg	Gly	Gly	Ser	His	Asp	Ala	Pro	Glu	Asn
35					40						45				
Thr	Leu	Ala	Ala	Ile	Arg	Gln	Ala	Ala	Lys	Asn	Gly	Ala	Thr	Gly	Val
50					55					60					65
Glu	Leu	Asp	Ile	Glu	Phe	Thr	Ser	Asp	Gly	Ile	Pro	Val	Leu	Met	His
			70						75					80	
Asp	Asn	Thr	Val	Asp	Arg	Thr	Thr	Asp	Gly	Thr	Gly	Arg	Leu	Cys	Asp
		85						90				95			
Leu	Thr	Phe	Glu	Gln	Ile	Arg	Lys	Leu	Asn	Pro	Ala	Ala	Asn	His	Arg
	100						105					110			
Leu	Arg	Asn	Asp	Phe	Pro	Asp	Glu	Lys	Ile	Pro	Thr	Leu	Met	Glu	Ala
	115					120					125				
Val	Ala	Glu	Cys	Leu	Asn	His	Asn	Leu	Thr	Ile	Phe	Phe	Asp	Val	Lys
130					135					140					145
Gly	His	Ala	His	Lys	Ala	Thr	Glu	Ala	Leu	Lys	Lys	Met	Tyr	Met	Glu
			150					155					160		
Phe	Pro	Gln	Leu	Tyr	Asn	Asn	Ser	Val	Val	Cys	Ser	Phe	Leu	Pro	Glu
		165					170					175			
Val	Ile	Tyr	Lys	Met	Arg	Gln	Thr	Asp	Arg	Asp	Val	Ile	Thr	Ala	Leu
	180					185						190			
Thr	His	Arg	Pro	Trp	Ser	Leu	Ser	His	Thr	Gly	Asp	Gly	Lys	Pro	Arg
	195					200					205				
Tyr	Asp	Thr	Phe	Trp	Lys	His	Phe	Ile	Phe	Val	Met	Met	Asp	Ile	Leu
210					215					220					225
Leu	Asp	Trp	Ser	Met	His	Asn	Ile	Leu	Trp	Tyr	Leu	Cys	Gly	Ile	Ser
			230					235						240	
Ala	Phe	Leu	Met	Gln	Lys	Asp	Phe	Val	Ser	Pro	Ala	Tyr	Leu	Lys	Lys
		245					250					255			
Trp	Ser	Ala	Lys	Gly	Ile	Gln	Val	Val	Gly	Trp	Thr	Val	Asn	Thr	Phe
	260					265						270			
Asp	Glu	Lys	Ser	Tyr	Tyr	Glu	Ser	His	Leu	Gly	Ser	Ser	Tyr	Ile	Thr
	275					280					285				
Asp	Ser	Met	Val	Glu	Asp	Cys	Glu	Pro	His	Phe					
290					295					300					

<210> 244
 <211> 274
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 244
 Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala
 -15 -10 -5
 Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
 1 5 10 15
 Arg Leu Gln Ser Pro Gln Gly Phe Ser Lys Ala Gly Gly Phe His Gly
 20 25 30
 Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Ala
 35 40 45
 Ala Ala Phe Phe Ile Thr Tyr Glu Tyr Val Lys Trp Phe Leu His Ala
 50 55 60
 Asp Ser Ser Ser Tyr Leu Thr Pro Met Lys His Met Leu Ala Ala Ser
 65 70 75
 Ala Gly Glu Val Val Ala Cys Leu Ile Arg Val Pro Ser Glu Val Val
 80 85 90 95
 Lys Gln Arg Ala Gln Val Ser Ala Ser Thr Arg Thr Phe Gln Ile Phe
 100 105 110
 Ser Asn Ile Leu Tyr Glu Glu Gly Ile Gln Gly Leu Tyr Arg Gly Tyr
 115 120 125
 Lys Ser Thr Val Leu Arg Glu Ile Pro Phe Ser Leu Val Gln Phe Pro
 130 135 140
 Leu Trp Glu Ser Leu Lys Ala Leu Trp Ser Trp Arg Gln Asp His Val
 145 150 155
 Val Asp Ser Trp Gln Ser Ala Val Cys Gly Ala Phe Ala Gly Gly Phe
 160 165 170 175
 Ala Ala Ala Val Thr Thr Pro Leu Asp Val Ala Lys Thr Arg Ile Met
 180 185 190
 Leu Ala Lys Ala Gly Ser Ser Thr Ala Asp Gly Asn Val Leu Ser Val
 195 200 205
 Leu His Gly Val Trp Arg Ser Gln Gly Leu Ala Gly Leu Phe Ala Gly
 210 215 220
 Val Phe Pro Arg Met Ala Ala Ile Ser Leu Gly Gly Phe Ile Phe Leu
 225 230 235
 Gly Ala Tyr Asp Arg Thr His Ser Leu Leu Leu Glu Val Gly Arg Lys
 240 245 250 255
 Ser Pro

<210> 245
 <211> 406
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -35..-1

<400> 245

Met	Arg	Gly	Ser	Val	Glu	Cys	Thr	Trp	Gly	Trp	Gly	His	Cys	Ala	Pro
-35					-30					-25					-20
Ser	Pro	Leu	Leu	Leu	Trp	Thr	Leu	Leu	Leu	Phe	Ala	Ala	Pro	Phe	Gly
				-15					-10					-5	
Leu	Leu	Gly	Glu	Lys	Thr	Arg	Gln	Val	Ser	Leu	Glu	Val	Ile	Pro	Asn
			1				5					10			
Trp	Leu	Gly	Pro	Leu	Gln	Asn	Leu	Leu	His	Ile	Arg	Ala	Val	Gly	Thr
15						20					25				
Asn	Ser	Thr	Leu	His	Tyr	Val	Trp	Ser	Ser	Leu	Gly	Pro	Leu	Ala	Val
30					35					40					45
Val	Met	Val	Ala	Thr	Asn	Thr	Pro	His	Ser	Thr	Leu	Ser	Val	Asn	Trp
				50					55					60	
Ser	Leu	Leu	Leu	Ser	Pro	Glu	Pro	Asp	Gly	Gly	Leu	Met	Val	Leu	Pro
			65					70					75		
Lys	Asp	Ser	Ile	Gln	Phe	Ser	Ser	Ala	Leu	Val	Phe	Thr	Arg	Leu	Leu
	80					85						90			
Glu	Phe	Asp	Ser	Thr	Asn	Val	Ser	Asp	Thr	Ala	Ala	Lys	Pro	Leu	Gly
95					100					105					
Arg	Pro	Tyr	Pro	Pro	Tyr	Ser	Leu	Ala	Asp	Phe	Ser	Trp	Asn	Asn	Ile
110					115					120					125
Thr	Asp	Ser	Leu	Asp	Pro	Ala	Thr	Leu	Ser	Ala	Thr	Phe	Gln	Gly	His
				130					135					140	
Pro	Met	Asn	Asp	Pro	Thr	Arg	Thr	Phe	Ala	Asn	Gly	Ser	Leu	Ala	Phe
		145						150					155		
Arg	Val	Gln	Ala	Phe	Ser	Arg	Ser	Ser	Arg	Pro	Ala	Gln	Pro	Pro	Arg
	160						165					170			
Leu	Leu	His	Thr	Ala	Asp	Thr	Cys	Gln	Leu	Glu	Val	Ala	Leu	Ile	Gly
175						180				185					
Ala	Ser	Pro	Arg	Gly	Asn	Arg	Ser	Leu	Phe	Gly	Leu	Glu	Val	Ala	Thr
190					195					200					205
Leu	Gly	Gln	Gly	Pro	Asp	Cys	Pro	Ser	Met	Gln	Glu	Gln	His	Ser	Ile
				210					215					220	
Asp	Asp	Glu	Tyr	Ala	Pro	Ala	Val	Phe	Gln	Leu	Asp	Gln	Leu	Leu	Trp
		225						230				235			
Gly	Ser	Leu	Pro	Ser	Gly	Phe	Ala	Gln	Trp	Arg	Pro	Val	Ala	Tyr	Ser
	240					245						250			
Gln	Lys	Pro	Gly	Gly	Arg	Glu	Ser	Ala	Leu	Pro	Cys	Gln	Ala	Ser	Pro
255					260						265				
Leu	His	Pro	Ala	Leu	Ala	Tyr	Ser	Leu	Pro	Gln	Ser	Pro	Ile	Val	Arg
270					275					280					285
Ala	Phe	Phe	Gly	Ser	Gln	Asn	Asn	Phe	Cys	Ala	Phe	Asn	Leu	Thr	Phe
				290					295					300	
Gly	Ala	Ser	Thr	Gly	Pro	Gly	Tyr	Trp	Asp	Gln	His	Tyr	Leu	Ser	Trp
			305				310						315		
Ser	Met	Leu	Leu	Gly	Val	Gly	Phe	Pro	Pro	Val	Asp	Gly	Leu	Ser	Pro
	320					325					330				
Leu	Val	Leu	Gly	Ile	Met	Ala	Val	Ala	Leu	Gly	Ala	Pro	Gly	Leu	Met
335					340						345				
Leu	Leu	Gly	Gly	Gly	Leu	Val	Leu	Leu	Leu	His	His	Lys	Lys	Tyr	Ser
350					355				360						365
Glu	Tyr	Gln	Ser	Ile	Asn										

370

<210> 246
 <211> 24
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 246
 Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala Ala Cys Thr
 -15 -10 -5
 Pro Ser Ala Ser Val Ile Arg Thr
 1 5

<210> 247
 <211> 348
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 247
 Met Ala Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met
 -25 -20 -15
 Leu Leu Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His
 -10 -5 1
 Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr
 5 10 15
 Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala
 20 25 30 35
 Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln
 40 45 50
 Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln
 55 60 65
 Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn
 70 75 80
 Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser
 85 90 95
 Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met
 100 105 110 115
 Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu
 120 125 130
 Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val
 135 140 145
 Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe
 150 155 160
 Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp
 165 170 175
 Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser

180		185		190		195									
Phe	Gly	Gly	Leu	Gln	Val	Val	Ile	Asn	Gly	Leu	Asn	Ser	Thr	Glu	Pro
		200		205		210									
Leu	Val	Lys	Glu	Tyr	Ala	Ala	Phe	Val	Leu	Gly	Ala	Ala	Phe	Ser	Ser
		215		220		225									
Asn	Pro	Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly	Ala	Leu	Gln	Lys
		230		235		240									
Leu	Leu	Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr	Ala	Lys	Lys	Lys
		245		250		255									
Val	Leu	Phe	Ala	Leu	Cys	Ser	Leu	Leu	Arg	His	Phe	Pro	Tyr	Ala	Gln
260				265		270									275
Arg	Gln	Phe	Leu	Lys	Leu	Gly	Gly	Leu	Gln	Val	Leu	Arg	Thr	Leu	Val
				280		285									290
Gln	Glu	Lys	Gly	Thr	Glu	Val	Leu	Ala	Val	Arg	Val	Val	Thr	Leu	Leu
		295		300		305									
Tyr	Asp	Leu	Val	Thr	Glu	Lys	Met	Phe	Ala	Glu	Glu				
		310		315											

<210> 248
 <211> 397
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 248
Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys Phe
-35 -30 -25
Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala
-20 -15 -10 -5
Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
1 5 10
Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly
15 20 25
Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu Gly
30 35 40
Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser Gly
45 50 55 60
Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile Ile
65 70 75
Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly His
80 85 90
Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr Gly
95 100 105
Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu Glu
110 115 120
Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser Leu
125 130 135 140
Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser Gln
145 150 155
Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser Ala
160 165 170

Ser	Arg	Lys	Arg	Leu	Asp	Lys	Lys	Arg	Ser	Val	Pro	Val	Ala	Thr	Val
		175					180					185			
Glu	Leu	Glu	Glu	Lys	Arg	Phe	Arg	Thr	Leu	Pro	Leu	Val	Pro	Ser	Pro
		190					195				200				
Leu	Gln	Gly	Leu	Thr	Asn	Gln	Asp	Leu	Gln	Glu	Gly	Glu	Asp	Trp	Glu
205					210				215						220
Gln	Glu	Asp	Glu	Asp	Met	Asp	Pro	Arg	Leu	Glu	His	Ser	Ser	Ser	Val
				225					230					235	
Gln	Glu	Asp	Ser	Glu	Ser	Pro	Ser	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Leu
			240					245					250		
Leu	Gln	Tyr	Arg	Ala	Ile	His	Ser	Ala	Glu	Gln	Gln	His	Ala	Tyr	Glu
		255					260					265			
Gln	Asp	Phe	Glu	Thr	Asp	Tyr	Ala	Glu	Tyr	Arg	Ile	Leu	His	Ala	Arg
	270					275					280				
Val	Gly	Thr	Ala	Ser	Gln	Arg	Phe	Ile	Glu	Leu	Gly	Ala	Glu	Ile	Lys
285					290					295					300
Arg	Val	Arg	Arg	Gly	Thr	Pro	Glu	Tyr	Lys	Val	Leu	Glu	Asp	Lys	Ile
				305					310					315	
Ile	Gln	Glu	Tyr	Lys	Lys	Phe	Arg	Lys	Gln	Tyr	Pro	Ser	Tyr	Arg	Glu
			320					325					330		
Glu	Lys	Arg	Arg	Cys	Glu	Tyr	Leu	His	Gln	Lys	Leu	Ser	His	Ile	Lys
		335					340					345			
Gly	Leu	Ile	Leu	Glu	Phe	Glu	Glu	Lys	Asn	Arg	Gly	Ser			
	350					355					360				

<210> 249

<211> 403

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -21...-1

<400> 249

Met	Val	Asn	Asp	Pro	Pro	Val	Pro	Ala	Leu	Leu	Trp	Ala	Gln	Glu	Val
	-20					-15					-10				
Gly	Gln	Val	Leu	Ala	Gly	Arg	Ala	Arg	Arg	Leu	Leu	Leu	Gln	Phe	Gly
-5					1				5					10	
Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Trp	Val	Ser	Val	Phe	Leu	
			15					20				25			
Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	Leu	Ser
		30					35					40			
Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	Thr	Ser
	45					50					55				
Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg
60					65					70					75
Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu
				80					85					90	
Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val
			95					100					105		
Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser
		110					115					120			
Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp

125		130		135											
Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys
140					145					150					155
Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Val
				160					165						170
Ser	Glu	Tyr	Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	Ser	Lys
			175					180					185		
Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	Phe	Thr
	190						195					200			
Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	Phe	Ile
	205					210					215				
Gly	Val	Ala	Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	Phe	Ser
220					225					230					235
Tyr	Met	Gln	Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	Phe	Ser
				240					245						250
Leu	Gln	Val	Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	Val	Gln
			255					260					265		
Arg	Arg	Ile	Ser	Ala	His	Gln	Pro	Gly	Ala	Gly	Pro	Glu	Gly	Gln	Glu
	270						275					280			
Glu	Ser	Thr	Pro	Gln	Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	Pro	Glu
	285					290					295				
Asp	Pro	Ser	Gly	Thr	Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Pro	Asp
300					305					310					315
Gln	Gln	Pro	Leu	Ser	Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala	Ser	Asp
				320					325						330
Gly	Ser	Gly	Ser	Trp	Glu	Asp	Ala	Ala	Leu	Leu	Thr	Glu	Ala	Asn	Leu
			335				340						345		
Pro	Ala	Pro	Ala	Pro	Ala	Ser	Ala	Ser	Ala	Pro	Val	Leu	Glu	Thr	Leu
	350					355						360			
Gly	Ser	Ser	Glu	Pro	Ala	Gly	Gly	Ala	Leu	Arg	Gln	Arg	Pro	Thr	Cys
	365					370					375				
Ser	Ser	Ser													
380															

<210> 250
 <211> 111
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 250															
Met	Pro	His	Leu	Met	Glu	Arg	Met	Val	Gly	Ser	Gly	Leu	Leu	Trp	Leu
-25					-20				-15						
Ala	Leu	Val	Ser	Cys	Ile	Leu	Thr	Gln	Ala	Ser	Ala	Val	Gln	Arg	Gly
-10					-5				1				5		
Tyr	Gly	Asn	Pro	Ile	Glu	Ala	Ser	Ser	Tyr	Gly	Leu	Asp	Leu	Asp	Cys
		10					15					20			
Gly	Ala	Pro	Gly	Thr	Pro	Glu	Ala	His	Val	Cys	Phe	Asp	Pro	Cys	Gln
	25					30					35				
Asn	Tyr	Thr	Leu	Leu	Asp	Leu	Gly	Pro	Ile	Thr	Arg	Arg	Gly	Ala	Gln
40						45					50				

Ser	Pro	Gly	Val	Met	Asn	Gly	Thr	Pro	Ser	Thr	Ala	Gly	Phe	Leu	Val
55					60					65					70
Ala	Trp	Pro	Met	Val	Leu	Leu	Thr	Val	Leu	Leu	Ala	Trp	Leu	Phe	
				75					80					85	

<210> 251
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

Met	Asp	Arg	Pro	Gly	Phe	Val	Ala	Ala	Leu	Val	Ala	Gly	Gly	Val	Ala
		-15					-10					-5			
Gly	Val	Ser	Val	Asp	Leu	Ile	Leu	Phe	Pro	Leu	Asp	Thr	Ile	Lys	Thr
1					5					10				15	
Arg	Leu	Gln	Ser	Pro	Gln	Gly	Phe	Asn	Lys	Ala	Gly	Gly	Phe	His	Gly
				20					25					30	
Ile	Tyr	Ala	Gly	Val	Pro	Ser	Ala	Ala	Ile	Gly	Ser	Phe	Pro	Asn	Gly
			35					40					45		
Cys	Leu	Pro	Asp	Ser	Ser	Ser	Ile								
			50				55								

<210> 252
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

Met	Lys	Phe	Thr	Thr	Leu	Leu	Phe	Leu	Ala	Ala	Val	Ala	Gly	Ala	Leu
-15					-10					-5					1
Val	Tyr	Ala	Glu	Asp	Ala	Ser	Ser	Asp	Ser	Thr	Gly	Ala	Asp	Pro	Ala
			5					10					15		
Gln	Glu	Ala	Gly	Thr	Ser	Lys	Pro	Asn	Glu	Glu	Ile	Ser	Gly	Pro	Ala
			20				25					30			
Glu	Pro	Ala	Ser	Pro	Pro	Glu	Thr	Thr	Thr	Thr	Ala	Gln	Glu	Thr	Ser
			35			40					45				
Ala	Ala	Ala	Val	Gln	Gly	Thr	Ala	Lys	Val	Thr	Ser	Ser	Arg	Gln	Glu
50					55				60					65	
Leu	Asn	Pro	Leu	Lys	Ser	Ile	Val	Glu	Lys	Ser	Ile	Leu	Leu	Thr	Glu
				70				75					80		
Gln	Ala	Leu	Ala	Lys	Ala	Gly	Lys	Gly	Met	His	Gly	Gly	Val	Pro	Gly
				85			90					95			
Gly	Lys	Gln	Phe	Ile	Glu	Asn	Gly	Ser	Glu	Phe	Ala	Gln	Lys	Leu	Leu
		100				105						110			
Lys	Lys	Phe	Ser	Leu	Leu	Lys	Pro	Trp	Ala						
						115									

<210> 253
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<220>
 <221> UNSURE
 <222> 45
 <223> Xaa = Glu,Gln

<220>
 <221> UNSURE
 <222> 44
 <223> Xaa = Lys,Asn

<400> 253
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
 -30 -25 -20
 Leu Leu Leu Val Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
 -15 -10 -5 1
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
 5 10 15
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
 20 25 30
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser Xaa Xaa Ala Pro Glu Asn
 35 40 45
 Thr Leu Ala Ala Ile Arg Gln Leu Arg Met Glu Gln Gln Ala Trp Ser
 50 55 60 65
 Trp Thr Leu Ser Leu Leu Leu Thr Gly Phe Leu Ser
 70 75

<210> 254
 <211> 147
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24..-1

<400> 254
 Met Val Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu
 -20 -15 -10
 Gly Leu Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His
 -5 1 5
 Phe Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg
 10 15 20
 Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys
 25 30 35 40

Asp	Ile	Asn	Thr	Phe	Ile	His	Gly	Asn	Lys	Arg	Thr	Ile	Lys	Ala	Ile
				45					50					55	
Cys	Glu	Asn	Lys	Asn	Gly	Asn	Pro	His	Arg	Glu	Asn	Leu	Arg	Ile	Ser
		60						65					70		
Lys	Ser	Ser	Phe	Gln	Val	Thr	Thr	Cys	Lys	Leu	His	Gly	Gly	Ser	Pro
		75					80					85			
Trp	Pro	Pro	Cys	Gln	Tyr	Arg	Ala	Thr	Ala	Gly	Phe	Arg	Asn	Val	Val
	90				95						100				
Val	Ala	Cys	Glu	Asn	Gly	Leu	Pro	Val	His	Leu	Asp	Gln	Ser	Ile	Phe
105					110					115					120
Arg	Arg	Pro													

<210> 255
 <211> 381
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 255															
Met	Ser	Trp	Thr	Val	Pro	Val	Val	Arg	Ala	Ser	Gln	Arg	Val	Ser	Ser
			-30					-25					-20		
Val	Gly	Ala	Asn	Phe	Leu	Cys	Leu	Gly	Met	Ala	Leu	Cys	Pro	Arg	Gln
		-15					-10					-5			
Ala	Thr	Arg	Ile	Pro	Leu	Asn	Gly	Thr	Trp	Leu	Phe	Thr	Pro	Val	Ser
1					5					10					15
Lys	Met	Ala	Thr	Val	Lys	Ser	Glu	Leu	Ile	Glu	Arg	Phe	Thr	Ser	Glu
			20						25					30	
Lys	Pro	Val	His	His	Ser	Lys	Val	Ser	Ile	Ile	Gly	Thr	Gly	Ser	Val
			35					40					45		
Gly	Met	Ala	Cys	Ala	Ile	Ser	Ile	Leu	Leu	Lys	Gly	Leu	Ser	Asp	Glu
		50					55					60			
Leu	Ala	Leu	Val	Asp	Leu	Asp	Glu	Asp	Lys	Leu	Lys	Gly	Glu	Thr	Met
		65				70					75				
Asp	Leu	Gln	His	Gly	Ser	Pro	Phe	Thr	Lys	Met	Pro	Asn	Ile	Val	Cys
80					85					90					95
Ser	Lys	Asp	Tyr	Phe	Val	Thr	Ala	Asn	Ser	Asn	Leu	Val	Ile	Ile	Thr
			100						105					110	
Ala	Gly	Ala	Arg	Gln	Glu	Lys	Gly	Glu	Thr	Arg	Leu	Asn	Leu	Val	Gln
			115					120					125		
Arg	Asn	Val	Ala	Ile	Phe	Lys	Leu	Met	Ile	Ser	Ser	Ile	Val	Gln	Tyr
		130					135					140			
Ser	Pro	His	Cys	Lys	Leu	Ile	Ile	Val	Ser	Asn	Pro	Val	Asp	Ile	Leu
		145				150					155				
Thr	Tyr	Val	Ala	Trp	Lys	Leu	Ser	Ala	Phe	Pro	Lys	Asn	Arg	Ile	Ile
160					165					170					175
Gly	Ser	Gly	Cys	Asn	Leu	Asp	Thr	Ala	Arg	Phe	Arg	Phe	Leu	Ile	Gly
				180					185					190	
Gln	Lys	Leu	Gly	Ile	His	Ser	Glu	Ser	Cys	His	Gly	Trp	Ile	Leu	Gly
			195					200					205		
Glu	His	Gly	Asp	Ser	Ser	Val	Pro	Val	Trp	Ser	Gly	Val	Asn	Ile	Ala
		210					215					220			

Gly	Val	Pro	Leu	Lys	Asp	Leu	Asn	Ser	Asp	Ile	Gly	Thr	Asp	Lys	Asp
225						230					235				
Pro	Glu	Gln	Trp	Lys	Asn	Val	His	Lys	Glu	Val	Thr	Ala	Thr	Ala	Tyr
240					245					250					255
Glu	Ile	Ile	Lys	Met	Lys	Gly	Tyr	Thr	Ser	Trp	Ala	Ile	Gly	Leu	Ser
				260					265					270	
Val	Ala	Asp	Leu	Thr	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Arg	Ile	His
			275					280					285		
Pro	Val	Ser	Thr	Ile	Ile	Lys	Gly	Leu	Tyr	Gly	Ile	Asp	Glu	Glu	Val
		290					295					300			
Phe	Leu	Ser	Ile	Pro	Cys	Ile	Leu	Gly	Glu	Asn	Gly	Ile	Thr	Asn	Leu
305						310					315				
Ile	Lys	Ile	Lys	Leu	Thr	Pro	Glu	Glu	Glu	Ala	His	Leu	Lys	Lys	Ser
320					325					330					335
Ala	Lys	Thr	Leu	Trp	Glu	Ile	Gln	Asn	Lys	Leu	Lys	Leu			
				340					345						

<210> 256
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

Met	Ser	Trp	Thr	Val	Pro	Val	Val	Arg	Ala	Ser	Gln	Arg	Met	Ser	Ser
			-30					-25					-20		
Val	Gly	Ala	Asn	Phe	Leu	Cys	Leu	Gly	Met	Ala	Leu	Cys	Leu	Arg	Gln
	-15					-10					-5				
Ala	Thr	Arg	Ile	Pro	Leu	Asn	Gly	Thr	Trp	Leu	Phe	Thr	Pro	Val	Ser
1				5					10					15	
Lys	Met	Ala	Thr	Val	Lys	Ser	Glu	Leu	Ile	Glu	Arg	Phe	Thr	Ser	Glu
				20				25						30	
Lys	Pro	Val	His	His	Ser	Lys	Val	Ser	Ile	Ile	Gly	Thr	Gly	Ser	Val
			35				40						45		
Gly	Met	Ala	Cys	Ala	Ile	Ser	Ile	Leu	Leu	Lys	Gly	Leu	Ser	Asp	Glu
	50					55						60			
Leu	Ala	Leu	Val	Asp	Leu	Asp	Glu	Asp	Lys	Leu	Lys	Gly	Glu	Thr	Met
	65				70					75					
Asp	Leu	Gln	His	Gly	Ser	Pro	Phe	Thr	Lys	Met	Pro	Ile	Leu	Phe	Val
80					85					90					95
Ala	Lys	Ile	Thr	Leu	Ser	Gln	Gln	Thr	Pro	Thr					
				100					105						

<210> 257
 <211> 265
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 257

```
Met Asn Phe Ile Leu Phe Ile Phe Ile Pro Gly Val Phe Ser Leu Lys
      -10                      -5                      1
Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro
      5                      10                      15
Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr
      20                      25                      30
Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp
      35                      40                      45                      50
Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser
      55                      60                      65
Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn
      70                      75                      80
Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala
      85                      90                      95
Ile Asn Gly Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His
      100                     105                     110
Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro
      115                     120                     125                     130
Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met
      135                     140                     145
Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu
      150                     155                     160
Tyr Lys Leu Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser
      165                     170                     175
Val Asn Pro Glu Leu Ala Thr Met Ser Tyr Phe His Pro Ser Glu Gly
      180                     185                     190
Val Ser Asp Thr Ser Phe Ser Lys Ser Ala Glu Ser Ser Thr Phe Leu
      195                     200                     205                     210
Gly Thr Thr Ser Ser Asp Met Arg Arg Ser Gly Thr Arg Thr Ser Glu
      215                     220                     225
Ser Lys Ile Met Thr Asp Ile Ile Ser Ile Gly Ser Asp Asn Glu Met
      230                     235                     240
His Glu Asn Asp Glu Ser Val Thr Arg
      245                     250
```

<210> 258

<211> 200

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 258

```
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
-20                      -15                      -10                      -5
Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
      1                      5                      10
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
      15                      20                      25
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
```

30		35		40												
Gly	Val	Ile	Phe	Leu	Phe	Thr	Leu	Leu	Lys	Pro	Tyr	Pro	Arg	Phe	Pro	
45					50					55					60	
Phe	Ile	Phe	Leu	Ser	Gly	Tyr	Pro	Phe	Trp	Gly	Ser	Val	Leu	Phe	Ile	
			65						70					75		
Asn	Ser	Gly	Ala	Phe	Leu	Ile	Ala	Val	Lys	Arg	Lys	Thr	Thr	Glu	Thr	
		80						85				90				
Leu	Ile	Ile	Leu	Ser	Arg	Ile	Met	Asn	Phe	Leu	Ser	Ala	Leu	Gly	Ala	
	95						100					105				
Ile	Ala	Gly	Ile	Ile	Leu	Leu	Thr	Phe	Gly	Phe	Ile	Leu	Asp	Gln	Asn	
	110					115					120					
Tyr	Ile	Cys	Gly	Tyr	Ser	His	Gln	Asn	Ser	Gln	Cys	Lys	Ala	Val	Thr	
125					130					135					140	
Val	Leu	Phe	Leu	Gly	Ile	Leu	Ile	Thr	Leu	Met	Thr	Phe	Ser	Ile	Ile	
			145						150					155		
Glu	Leu	Phe	Ile	Ser	Leu	Pro	Phe	Ser	Ile	Leu	Gly	Cys	His	Ser	Glu	
			160					165					170			
Asp	Cys	Asp	Cys	Glu	Gln	Cys	Cys									
	175						180									

<210> 259
 <211> 394
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 259																
Met	Ala	Thr	Ala	Gln	Leu	Gln	Arg	Thr	Pro	Met	Ser	Ala	Leu	Val	Phe	
			-35					-30						-25		
Pro	Asn	Lys	Ile	Ser	Thr	Glu	His	Gln	Ser	Leu	Val	Leu	Val	Lys	Arg	
		-20					-15					-10				
Leu	Leu	Ala	Val	Ser	Val	Ser	Cys	Ile	Thr	Tyr	Leu	Arg	Gly	Ile	Phe	
	-5					1			5							
Pro	Glu	Cys	Ala	Tyr	Gly	Thr	Arg	Tyr	Leu	Asp	Asp	Leu	Cys	Val	Lys	
10			15					20						25		
Ile	Leu	Arg	Glu	Asp	Lys	Asn	Cys	Pro	Gly	Ser	Thr	Gln	Leu	Val	Lys	
			30					35					40			
Trp	Ile	Leu	Gly	Cys	Tyr	Asp	Ala	Leu	Gln	Lys	Lys	Tyr	Leu	Arg	Met	
		45					50						55			
Val	Val	Leu	Ala	Val	Tyr	Thr	Asn	Pro	Glu	Asp	Pro	Gln	Thr	Ile	Ser	
	60						65				70					
Glu	Cys	Tyr	Gln	Phe	Lys	Phe	Lys	Tyr	Thr	Asn	Asn	Gly	Pro	Leu	Met	
	75				80					85						
Asp	Phe	Ile	Ser	Lys	Asn	Gln	Ser	Asn	Glu	Ser	Ser	Met	Leu	Ser	Thr	
90					95				100					105		
Asp	Thr	Lys	Lys	Ala	Ser	Ile	Leu	Leu	Ile	Arg	Lys	Ile	Tyr	Ile	Leu	
			110					115					120			
Met	Gln	Asn	Leu	Gly	Pro	Leu	Pro	Asn	Asp	Val	Cys	Leu	Thr	Met	Lys	
		125					130					135				
Leu	Phe	Tyr	Tyr	Asp	Glu	Val	Thr	Pro	Pro	Asp	Tyr	Gln	Pro	Pro	Gly	
	140						145					150				

Phe	Lys	Asp	Gly	Asp	Cys	Glu	Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro	Met
155						160					165				
Tyr	Leu	Asn	Val	Gly	Glu	Val	Ser	Thr	Pro	Phe	His	Ile	Phe	Lys	Val
170					175					180					185
Lys	Val	Thr	Thr	Glu	Arg	Glu	Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr	Ile
				190					195					200	
Leu	Ser	Pro	Lys	Gln	Ile	Lys	Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg	Asp
			205					210						215	
Lys	Asp	Val	Glu	Asp	Glu	Gln	Glu	His	Tyr	Thr	Ser	Asp	Asp	Leu	Asp
		220					225					230			
Ile	Glu	Thr	Lys	Met	Glu	Glu	Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser	Glu
235					240						245				
Leu	Glu	Glu	Pro	Ser	Leu	Val	Cys	Glu	Glu	Asp	Glu	Ile	Met	Arg	Ser
250					255					260					265
Lys	Glu	Ser	Pro	Asp	Leu	Ser	Ile	Ser	His	Ser	Gln	Val	Glu	Gln	Leu
				270					275					280	
Val	Asn	Lys	Thr	Ser	Glu	Leu	Asp	Met	Ser	Glu	Ser	Lys	Thr	Arg	Ser
			285					290					295		
Gly	Lys	Val	Phe	Gln	Asn	Lys	Met	Ala	Asn	Gly	Asn	Gln	Pro	Val	Lys
		300					305					310			
Ser	Ser	Lys	Glu	Asn	Arg	Lys	Arg	Ser	Gln	His	Glu	Ser	Gly	Arg	Ile
		315				320					325				
Val	Leu	His	His	Phe	Asp	Ser	Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys	Arg
330					335					340					345
Arg	Lys	Phe	Ser	Glu	Pro	Lys	Glu	His	Ile						
				350					355						

<210> 260
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 260															
Met	Ala	Leu	Glu	Val	Leu	Met	Leu	Leu	Ala	Val	Leu	Ile	Trp	Thr	Gly
	-15					-10						-5			
Ala	Glu	Asn	Leu	His	Val	Lys	Ile	Ser	Cys	Ser	Leu	Asp	Trp	Leu	Met
1				5					10					15	
Val	Ser	Val	Ile	Pro	Val	Ala	Glu	Ser	Arg	Asn	Leu	Tyr	Ile	Phe	Ala
				20					25					30	
Asp	Glu	Leu	His	Leu	Gly	Met	Gly	Cys	Pro	Ala	Asn	Arg	Ile	His	Thr
			35				40					45			
Tyr	Val	Tyr	Glu	Phe	Ile	Tyr	Leu	Val	Arg	Asp	Cys	Gly	Ile	Arg	Thr
	50					55					60				
Arg	Val	Val	Ser	Glu	Glu	Thr	Leu	Leu	Phe	Gln	Thr	Glu	Leu	Tyr	Phe
	65					70					75				
Thr	Pro	Arg	Asn	Ile	Asp	His	Asp	Pro	Gln	Glu	Ile	His	Leu	Glu	Cys
80					85					90				95	
Ser	Thr	Ser	Arg	Lys	Ser	Val	Trp	Leu	Thr	Pro	Val	Ser	Thr	Glu	Asn
				100					105					110	
Glu	Ile	Lys	Leu	Asp	Pro	Ser	Pro	Phe	Ile	Ala	Asp	Phe	Gln	Thr	Thr

	115		120		125
Ala	Glu	Glu	Leu	Gly	Leu
	130		135		140

<210> 261
 <211> 233
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 261

Met	Ala	Thr	Pro	Pro	Phe	Arg	Leu	Ile	Arg	Lys	Met	Phe	Ser	Phe	Lys
		-30					-25					-20			
Val	Ser	Arg	Trp	Met	Gly	Leu	Ala	Cys	Phe	Arg	Ser	Leu	Ala	Ala	Ser
		-15				-10					-5				
Ser	Pro	Ser	Ile	Arg	Gln	Lys	Lys	Leu	Met	His	Lys	Leu	Gln	Glu	Glu
1			5					10					15		
Lys	Ala	Phe	Arg	Glu	Glu	Met	Lys	Ile	Phe	Arg	Glu	Lys	Ile	Glu	Asp
		20					25					30			
Phe	Arg	Glu	Met	Trp	Thr	Phe	Arg	Gly	Lys	Ile	His	Ala	Phe	Arg	
	35				40					45					
Gly	Gln	Ile	Leu	Gly	Phe	Trp	Glu	Glu	Glu	Arg	Pro	Phe	Trp	Glu	Glu
	50				55					60					
Glu	Lys	Thr	Phe	Trp	Lys	Glu	Glu	Lys	Ser	Phe	Trp	Glu	Met	Glu	Lys
65				70					75					80	
Ser	Phe	Arg	Glu	Glu	Glu	Lys	Thr	Phe	Trp	Lys	Lys	Tyr	Arg	Thr	Phe
			85				90					95			
Trp	Lys	Glu	Asp	Lys	Ala	Phe	Trp	Lys	Glu	Asp	Asn	Ala	Leu	Trp	Glu
		100					105					110			
Arg	Asp	Arg	Asn	Leu	Leu	Gln	Glu	Asp	Lys	Ala	Leu	Trp	Glu	Glu	Glu
		115				120						125			
Lys	Ala	Leu	Trp	Val	Glu	Glu	Arg	Ala	Leu	Leu	Glu	Gly	Glu	Lys	Ala
	130				135						140				
Leu	Trp	Glu	Asp	Lys	Thr	Ser	Leu	Trp	Glu	Glu	Asn	Ala	Leu	Trp	
145				150					155					160	
Glu	Glu	Glu	Arg	Ala	Phe	Trp	Met	Glu	Asn	Asn	Gly	His	Ile	Ala	Gly
			165					170					175		
Glu	Gln	Met	Leu	Glu	Asp	Gly	Pro	His	Asn	Ala	Asn	Arg	Gly	Gln	Arg
		180				185							190		
Leu	Leu	Ala	Phe	Ser	Arg	Gly	Arg	Ala							
	195					200									

<210> 262
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 262
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
-20 -15 -10 -5
Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
1 5 10
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
15 20 25
Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys Ser Leu Ile Leu
30 35 40
Glu Pro Ser
45

<210> 263
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 263
Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu Ser
-25 -20 -15 -10
His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys Pro
-5 1 5
Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu Arg
10 15 20
Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val Ser
25 30 35
Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu Pro
40 45 50 55
Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
60 65

<210> 264
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 264
Met Phe Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys
-15 -10 -5
Val Ser Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg
1 5 10
Arg Leu Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln
15 20 25
Leu Leu Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn
30 35 40 45
Ala Ser Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys

15					20				25					30	
Thr	Gly	His	Gly	Val	Ala	Pro	Gly	Thr	Gly	Pro	Val	Ile	Asn	Lys	Gly
				35					40					45	
Cys	Leu	Arg	Ala	Thr	Ser	Cys	Gly	Leu	Glu	Glu	Pro	Val	Ser	Tyr	Arg
			50					55					60		
Gly	Val	Thr	Tyr	Ser	Leu	Thr	Thr	Asn	Cys	Cys	Thr	Gly	Arg	Leu	Cys
		65					70					75			
Asn	Arg	Ala	Pro	Ser	Ser	Gln	Thr	Val	Gly	Ala	Thr	Thr	Ser	Leu	Ala
	80					85					90				
Leu	Gly	Leu	Gly	Met	Leu	Leu	Pro	Pro	Arg	Leu	Leu				
95					100					105					

<210> 267
 <211> 261
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 267

Met	Glu	Asn	Phe	Ser	Leu	Leu	Ser	Ile	Ser	Gly	Pro	Pro	Ile	Ser	Ser
	-15					-10					-5				
Ser	Ala	Leu	Ser	Ala	Phe	Pro	Asp	Ile	Met	Phe	Ser	Arg	Ala	Thr	Ser
1				5				10						15	
Leu	Pro	Asp	Ile	Ala	Lys	Thr	Ala	Val	Pro	Thr	Glu	Ala	Ser	Ser	Pro
			20					25					30		
Ala	Gln	Ala	Leu	Pro	Pro	Gln	Tyr	Gln	Ser	Ile	Ile	Val	Arg	Gln	Gly
	35					40						45			
Ile	Gln	Asn	Thr	Val	Leu	Ser	Pro	Asp	Cys	Ser	Leu	Gly	Asp	Thr	Gln
	50					55					60				
His	Gly	Glu	Lys	Leu	Arg	Arg	Asn	Cys	Thr	Ile	Tyr	Arg	Pro	Trp	Phe
65					70					75				80	
Ser	Pro	Tyr	Ser	Tyr	Phe	Val	Cys	Ala	Asp	Lys	Glu	Ser	Gln	Leu	Glu
			85					90						95	
Ala	Tyr	Asp	Phe	Pro	Glu	Val	Gln	Gln	Asp	Glu	Gly	Lys	Trp	Asp	Asn
			100					105					110		
Cys	Leu	Ser	Glu	Asp	Met	Ala	Glu	Asn	Ile	Cys	Ser	Ser	Ser	Ser	Ser
		115					120					125			
Pro	Glu	Asn	Thr	Cys	Pro	Arg	Glu	Ala	Thr	Lys	Lys	Ser	Arg	His	Gly
	130					135						140			
Leu	Asp	Ser	Ile	Thr	Ser	Gln	Asp	Ile	Leu	Met	Ala	Ser	Arg	Trp	His
145					150					155				160	
Pro	Ala	Gln	Gln	Asn	Gly	Tyr	Lys	Cys	Val	Ala	Cys	Cys	Arg	Met	Tyr
			165					170						175	
Pro	Thr	Leu	Asp	Phe	Leu	Lys	Ser	His	Ile	Lys	Arg	Gly	Phe	Arg	Glu
			180					185					190		
Gly	Phe	Ser	Cys	Lys	Val	Tyr	Tyr	Arg	Lys	Leu	Lys	Ala	Leu	Trp	Ser
		195					200					205			
Lys	Glu	Gln	Lys	Ala	Arg	Leu	Gly	Asp	Arg	Leu	Ser	Ser	Gly	Ser	Cys
	210					215					220				
Gln	Ala	Phe	Asn	Ser	Pro	Ala	Glu	His	Leu	Arg	Gln	Ile	Gly	Gly	Glu
225					230					235					240

Ala Tyr Leu Cys Leu
245

<210> 268 .
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 268
Met Cys Met Ser Leu Ser Met Lys Val Pro Cys Cys Leu Cys Ala Leu
-25 -20 -15 -10
Leu Ser Asn Phe Cys Pro Ser Thr Thr Val Lys Gly Asp Val Val Thr
-5 1 5
Ser Phe Phe Arg Ala Asp Tyr Asp Leu Ala Ser Arg Ser Ala Asp Gln
10 15 20
Ser Ser Gln Lys Val Lys Leu Arg Met Phe Thr Gly Arg Leu Pro Ile
25 30 35
Gly Pro Phe Ala Ser Val Gly Asn Ala Ala Glu Leu
40 45 50

<210> 269
<211> 199
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 269
Met Glu Thr Phe Pro Leu Leu Leu Ser Leu Gly Leu Val Leu Ala
-15 -10 -5
Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe Thr Asp
1 5 10 15
Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys Gln Thr
20 25 30
Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr Ser Leu
35 40 45
Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe Arg Ser
50 55 60
Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp Lys Glu
65 70 75 80
Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala Asn Gly
85 90 95
Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu Val Met
100 105 110
Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn Pro Gly
115 120 125
Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys Gln Phe
130 135 140

Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val Thr Ser
 145 150 155 160
 Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met Ser Trp
 165 170 175
 Leu Val Cys Gly Ser Lys Leu
 180

<210> 270
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 270
 Met Ala Ser Val Val Pro Val Lys Asp Lys Lys Leu Leu Glu Val Lys
 -35 -30 -25
 Leu Gly Glu Leu Pro Ser Trp Ile Leu Met Arg Asp Phe Ser Pro Ser
 -20 -15 -10 -5
 Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr Tyr Arg Tyr Tyr Asn Lys
 1 5 10
 Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser Gly Ile Thr Met Val Leu
 15 20 25
 Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe Ser Tyr Lys His Leu Lys
 30 35 40
 His Glu Arg Leu Arg Lys Tyr His
 45 50

<210> 271
 <211> 481
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 271
 Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu Ala Leu Leu
 -25 -20 -15 -10
 Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly Leu Val Ala
 -5 1 5
 Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu Gly Leu Leu
 10 15 20
 Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp Phe Thr Gly
 25 30 35
 Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu Phe His Ser
 40 45 50 55
 Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu Arg Pro Val
 60 65 70
 Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser Ile Arg Val
 75 80 85

<221> SIGNAL
 <222> -43...-1

<400> 272
 Met Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp
 -40 -35 -30
 Ser Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val
 -25 -20 -15
 Ser Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val
 -10 -5 1 5
 His Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg
 10 15 20
 Glu Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Ala Thr Arg Gln Gln
 25 30 35
 Phe Tyr Thr Asp Met Tyr Cys Pro Ile Cys Leu His Gln Ala Ser Phe
 40 45 50
 Pro Val Glu Thr Asn Cys Gly His Leu Phe Cys Gly Ala Cys Ile Ile
 55 60 65
 Ala Tyr Trp Arg Tyr Gly Ser Trp Leu Gly Ala Ile Ser Cys Pro Ile
 70 75 80 85
 Cys Arg Gln Thr Arg His Gly His Ile Ala Leu Ser Arg Thr Ala
 90 95 100

<210> 273
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 273
 Met Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp
 1 5 10 15
 Ser Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val
 20 25 30
 Ser Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val
 35 40 45
 His Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg
 50 55 60
 Glu Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Asp Ser Thr Ala Val
 65 70 75 80
 Leu His

<210> 274
 <211> 373
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 274
 Met Ala Thr Gln Ala His Ser Leu Ser Tyr Ala Gly Cys Asn Phe Leu
 -25 -20 -15
 Cys Gln Arg Leu Val Leu Ser Thr Leu Ser Gly Arg Pro Val Lys Ile

-10					-5					1				5
Arg	Lys	Ile	Arg	Ala	Arg	Asp	Asp	Asn	Pro	Gly	Leu	Arg	Asp	Phe
				10					15					20
Ala	Ser	Phe	Ile	Arg	Leu	Leu	Asp	Lys	Ile	Thr	Asn	Gly	Ser	Arg
			25					30					35	
Glu	Ile	Asn	Gln	Thr	Gly	Thr	Thr	Leu	Tyr	Tyr	Gln	Pro	Gly	Leu
		40					45				50			Leu
Tyr	Gly	Gly	Ser	Val	Glu	His	Asp	Cys	Ser	Val	Leu	Arg	Gly	Ile
	55				60						65			Gly
Tyr	Tyr	Leu	Glu	Ser	Leu	Leu	Cys	Leu	Ala	Pro	Phe	Met	Lys	His
70					75					80				85
Leu	Lys	Ile	Val	Leu	Arg	Gly	Val	Thr	Asn	Asp	Gln	Ile	Asp	Pro
			90						95					100
Val	Asp	Val	Leu	Lys	Ala	Thr	Ala	Leu	Pro	Leu	Leu	Lys	Gln	Phe
			105					110					115	Gly
Ile	Asp	Gly	Glu	Ser	Phe	Glu	Leu	Lys	Ile	Val	Arg	Arg	Gly	Met
	120					125					130			Pro
Pro	Gly	Gly	Gly	Gly	Glu	Val	Val	Phe	Ser	Cys	Pro	Val	Arg	Lys
	135				140						145			Val
Leu	Lys	Pro	Ile	Gln	Leu	Thr	Asp	Pro	Gly	Lys	Ile	Lys	Arg	Ile
150				155					160					165
Gly	Met	Ala	Tyr	Ser	Val	Arg	Val	Ser	Pro	Gln	Met	Ala	Asn	Arg
			170						175					180
Val	Asp	Ser	Ala	Arg	Ser	Ile	Leu	Asn	Lys	Phe	Ile	Pro	Asp	Ile
		185						190				195		Tyr
Ile	Tyr	Thr	Asp	His	Ile	Lys	Gly	Val	Asn	Ser	Gly	Lys	Ser	Pro
	200					205					210			Gly
Phe	Gly	Leu	Ser	Leu	Val	Ala	Glu	Thr	Thr	Ser	Gly	Thr	Phe	Leu
	215				220						225			Ser
Ala	Glu	Leu	Ala	Ser	Asn	Pro	Gln	Gly	Gln	Gly	Ala	Ala	Val	Leu
230				235					240					245
Glu	Asp	Leu	Gly	Arg	Asn	Cys	Ala	Arg	Leu	Leu	Leu	Glu	Glu	Ile
			250					255						260
Arg	Gly	Gly	Cys	Val	Asp	Ser	Thr	Asn	Gln	Ser	Leu	Ala	Leu	Leu
		265					270				275			Leu
Met	Thr	Leu	Gly	Gln	Gln	Asp	Val	Ser	Lys	Val	Leu	Leu	Gly	Pro
	280					285					290			Leu
Ser	Pro	Tyr	Thr	Ile	Glu	Phe	Leu	Arg	His	Leu	Lys	Ser	Phe	Phe
	295			300						305				Gln
Ile	Met	Phe	Lys	Ile	Glu	Thr	Lys	Pro	Cys	Gly	Glu	Glu	Leu	Lys
310				315						320				325
Gly	Asp	Lys	Val	Leu	Met	Thr	Cys	Val	Gly	Ile	Gly	Phe	Ser	Asn
			330					335						340
Ser	Arg	Thr	Leu	Lys										
			345											

<210> 275
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 275

```
Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
-25                -20                -15                -10
Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
                -5                1                5
Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
    10                15                20
Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
    25                30                35
Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
40                45                50                55
Val Ser Cys Ser Val Ala Ala Pro Leu Phe Pro Phe Leu Gly
                60                65
```

<210> 276

<211> 197

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -20...-1

<400> 276

```
Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
-20                -15                -10                -5
Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
                1                5                10
Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
    15                20                25
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
    30                35                40
Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
45                50                55                60
Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
                65                70                75
Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala
    80                85                90
Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys
    95                100                105
Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr
    110                115                120
Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp
125                130                135                140
Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn
                145                150                155
Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser
                160                165                170
Leu Phe Ser Pro Ala
    175
```

<210> 277

<211> 344

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 277

Met	Asp	Phe	Leu	Val	Leu	Phe	Leu	Phe	Tyr	Leu	Ala	Ser	Val	Leu	Met
			-25						-20					-15	
Gly	Leu	Val	Leu	Ile	Cys	Val	Cys	Ser	Lys	Thr	His	Ser	Leu	Lys	Gly
		-10						-5					1		
Leu	Ala	Arg	Gly	Gly	Ala	Gln	Ile	Phe	Ser	Cys	Ile	Ile	Pro	Glu	Cys
5					10					15					
Leu	Gln	Arg	Ala	Val	His	Gly	Leu	Leu	His	Tyr	Leu	Phe	His	Thr	Arg
20				25						30				35	
Asn	His	Thr	Phe	Ile	Val	Leu	His	Leu	Val	Leu	Gln	Gly	Met	Val	Tyr
			40					45						50	
Thr	Glu	Tyr	Thr	Trp	Glu	Val	Phe	Gly	Tyr	Cys	Gln	Glu	Leu	Glu	Leu
		55						60					65		
Ser	Leu	His	Tyr	Leu	Leu	Leu	Pro	Tyr	Leu	Leu	Leu	Gly	Val	Asn	Leu
	70						75					80			
Phe	Phe	Phe	Thr	Leu	Thr	Cys	Gly	Thr	Asn	Pro	Gly	Ile	Ile	Thr	Lys
85					90						95				
Ala	Asn	Glu	Leu	Leu	Phe	Leu	His	Val	Tyr	Glu	Phe	Asp	Glu	Val	Met
100					105					110					115
Phe	Pro	Lys	Asn	Val	Arg	Cys	Ser	Thr	Cys	Asp	Leu	Arg	Lys	Pro	Ala
			120						125					130	
Arg	Ser	Lys	His	Cys	Ser	Val	Cys	Asn	Trp	Cys	Val	His	Arg	Phe	Asp
			135					140					145		
His	His	Cys	Val	Trp	Val	Asn	Asn	Cys	Ile	Gly	Ala	Trp	Asn	Ile	Arg
		150					155						160		
Tyr	Phe	Leu	Ile	Tyr	Val	Leu	Thr	Leu	Thr	Ala	Ser	Ala	Ala	Thr	Val
	165					170					175				
Ala	Ile	Val	Ser	Thr	Thr	Phe	Leu	Val	His	Leu	Val	Val	Met	Ser	Asp
180					185					190					195
Leu	Tyr	Gln	Glu	Thr	Tyr	Ile	Asp	Asp	Leu	Gly	His	Leu	His	Val	Met
			200					205						210	
Asp	Thr	Val	Phe	Leu	Ile	Gln	Tyr	Leu	Phe	Leu	Thr	Phe	Pro	Arg	Ile
			215					220					225		
Val	Phe	Met	Leu	Gly	Phe	Val	Val	Val	Leu	Ser	Phe	Leu	Leu	Gly	Gly
	230						235					240			
Tyr	Leu	Leu	Phe	Val	Leu	Tyr	Leu	Ala	Ala	Thr	Asn	Gln	Thr	Thr	Asn
	245					250					255				
Glu	Trp	Tyr	Arg	Gly	Asp	Trp	Ala	Trp	Cys	Gln	Arg	Cys	Pro	Leu	Val
260					265					270					275
Ala	Trp	Pro	Pro	Ser	Ala	Glu	Pro	Gln	Val	His	Arg	Asn	Ile	His	Ser
				280					285					290	
His	Gly	Leu	Arg	Ser	Asn	Leu	Gln	Glu	Ile	Phe	Leu	Pro	Ala	Phe	Pro
		295						300					305		
Cys	His	Glu	Arg	Lys	Lys	Gln	Glu								
		310					315								

<210> 278

<211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 278

Met	Gly	Ser	Gln	Glu	Val	Leu	Gly	His	Ala	Ala	Arg	Leu	Ser	Ser	Ser
			-25					-20					-15		
Gly	Leu	Leu	Leu	Gln	Val	Leu	Phe	Arg	Leu	Ile	Thr	Phe	Val	Leu	Asn
		-10					-5					1			
Ala	Phe	Ile	Leu	Arg	Phe	Leu	Ser	Lys	Glu	Ile	Val	Gly	Val	Val	Asn
5					10					15					20
Val	Arg	Leu	Thr	Leu	Leu	Tyr	Ser	Thr	Thr	Leu	Phe	Leu	Ala	Arg	Glu
				25					30					35	
Ala	Phe	Arg	Arg	Ala	Cys	Leu	Ser	Gly	Gly	Thr	Gln	Arg	Asp	Trp	Ser
			40					45					50		
Gln	Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp
		55					60					65			
Ser	Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp
	70				75						80				
Pro	Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu
85					90					95					100
Ser	Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln
				105					110					115	
Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val
			120					125					130		
Ile	Leu	Lys	Thr	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His
		135					140					145			
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val
	150					155					160				
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro
165					170					175					180
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu
			185						190					195	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala
		200						205					210		
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu
	215						220					225			
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
	230					235					240				
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val
245					250					255					260
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe
				265					270					275	
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu
			280					285					290		
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala
	295						300					305			
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln
	310					315					320				
Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly

325					330					335					340
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile
				345					350					355	
Asn	Gly	Val	Thr	Glu	Cys	Phe	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu
			360					365					370		
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu
	375						380					385			
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile
	390					395					400				
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys
405					410					415					420
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly
			425					430						435	
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly
		440					445					450			
Val	Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Glu	Gln	Gly	Trp	Pro
	455					460						465			
Ala	Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr
	470				475					480					
Leu	Gly	Thr	Ala	Phe	Leu	Thr	Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg
485					490				495						500
Thr	Gln	Leu	Gly	Val	Pro	Arg	Arg	Thr	Asp	Lys	Met	Thr			
				505				510							

<210> 279

<211> 267

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 279

Met	Ala	Arg	Phe	Leu	Thr	Leu	Cys	Thr	Trp	Leu	Leu	Leu	Leu	Gly	Pro
				-20	.			-15						-10	
Gly	Leu	Leu	Ala	Thr	Val	Arg	Ala	Glu	Cys	Ser	Gln	Asp	Cys	Ala	Thr
		-5					1				5				
Cys	Ser	Tyr	Arg	Leu	Val	Arg	Pro	Ala	Asp	Ile	Asn	Phe	Leu	Ala	Cys
	10					15					20				
Val	Met	Glu	Cys	Glu	Gly	Lys	Leu	Pro	Ser	Leu	Lys	Ile	Trp	Glu	Thr
25					30					35					40
Cys	Lys	Glu	Leu	Leu	Gln	Leu	Ser	Lys	Pro	Asp	Leu	Pro	Gln	Asp	Gly
			45					50						55	
Thr	Ser	Thr	Leu	Arg	Glu	Asn	Ser	Lys	Pro	Glu	Glu	Ser	His	Leu	Leu
		60						65					70		
Ala	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys
	75					80					85				
Lys	Met	Asp	Glu	Leu	Tyr	Pro	Met	Glu	Pro	Glu	Glu	Glu	Ala	Asn	Gly
	90					95				100					
Ser	Glu	Ile	Leu	Ala	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys	Lys	Asp	Ala
105					110					115					120
Glu	Glu	Asp	Asp	Ser	Leu	Ala	Asn	Ser	Ser	Asp	Leu	Leu	Lys	Glu	Leu
				125				130						135	

Leu	Glu	Thr	Gly	Asp	Asn	Arg	Glu	Arg	Ser	His	His	Gln	Asp	Gly	Ser
			140					145					150		
Asp	Asn	Glu	Glu	Glu	Val	Ser	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Arg	Gly
		155					160					165			
Leu	Lys	Arg	Ser	Pro	Gln	Leu	Glu	Asp	Glu	Ala	Lys	Glu	Leu	Gln	Lys
	170					175					180				
Arg	Tyr	Gly	Gly	Phe	Met	Arg	Arg	Val	Gly	Arg	Pro	Glu	Trp	Trp	Met
185					190					195					200
Asp	Tyr	Gln	Lys	Arg	Tyr	Gly	Gly	Phe	Leu	Lys	Arg	Phe	Ala	Glu	Ala
			205					210						215	
Leu	Pro	Ser	Asp	Glu	Glu	Gly	Glu	Ser	Tyr	Ser	Lys	Glu	Val	Pro	Glu
			220				225						230		
Met	Glu	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Arg	Phe					
		235					240								

<210> 280
 <211> 362
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40..-1

<400> 280

Met	Pro	Phe	Ala	Tyr	Phe	Phe	Thr	Glu	Ser	Glu	Gly	Phe	Ala	Gly	Ser
-40					-35					-30					-25
Arg	Lys	Gly	Val	Leu	Gly	Arg	Val	Tyr	Glu	Thr	Val	Val	Met	Leu	Met
			-20					-15						-10	
Leu	Leu	Thr	Leu	Leu	Val	Leu	Gly	Met	Val	Trp	Val	Ala	Ser	Ala	Ile
		-5					1				5				
Val	Asp	Lys	Asn	Lys	Ala	Asn	Arg	Glu	Ser	Leu	Tyr	Asp	Phe	Trp	Glu
10					15					20					
Tyr	Tyr	Leu	Pro	Tyr	Leu	Tyr	Ser	Cys	Ile	Ser	Phe	Leu	Gly	Val	Leu
25				30				35						40	
Leu	Leu	Leu	Val	Cys	Thr	Pro	Leu	Gly	Leu	Ala	Arg	Met	Phe	Ser	Val
			45					50					55		
Thr	Gly	Lys	Leu	Leu	Val	Lys	Pro	Arg	Leu	Leu	Glu	Asp	Leu	Glu	Glu
		60					65					70			
Gln	Leu	Tyr	Cys	Ser	Ala	Phe	Glu	Glu	Ala	Ala	Leu	Thr	Arg	Arg	Ile
	75					80					85				
Cys	Asn	Pro	Thr	Ser	Cys	Trp	Leu	Pro	Leu	Asp	Met	Glu	Leu	Leu	His
	90				95					100					
Arg	Gln	Val	Leu	Ala	Leu	Gln	Thr	Gln	Arg	Val	Leu	Leu	Glu	Lys	Arg
105				110					115					120	
Arg	Lys	Ala	Ser	Ala	Trp	Gln	Arg	Asn	Leu	Gly	Tyr	Pro	Leu	Ala	Met
			125				130						135		
Leu	Cys	Leu	Leu	Val	Leu	Thr	Gly	Leu	Ser	Val	Leu	Ile	Val	Ala	Ile
		140				145					150				
His	Ile	Leu	Glu	Leu	Leu	Ile	Asp	Glu	Ala	Ala	Met	Pro	Arg	Gly	Met
	155				160						165				
Gln	Gly	Thr	Ser	Leu	Gly	Gln	Val	Ser	Phe	Ser	Lys	Leu	Gly	Ser	Phe
170					175					180					
Gly	Ala	Val	Ile	Gln	Val	Val	Leu	Ile	Phe	Tyr	Leu	Met	Val	Ser	Ser

185					190				195				200
Val	Val	Gly	Phe	Tyr	Ser	Ser	Pro	Leu	Phe	Arg	Ser	Leu	Arg
				205					210				215
Trp	His	Asp	Thr	Ala	Met	Thr	Gln	Ile	Ile	Gly	Asn	Cys	Val
			220				225					230	
Leu	Val	Leu	Ser	Ser	Ala	Leu	Pro	Val	Phe	Ser	Arg	Thr	Leu
		235					240					245	
Thr	Arg	Phe	Asp	Leu	Leu	Gly	Asp	Phe	Gly	Arg	Phe	Asn	Trp
	250					255					260		
Asn	Phe	Tyr	Ile	Val	Phe	Leu	Tyr	Asn	Ala	Ala	Phe	Ala	Gly
265						270				275			280
Thr	Leu	Tyr	Leu	Val	Lys	Thr	Phe	Thr	Ala	Ala	Val	Arg	Ala
				285					290				295
Ile	Arg	Ala	Phe	Gly	Leu	Asp	Arg	Leu	Pro	Leu	Pro	Val	Ser
			300					305					310
Pro	Gln	Ala	Ser	Arg	Lys	Thr	Gln	His	Gln				
			315				320						

<210> 281
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 281
Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr
-20 -15 -10
Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp Gln Gln
-5 1 5 10
Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln Ile Arg Lys
15 20 25
Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile Leu Thr Glu Gln
30 35 40
Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala Lys Gly Ser Gln Lys
45 50 55
Ser
60

<210> 282
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 282
Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser
-25 -20 -15
Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn

		-10					-5					1				
Ala 5	Phe	Ile	Leu	Arg	Phe 10	Leu	Ser	Lys	Glu	Ile 15	Val	Gly	Val	Val	Asn 20	
Val	Arg	Leu	Thr	Leu 25	Leu	Tyr	Ser	Thr	Thr 30	Leu	Phe	Leu	Ala	Arg	Glu 35	
Ala	Phe	Arg	Arg	Ala 40	Cys	Leu	Ser	Gly	Gly 45	Thr	Gln	Arg	Asp	Trp	Ser 50	
Gln	Thr	Leu	Asn	Leu 55	Leu	Trp	Leu	Thr	Val 60	Pro	Leu	Gly	Val	Phe	Trp 65	
Ser	Leu	Phe	Leu	Gly 70	Trp	Ile	Trp	Leu	Gln 75	Leu	Leu	Glu	Val	Pro	Asp 80	
Pro 85	Asn	Val	Val	Pro 90	His	Tyr	Ala	Thr	Gly 95	Val	Val	Leu	Phe	Gly	Leu 100	
Ser	Ala	Val	Val	Glu 105	Leu	Leu	Gly	Glu	Pro 110	Phe	Trp	Val	Leu	Ala	Gln 115	
Ala	His	Met	Phe	Val 120	Lys	Leu	Lys	Val	Ile 125	Ala	Glu	Ser	Leu	Ser	Val 130	
Ile	Leu	Lys	Ser	Val 135	Leu	Thr	Ala	Phe	Leu 140	Val	Leu	Trp	Leu	Pro	His 145	
Trp	Gly	Leu	Tyr	Ile 150	Phe	Ser	Leu	Ala	Gln 155	Leu	Phe	Tyr	Thr	Thr	Val 160	
Leu 165	Val	Leu	Cys	Tyr 170	Val	Ile	Tyr	Phe	Thr 175	Lys	Leu	Leu	Gly	Ser	Pro 180	
Glu	Ser	Thr	Lys	Leu 185	Gln	Thr	Leu	Pro	Val 190	Ser	Arg	Ile	Thr	Asp	Leu 195	
Leu	Pro	Asn	Ile	Thr 200	Arg	Asn	Gly	Ala	Phe 205	Ile	Asn	Trp	Lys	Glu	Ala 210	
Lys	Leu	Thr	Trp	Ser 215	Phe	Phe	Lys	Gln	Ser 220	Phe	Leu	Lys	Gln	Ile	Leu 225	
Thr	Glu	Gly	Glu	Arg 230	Tyr	Val	Met	Thr	Phe 235	Leu	Asn	Val	Leu	Asn	Phe 240	
Gly 245	Asp	Gln	Gly	Val 250	Tyr	Asp	Ile	Val	Asn 255	Asn	Leu	Gly	Ser	Leu	Val 260	
Ala	Arg	Leu	Ile	Phe 265	Gln	Pro	Ile	Glu	Glu 270	Ser	Phe	Tyr	Ile	Phe	Phe 275	
Ala	Lys	Val	Leu	Glu 280	Arg	Gly	Lys	Asp	Ala 285	Thr	Leu	Gln	Lys	Gln	Glu 290	
Asp	Val	Ala	Val	Ala 295	Ala	Ala	Ala	Val	Leu 300	Glu	Ser	Leu	Leu	Lys	Leu 305	
Leu	Leu	Ala	Gly	Leu 310	Thr	Ile	Thr	Val	Phe 315	Gly	Phe	Ala	Tyr	Ser	Gln 320	
Leu 325	Ala	Leu	Asp	Ile 330	Asn	Gly	Gly	Thr	Met 335	Leu	Ser	Ser	Gly	Ser	Gly 340	
Pro	Val	Leu	Leu	Arg 345	Ser	Tyr	Cys	Leu	Tyr 350	Val	Leu	Leu	Leu	Ala	Ile 355	
Asn	Gly	Val	Thr	Glu 360	Cys	Phe	Thr	Phe	Ala 365	Ala	Ala	Met	Ser	Lys	Glu 370	
Val	Asp	Arg	Tyr	Asn 375	Phe	Val	Met	Leu	Ala 380	Leu	Ser	Ser	Ser	Phe	Leu 385	
Val	Leu	Ser	Tyr	Leu 390	Leu	Thr	Arg	Trp	Cys 395	Gly	Ser	Val	Gly	Phe	Ile 400	
Leu 405	Ala	Asn	Cys	Phe 410	Asn	Met	Gly	Ile	Arg 415	Ile	Thr	Gln	Ser	Leu	Cys 420	
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	

				425				430					435				
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly		
			440					445					450				
Val	Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Glu	Gln	Gly	Trp	Pro		
		455					460					465					
Ala	Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr		
	470					475					480						
Leu	Gly	Thr	Ala	Phe	Leu	Thr	Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg		
485					490					495					500		
Thr	Gln	Leu	Gly	Val	Pro	Arg	Arg	Thr	Asp	Lys	Met	Thr					
				505				510									

<210> 283
 <211> 468
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 283

Met	Gly	Thr	Gln	Glu	Gly	Trp	Cys	Leu	Leu	Leu	Cys	Leu	Ala	Leu	Ser		
	-20					-15					-10						
Gly	Ala	Ala	Glu	Thr	Lys	Pro	His	Pro	Ala	Glu	Gly	Gln	Trp	Arg	Ala		
-5					1				5					10			
Val	Asp	Val	Val	Leu	Asp	Cys	Phe	Leu	Val	Lys	Asp	Gly	Ala	His	Arg		
		15						20					25				
Gly	Ala	Leu	Ala	Ser	Ser	Glu	Asp	Arg	Ala	Arg	Ala	Ser	Leu	Val	Leu		
	30					35						40					
Lys	Gln	Val	Pro	Val	Leu	Asp	Asp	Gly	Ser	Leu	Glu	Asp	Phe	Thr	Asp		
	45					50					55						
Phe	Gln	Gly	Gly	Thr	Leu	Ala	Gln	Asp	Asp	Pro	Pro	Ile	Ile	Phe	Glu		
60					65					70					75		
Ala	Ser	Val	Asp	Leu	Val	Gln	Ile	Pro	Gln	Ala	Glu	Ala	Leu	Leu	His		
				80					85					90			
Ala	Asp	Cys	Ser	Gly	Lys	Glu	Val	Thr	Cys	Glu	Ile	Ser	Arg	Tyr	Phe		
		95						100					105				
Leu	Gln	Met	Thr	Glu	Thr	Thr	Val	Lys	Thr	Ala	Ala	Trp	Phe	Met	Ala		
	110						115					120					
Asn	Val	Gln	Val	Ser	Gly	Gly	Pro	Ser	Ile	Ser	Leu	Val	Met	Lys			
	125					130				135							
Thr	Pro	Arg	Val	Ala	Lys	Asn	Glu	Val	Leu	Trp	His	Pro	Thr	Leu	Asn		
140					145					150					155		
Leu	Pro	Leu	Ser	Pro	Gln	Gly	Thr	Val	Arg	Thr	Ala	Val	Glu	Phe	Gln		
				160					165					170			
Val	Met	Thr	Gln	Thr	Gln	Ser	Leu	Ser	Phe	Leu	Leu	Gly	Ser	Ser	Ala		
			175						180				185				
Ser	Leu	Asp	Cys	Gly	Phe	Ser	Met	Ala	Pro	Gly	Leu	Asp	Leu	Ile	Ser		
	190						195					200					
Val	Glu	Trp	Arg	Leu	Gln	His	Lys	Gly	Arg	Gly	Gln	Leu	Val	Tyr	Ser		
	205					210					215						
Trp	Thr	Ala	Gly	Gln	Gly	Gln	Ala	Val	Arg	Lys	Gly	Ala	Thr	Leu	Glu		
220					225					230					235		

Pro Ala Gln Leu Gly Met Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly
 240 245 250
 Leu Thr Ile Gln Asp Glu Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser
 255 260 265
 Leu Tyr Arg Ala Gln Gln Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro
 270 275 280
 Lys Val Arg Leu Ser Leu Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile
 285 290 295
 Cys Asp Ile Ala Gly Tyr Tyr Pro Leu Asp Val Val Val Thr Trp Thr
 300 305 310 315
 Arg Glu Glu Leu Gly Gly Ser Pro Ala Gln Val Ser Gly Ala Ser Phe
 320 325 330
 Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser
 335 340 345
 Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val
 350 355 360
 Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val
 365 370 375
 Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu
 380 385 390 395
 Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro
 400 405 410
 Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys
 415 420 425
 Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val
 430 435 440
 Ser Gln Pro Ser
 445

<210> 284
 <211> 406
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

<400> 284
 Met Val Arg Ile Gln Arg Arg Lys Leu Leu Ala Ser Cys Leu Cys Val
 -30 -25 -20
 Thr Ala Thr Val Phe Leu Leu Val Thr Leu Gln Ala Leu Asp Thr Val
 -15 -10 -5 1
 Glu Asn Leu Met Lys Val Thr Gly Pro Pro Gln Gly Val Thr Asp Ser
 5 10 15
 Met Gln Cys Phe Asn Asp Gln Trp Pro Leu Ser Asn Thr Arg Ser Ser
 20 25 30
 Glu His Ile Lys Glu Val Met Val Glu Leu Gly Lys Phe Glu Arg Lys
 35 40 45
 Glu Phe Lys Ser Ser Ser Leu Gln Asp Gly His Thr Lys Met Glu Glu
 50 55 60 65
 Ala Pro Thr His Leu Asn Ser Phe Leu Lys Lys Glu Gly Leu Thr Phe
 70 75 80
 Asn Arg Lys Arg Lys Trp Glu Leu Asp Ser Tyr Pro Ile Met Leu Trp

Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
 25 30 35
 Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
 40 45 50
 Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
 55 60 65 70
 Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
 75 80 85
 Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
 90 95 100
 Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val
 105 110 115
 Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
 120 125 130
 Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala
 135 140 145 150
 Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu
 155 160 165
 Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys
 170 175 180
 Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu
 185 190 195
 Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp
 200 205 210
 Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe
 215 220 225 230
 Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp
 235 240 245
 Val Leu Val Leu Leu Cys Gly Pro Pro Pro Met Val Gln Leu Ala Cys
 250 255 260
 His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr
 265 270 275
 Tyr

<210> 286
 <211> 442
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<220>
 <221> UNSURE
 <222> 132
 <223> Xaa = Pro,Arg

<400> 286
 Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser
 -20 -15 -10
 Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Leu Arg Ala
 -5 1 5 10
 Val Asp Val Val Leu Asp Cys Phe Leu Ala Lys Asp Gly Ala His Arg

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48...-1

<400> 287
 Met Asn Pro Ala Ser Asp Gly Gly Thr Ser Glu Ser Ile Phe Asp Leu
 -45 -40 -35
 Asp Tyr Ala Ser Trp Gly Ile Arg Ser Thr Leu Met Val Ala Gly Phe
 -30 -25 -20
 Val Phe Tyr Leu Gly Val Phe Val Val Cys His Gln Leu Ser Ser Ser
 -15 -10 -5
 Leu Asn Ala Thr Tyr Arg Ser Leu Val Ala Arg Glu Lys Val Phe Trp
 1 5 10 15
 Asp Leu Ala Ala Thr Arg Ala Val Phe Gly Val Gln Ser Thr Ala Ala
 20 25 30
 Gly Leu Trp Ala Leu Leu Gly Asp Pro Val Leu His Ala Asp Lys Ala
 35 40 45
 Arg Gly Gln Gln Asn Trp Cys Trp Phe His Ile Thr Thr Ala Thr Gly
 50 55 60
 Phe Phe Cys Phe Glu Asn Val Ala Val His Leu Ser Asn Leu Ile Phe
 65 70 75 80
 Arg Thr Phe Asp Leu Phe Leu Val Ile His His Leu Phe Ala Phe Leu
 85 90 95
 Gly Phe Leu Gly Cys Leu Val Asn Leu Gln Ala Gly His Tyr Leu Ala
 100 105 110
 Met Thr Thr Leu Leu Leu Glu Met Ser Thr Pro Phe Thr Cys Val Ser
 115 120 125
 Trp Met Leu Leu Lys Ala Gly Trp Ser Glu Ser Leu Phe Trp Lys Leu
 130 135 140
 Asn Gln Trp Leu Met Ile His Met Phe His Cys Arg Met Val Leu Thr
 145 150 155 160
 Tyr His Met Trp Trp Val Cys Phe Trp His Trp Asp Gly Leu Val Ser
 165 170 175
 Ser Leu Tyr Leu Pro His Leu Thr Leu Phe Leu Val Gly Leu Ala Leu
 180 185 190
 Leu Thr Leu Ile Ile Asn Pro Tyr Trp Thr His Lys Lys Thr Gln Gln
 195 200 205
 Leu Leu Asn Pro Val Asp Trp Asn Phe Ala Gln Pro Glu Ala Lys Ser
 210 215 220
 Arg Pro Glu Gly Asn Gly Gln Leu Leu Arg Lys Lys Arg Pro
 225 230 235

<210> 288
 <211> 398
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 288

Met	Val	Asn	Asp	Pro	Pro	Val	Pro	Ala	Leu	Leu	Trp	Ala	Gln	Glu	Val
-20						-15					-10				
Gly	Gln	Val	Leu	Ala	Gly	Arg	Ala	Arg	Arg	Leu	Leu	Leu	Gln	Phe	Gly
-5					1			5						10	
Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Trp	Val	Ser	Val	Phe	Leu	
			15				20					25			
Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	Leu	Ser
		30				35						40			
Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	Thr	Ser
	45					50				55					
Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg
60					65					70					75
Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu
				80					85					90	
Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val
			95					100					105		
Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser
	110						115					120			
Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp
	125					130					135				
Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys
140						145				150					155
Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Tyr
				160					165					170	
Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	Ser	Lys	Arg	Ile	Gln
			175					180					185		
Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	Phe	Thr	Gly	Leu	Arg
	190						195					200			
Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	Phe	Ile	Gly	Val	Ala
	205					210					215				
Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	Phe	Ser	Tyr	Met	Gln
220						225				230					235
Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	Phe	Ser	Leu	Gln	Val
				240					245					250	
Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	Val	Gln	Arg	Arg	Ile
			255					260					265		
Ser	Ala	His	Gln	Pro	Gly	Pro	Glu	Gly	Gln	Glu	Glu	Ser	Thr	Pro	Gln
	270						275					280			
Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	Pro	Glu	Asp	Pro	Ser	Gly	Thr
	285					290				295					
Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Pro	Asp	Gln	Gln	Pro	Leu	Ser
300					305					310					315
Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala	Ser	Asp	Gly	Ser	Gly	Ser	Trp
				320					325					330	
Glu	Asp	Ala	Ala	Leu	Leu	Thr	Glu	Ala	Asn	Leu	Pro	Ala	Pro	Ala	Pro
			335					340					345		
Ala	Ser	Ala	Ser	Ala	Pro	Val	Leu	Glu	Thr	Leu	Gly	Ser	Ser	Glu	Pro
	350						355					360			
Ala	Gly	Gly	Ala	Leu	Arg	Gln	Arg	Pro	Thr	Cys	Ser	Ser	Ser		
	365					370					375				

<210> 289

<211> 130

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 289
 Met Arg Gln Lys Ala Val Ser Leu Phe Phe Cys Tyr Leu Leu Leu Phe
 -20 -15 -10 -5
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser
 1 5 10
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
 15 20 25
 Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
 30 35 40
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala
 45 50 55 60
 Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu
 65 70 75
 Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly
 80 85 90
 Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp
 95 100 105
 Glu Glu
 110

<210> 290
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 290
 Met Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly
 -20 -15 -10 -5
 Phe Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met
 1 5 10
 Ser Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu
 15 20 25
 Val Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile
 30 35 40
 Gly Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp
 45 50 55 60
 Ser Glu Glu Asp Glu Glu
 65

<210> 291
 <211> 207
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

 <400> 291
 Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
 -20 -15 -10
 Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
 -5 1 5
 Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
 10 15 20 25
 Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
 30 35 40
 Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
 45 50 55
 Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
 60 65 70
 His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
 75 80 85
 Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
 90 95 100 105
 Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
 110 115 120
 Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys
 125 130 135
 Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
 140 145 150
 Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
 155 160 165
 Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
 170 175 180

<210> 292
 <211> 111
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

 <400> 292
 Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser Phe Val Val Phe Ser
 -20 -15 -10
 Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val Val Tyr Ala Asp Ile
 -5 1 5
 Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala Phe Pro Leu Gln Arg
 10 15 20
 Ser Val Ser Phe Asn Phe Ser Thr Val His Lys Ser Cys Pro Ala Lys
 25 30 35 40
 Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp Ile Ala Glu Thr Lys
 45 50 55
 Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala Ile Asn Asn Ser Tyr

		60						65					70				
Leu	Met	Val	Ile	Gln	Asp	Ile	Thr	Ala	Met	Val	Arg	Phe	Asn	Ile			
		75					80						85				

<210> 293
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 293																	
Met	Glu	Ala	Val	Val	Phe	Val	Phe	Ser	Leu	Leu	Asp	Cys	Cys	Ala	Leu		
-15					-10				-5						1		
Ile	Phe	Leu	Ser	Val	Tyr	Phe	Ile	Ile	Thr	Leu	Ser	Asp	Leu	Glu	Cys		
		5					10					15					
Asp	Tyr	Ile	Asn	Ala	Arg	Ser	Cys	Cys	Ser	Lys	Leu	Asn	Lys	Trp	Val		
	20					25					30						
Ile	Pro	Glu	Leu	Ile	Gly	His	Thr	Ile	Val	Thr	Val	Leu	Leu	Leu	Met		
	35				40					45							
Ser	Leu	His	Trp	Phe	Ile	Phe	Leu	Leu	Asn	Leu	Pro	Val	Ala	Thr	Trp		
50				55					60						65		
Asn	Ile	Tyr	Arg	Tyr	Ile	Met	Val	Pro	Ser	Gly	Asn	Met	Gly	Val	Phe		
		70						75					80				
Asp	Pro	Thr	Glu	Ile	His	Asn	Arg	Gly	Gln	Leu	Lys	Ser	His	Met	Lys		
		85					90					95					
Glu	Ala	Met	Ile	Lys	Leu	Gly	Phe	His	Leu	Leu	Cys	Phe	Phe	Met	Tyr		
	100					105						110					
Leu	Tyr	Ser	Met	Ile	Leu	Ala	Leu	Ile	Asn	Asp							
	115					120											

<210> 294
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 294																	
Met	Gln	Arg	Val	Ser	Gly	Leu	Leu	Ser	Trp	Thr	Leu	Ser	Arg	Val	Leu		
	-25					-20					-15						
Trp	Leu	Ser	Gly	Leu	Ser	Glu	Pro	Gly	Ala	Ala	Arg	Gln	Pro	Arg	Ile		
	-10				-5					1					5		
Met	Glu	Glu	Lys	Ala	Leu	Glu	Val	Tyr	Asp	Leu	Ile	Arg	Thr	Ile	Arg		
			10					15					20				
Asp	Pro	Glu	Lys	Pro	Asn	Thr	Leu	Glu	Glu	Leu	Glu	Val	Val	Ser	Glu		
		25				30						35					
Ser	Cys	Val	Glu	Val	Gln	Glu	Ile	Asn	Glu	Glu	Glu	Tyr	Leu	Val	Ile		
	40					45						50					
Ile	Arg	Phe	Thr	Pro	Thr	Val	Pro	His	Cys	Ser	Leu	Ala	Thr	Leu	Ile		

55		60		65											
Gly	Leu	Cys	Leu	Arg	Val	Lys	Leu	Gln	Arg	Cys	Leu	Pro	Phe	Lys	His
70					75					80					85
Lys	Leu	Glu	Ile	Tyr	Ile	Ser	Glu	Gly	Thr	His	Ser	Thr	Glu	Glu	Asp
			90					95						100	
Ile	Asn	Lys	Gln	Ile	Asn	Asp	Lys	Glu	Arg	Val	Ala	Ala	Ala	Met	Glu
		105						110					115		
Asn	Pro	Asn	Leu	Arg	Glu	Ile	Val	Glu	Gln	Cys	Val	Leu	Glu	Pro	Asp
		120					125					130			

<210> 295
 <211> 181
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 295															
Met	Pro	Pro	Phe	Leu	Leu	Leu	Thr	Cys	Leu	Phe	Ile	Thr	Gly	Thr	Ser
	-15					-10					-5				
Val	Ser	Pro	Val	Ala	Leu	Asp	Pro	Cys	Ser	Ala	Tyr	Ile	Ser	Leu	Asn
1			5					10					15		
Glu	Pro	Trp	Arg	Asn	Thr	Asp	His	Gln	Leu	Asp	Glu	Ser	Gln	Gly	Pro
			20					25					30		
Pro	Leu	Cys	Asp	Asn	His	Val	Asn	Gly	Glu	Trp	Tyr	His	Phe	Thr	Gly
		35					40					45			
Met	Ala	Gly	Asp	Ala	Met	Pro	Thr	Phe	Cys	Ile	Pro	Glu	Asn	His	Cys
	50					55					60				
Gly	Thr	His	Ala	Pro	Val	Trp	Leu	Asn	Gly	Ser	His	Pro	Leu	Glu	Gly
65					70					75					80
Asp	Gly	Ile	Val	Gln	Arg	Gln	Ala	Cys	Ala	Ser	Phe	Asn	Gly	Asn	Cys
				85				90						95	
Cys	Leu	Trp	Asn	Thr	Thr	Val	Glu	Val	Lys	Ala	Cys	Pro	Gly	Gly	Tyr
			100					105					110		
Tyr	Val	Tyr	Arg	Leu	Thr	Lys	Pro	Ser	Val	Cys	Phe	His	Val	Tyr	Cys
		115				120						125			
Gly	Arg	Glu	Tyr	Leu	Pro	Cys	Ala	Leu	Phe	Leu	His	Gln	Gln	Gly	His
	130					135					140				
Arg	Trp	Ser	Pro	Lys	Val	Pro	Asn	Tyr	Arg	Ile	Cys	Ser	Tyr	Ser	Gly
145					150					155					160
Asn	Tyr	Ile	Ser	Ile											
				165											

<210> 296
 <211> 247
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 296

```
Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser Ser
      -15                      -10                      -5
Phe Ser Lys Ala Arg Glu Glu Ile Thr Pro Val Val Ser Ile Ala
      1                      5                      10
Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val Leu Ile Thr
15                      20                      25                      30
Cys Cys Ala Pro Gln Pro Pro Pro Pro Ile Thr Tyr Ser Leu Cys Gly
      35                      40                      45
Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val Lys Thr His Glu Pro
      50                      55                      60
Ala Ser Phe Asn Leu Asn Val Thr Leu Lys Ser Ser Pro Asp Leu Leu
      65                      70                      75
Thr Tyr Phe Cys Arg Ala Ser Ser Thr Ser Gly Ala His Val Asp Ser
      80                      85                      90
Ala Arg Leu Gln Met His Trp Glu Leu Trp Ser Lys Pro Val Ser Glu
95                      100                      105                      110
Leu Arg Ala Asn Phe Thr Leu Gln Asp Arg Gly Ala Gly Pro Arg Val
      115                      120                      125
Glu Met Ile Cys Gln Ala Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser
      130                      135                      140
Leu Ile Gly Lys Asp Gly Gln Val His Leu Gln Gln Arg Pro Cys His
145                      150                      155
Arg Gln Pro Ala Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp
160                      165                      170
Phe Trp Cys Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu
175                      180                      185                      190
Thr Val Val Pro Pro Gly Gly Leu Pro Arg Ala Pro Thr Ile Val Leu
      195                      200                      205
Val Gly Ser Leu Ala Ser Thr Ala Ala Ile Thr Ser Arg Met Leu Gly
      210                      215                      220
Trp Thr Thr Trp Ala Arg Trp
      225
```

<210> 297

<211> 132

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -41...-1

<400> 297

```
Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe Asp
      -40                      -35                      -30
Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val Ser
-25                      -20                      -15                      -10
Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly Tyr
      -5                      1                      5
Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg Asn
      10                      15                      20
Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe Leu
      25                      30                      35
```

Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile Ser
40 45 50 55
Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val Ser
60 65 70
Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu Gly
75 80 85
Cys Pro Gly Pro
90

<210> 298
<211> 251
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24...-1

<400> 298
Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser Val
-20 -15 -10
Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
-5 1 5
Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
10 15 20
Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
25 30 35 40
Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
45 50 55
Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
60 65 70
Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
75 80 85
Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
90 95 100
Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
105 110 115 120
Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
125 130 135
Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
140 145 150
His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
155 160 165
Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
170 175 180
Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
185 190 195 200
Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
205 210 215
Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
220 225

<210> 299
<211> 137

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 299
 Met Leu Ser Gly Arg Leu Val Leu Gly Leu Val Ser Met Ala Gly Arg
 -20 -15 -10
 Val Cys Leu Cys Gln Gly Ser Ala Gly Ser Gly Ala Ile Gly Pro Val
 -5 1 5 10
 Glu Ala Ala Ile Arg Thr Lys Leu Glu Glu Ala Leu Ser Pro Glu Val
 15 20 25
 Leu Glu Leu Arg Asn Glu Ser Gly Gly His Ala Val Pro Pro Gly Ser
 30 35 40
 Glu Thr His Phe Arg Val Ala Val Val Ser Ser Arg Phe Glu Gly Leu
 45 50 55
 Ser Pro Leu Gln Arg His Arg Leu Val His Ala Ala Leu Ala Glu Glu
 60 65 70
 Leu Gly Gly Pro Val His Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala
 75 80 85 90
 Gln Trp Arg Glu Asn Ser Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly
 95 100 105
 Gly Asn Lys Lys Thr Leu Gly Thr Pro
 110 115

<210> 300
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 300
 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser
 -25 -20 -15
 Gly Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn
 -10 -5 1
 Ala Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn
 5 10 15 20
 Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu
 25 30 35
 Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser
 40 45 50
 Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp
 55 60 65
 Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp
 70 75 80
 Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu
 85 90 95 100
 Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln

				105				110				115			
Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val
			120					125					130		
Ile	Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His
		135					140					145			
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val
	150					155					160				
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro
165					170					175					180
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu
			185						190					195	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala
		200						205					210		
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu
	215						220					225			
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
	230					235					240				
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val
245					250				255						260
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe
			265					270						275	
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu
		280						285					290		
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala
	295						300					305			
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln
	310					315					320				
Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly
325					330					335					340
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile
			345						350					355	
Asn	Gly	Val	Thr	Glu	Cys	Leu	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu
		360						365					370		
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu
	375						380					385			
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile
	390					395					400				
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys
405					410					415					420
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly
			425						430					435	
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly
		440						445					450		
Val	Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Asp	Gln	Gly	Trp	Pro
	455						460					465			
Ala	Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr
	470					475					480				
Leu	Gly	Thr	Ala	Phe	Leu	Thr	Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg
485					490					495					500
Thr	Gln	Leu	Gly	Val	Pro	Arg	Arg	Thr	Asp	Lys	Met	Thr			
			505					510							

<210> 301

<211> 287

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17..-1

<400> 301
 Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu Ala Phe Val Gln
 -15 -10 -5
 Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp Glu Val Ile Phe
 1 5 10 15
 Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro Ser Gly Pro Ser
 20 25 30
 Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met Met Glu Ala Tyr
 35 40 45
 Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile Gly Asp Met Met
 50 55 60
 Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn Lys Glu Asn Leu
 65 70 75
 Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro Ile Ser Pro Glu
 80 85 90 95
 Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr Arg Ser Ser Ala
 100 105 110
 Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly Ala Glu Glu Glu
 115 120 125
 Leu Leu Pro Gly Val Asp Val Leu Leu Glu Val Phe Pro Thr Cys Ser
 130 135 140
 Val Glu Gln Ala Gln Trp Val Leu Ala Lys Ala Arg Gly Asp Leu Glu
 145 150 155
 Glu Ala Val Gln Met Leu Val Glu Gly Lys Glu Glu Gly Pro Ala Ala
 160 165 170 175
 Trp Glu Gly Pro Asn Gln Asp Leu Pro Arg Arg Leu Arg Gly Pro Gln
 180 185 190
 Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr Met Met Val Asp
 195 200 205
 Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala Pro Lys Glu Ala
 210 215 220
 Pro Lys Lys Leu Ile Arg Tyr Ile Asp Asn Gln Val Val Ser Thr Lys
 225 230 235
 Gly Glu Arg Phe Lys Asp Val Arg Asn Pro Glu Ala Glu Glu Met Lys
 240 245 250 255
 Ala Thr Tyr Ile Asn Leu Lys Pro Ala Arg Lys Tyr Arg Phe His
 260 265 270

<210> 302
 <211> 165
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35..-1

<400> 302

Met	Met	Arg	Cys	Cys	Arg	Arg	Arg	Cys	Cys	Cys	Arg	Gln	Pro	Pro	His
-35					-30					-25					-20
Ala	Leu	Arg	Pro	Leu	Leu	Leu	Leu	Pro	Leu	Val	Leu	Leu	Pro	Pro	Leu
				-15					-10					-5	
Ala	Ala	Ala	Ala	Ala	Gly	Pro	Asn	Arg	Cys	Asp	Thr	Ile	Tyr	Gln	Gly
			1				5					10			
Phe	Ala	Glu	Cys	Leu	Ile	Arg	Leu	Gly	Asp	Ser	Met	Gly	Arg	Gly	Gly
15					20					25					
Glu	Leu	Glu	Thr	Ile	Cys	Arg	Ser	Trp	Asn	Tyr	Phe	His	Ala	Cys	Ala
30					35					40					45
Ser	Gln	Val	Leu	Ser	Gly	Cys	Pro	Glu	Glu	Ala	Ala	Ala	Val	Trp	Glu
				50					55					60	
Ser	Leu	Gln	Gln	Glu	Ala	Arg	Gln	Ala	Pro	Arg	Pro	Asn	Asn	Leu	His
			65					70					75		
Thr	Leu	Cys	Gly	Ala	Pro	Val	His	Val	Arg	Glu	Arg	Gly	Thr	Gly	Ser
		80					85					90			
Glu	Thr	Asn	Gln	Glu	Thr	Leu	Arg	Ala	Thr	Ala	Pro	Ala	Leu	Pro	Met
95						100				105					
Ala	Pro	Ala	Pro	Pro	Leu	Leu	Ala	Ala	Ala	Leu	Ala	Leu	Ala	Tyr	Leu
110					115					120					125
Leu	Arg	Pro	Leu	Ala											
				130											

<210> 303

<211> 148

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 303

Met	Ala	Ser	Val	Val	Leu	Ala	Leu	Arg	Thr	Arg	Thr	Ala	Val	Thr	Ser
-25					-20					-15					-10
Leu	Leu	Ser	Pro	Thr	Pro	Ala	Thr	Ala	Leu	Ala	Val	Arg	Tyr	Ala	Ser
				-5				1				5			
Lys	Lys	Ser	Gly	Gly	Ser	Ser	Lys	Asn	Leu	Gly	Gly	Lys	Ser	Ser	Gly
		10					15					20			
Arg	Arg	Gln	Gly	Ile	Lys	Lys	Met	Glu	Gly	His	Tyr	Val	His	Ala	Gly
		25				30					35				
Asn	Ile	Ile	Ala	Thr	Gln	Arg	His	Phe	Arg	Trp	His	Pro	Gly	Ala	His
40					45					50					55
Val	Gly	Val	Gly	Lys	Asn	Lys	Cys	Leu	Tyr	Ala	Leu	Glu	Glu	Gly	Ile
				60					65					70	
Val	Arg	Tyr	Thr	Lys	Glu	Val	Tyr	Val	Pro	His	Pro	Arg	Asn	Thr	Glu
			75				80						85		
Ala	Val	Asp	Leu	Ile	Thr	Arg	Leu	Pro	Lys	Gly	Ala	Val	Leu	Tyr	Lys
		90				95					100				
Thr	Phe	Val	His	Val	Val	Pro	Ala	Lys	Pro	Glu	Gly	Thr	Phe	Lys	Leu
	105					110					115				
Val	Ala	Met	Leu												
120															

<210> 304
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 304
 Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu
 -30 -25 -20
 Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Leu Thr
 -15 -10 -5
 Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys
 1 5 10
 Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr
 15 20 25 30
 Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr
 35 40 45
 Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu
 50 55 60
 Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile
 65 70 75
 Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys
 80 85 90
 Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu
 95 100 105 110
 Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys
 115 120 125
 Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn
 130 135 140
 Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn
 145 150 155
 Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys
 160 165 170
 Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr
 175 180 185 190
 Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp
 195 200 205
 Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe
 210 215 220
 Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe
 225 230 235
 Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr
 240 245 250
 Asn Met Ser
 255

<210> 305
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49..-1

<400> 305
 Met Glu Gly Ala Gly Ala Gly Ser Gly Phe Arg Lys Glu Leu Val Ser
 -45 -40 -35
 Arg Leu Leu His Leu His Phe Lys Asp Asp Lys Thr Lys Val Ser Gly
 -30 -25 -20
 Asp Ala Leu Gln Leu Met Val Glu Leu Leu Lys Val Phe Val Val Glu
 -15 -10 -5
 Ala Ala Val Arg Gly Val Arg Gln Ala Gln Ala Glu Asp Ala Leu Arg
 1 5 10 15
 Val Asp Val Asp Gln Leu Glu Lys Val Leu Pro Gln Leu Leu Leu Asp
 20 25 30
 Phe

<210> 306
 <211> 233
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30..-1

<400> 306
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val
 -30 -25 -20 -15
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp
 -10 -5 1
 Pro Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu
 5 10 15
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu
 20 25 30
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu
 35 40 45 50
 Thr Leu Arg Ile Asp Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser
 55 60 65
 Ala Lys Glu Lys Trp Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val
 70 75 80
 Glu Asp Phe Asn Tyr Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly
 85 90 95
 Tyr Thr Glu Glu Asn Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala
 100 105 110
 Ile Glu Ile Ala Arg Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile
 115 120 125 130
 Ser Val Gln Asp Lys Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu
 135 140 145
 Lys Arg Ala Asp Ser Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu
 150 155 160
 Lys Gly Ala Asp Ser Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu
 165 170 175

Asp Lys Thr Asp Lys Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu
 180 185 190
 Ile Asn Lys Ser Gly Glu Lys Ala Met
 195 200

<210> 307
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 307
 Met Arg Gln Lys Ala Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe
 -20 -15 -10 -5
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser
 1 5 10
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
 15 20 25
 Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
 30 35 40
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala
 45 50 55 60
 Ile Leu Asn Gly Gly
 65

<210> 308
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

<400> 308
 Met Gly Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys
 -40 -35 -30
 Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly
 -25 -20 -15
 Ser Leu Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr
 -10 -5 1 5
 Ser Ser Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys
 10 15 20
 Leu Gly Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys
 25 30 35
 Glu Asp Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro
 40 45 50
 Pro Leu Lys Ser Glu Lys His Glu Glu
 55 60

<210> 309

<211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34..-1

<400> 309
 Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu
 -30 -25 -20
 Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Leu Thr
 -15 -10 -5
 Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys
 1 5 10
 Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr
 15 20 25 30
 Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Val Phe Thr
 35 40 45
 Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu
 50 55 60
 Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile
 65 70 75
 Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys
 80 85 90
 Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu
 95 100 105 110
 Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys
 115 120 125
 Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn
 130 135 140
 Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn
 145 150 155
 Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys
 160 165 170
 Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr
 175 180 185 190
 Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp
 195 200 205
 Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe
 210 215 220
 Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe
 225 230 235
 Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr
 240 245 250
 Asn Met Ser
 255

<210> 310
 <211> 426
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
 <222> -28...-1

<400> 310

Met	Ser	Pro	Ala	Phe	Arg	Ala	Met	Asp	Val	Glu	Pro	Arg	Ala	Lys	Gly
			-25					-20					-15		
Val	Leu	Leu	Glu	Pro	Phe	Val	His	Gln	Val	Gly	Gly	His	Ser	Cys	Val
		-10					-5					1			
Leu	Arg	Phe	Asn	Glu	Thr	Thr	Leu	Cys	Lys	Pro	Leu	Val	Pro	Arg	Glu
5					10					15					20
His	Gln	Phe	Tyr	Glu	Thr	Leu	Pro	Ala	Glu	Met	Arg	Lys	Phe	Thr	Pro
			25					30						35	
Gln	Tyr	Lys	Gly	Val	Val	Ser	Val	Arg	Phe	Glu	Glu	Asp	Glu	Asp	Arg
			40					45					50		
Asn	Leu	Cys	Leu	Ile	Ala	Tyr	Pro	Leu	Lys	Gly	Asp	His	Gly	Ile	Val
		55					60					65			
Asp	Ile	Val	Asp	Asn	Ser	Asp	Cys	Glu	Pro	Lys	Ser	Lys	Leu	Leu	Arg
	70					75					80				
Trp	Thr	Thr	Asn	Lys	Lys	His	His	Val	Leu	Glu	Thr	Glu	Lys	Thr	Pro
85					90					95					100
Lys	Asp	Trp	Val	Arg	Gln	His	Arg	Lys	Glu	Glu	Lys	Met	Lys	Ser	His
			105						110					115	
Lys	Leu	Glu	Glu	Glu	Phe	Glu	Trp	Leu	Lys	Lys	Ser	Glu	Val	Leu	Tyr
			120					125					130		
Tyr	Thr	Val	Glu	Lys	Lys	Gly	Asn	Ile	Ser	Ser	Gln	Leu	Lys	His	Tyr
		135					140					145			
Asn	Pro	Trp	Ser	Met	Lys	Cys	His	Gln	Gln	Gln	Leu	Gln	Arg	Met	Lys
	150					155					160				
Glu	Asn	Ala	Lys	His	Arg	Asn	Gln	Tyr	Lys	Phe	Ile	Leu	Leu	Glu	Asn
165					170					175					180
Leu	Thr	Ser	Arg	Tyr	Glu	Val	Pro	Cys	Val	Leu	Asp	Leu	Lys	Met	Gly
			185						190					195	
Thr	Arg	Gln	His	Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln
			200					205					210		
Ile	Arg	Lys	Cys	Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val
		215					220					225			
Cys	Gly	Met	Gln	Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met
	230					235					240				
Asn	Lys	Tyr	His	Gly	Arg	Lys	Leu	Ser	Met	Gln	Gly	Phe	Lys	Glu	Ala
245					250					255					260
Leu	Phe	Gln	Phe	Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu
			265						270					275	
Gly	Pro	Val	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg
			280					285					290		
Gln	Glu	Ser	Tyr	Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp
		295					300					305			
Gly	Lys	Glu	Arg	Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu
	310					315					320				
Glu	Asp	Leu	Ser	Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala
325					330					335					340
Tyr	Lys	Pro	Ile	Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe
			345						350					355	
Ala	His	Thr	Thr	Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu
			360					365					370		

Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile
 375 380 385
 Val Thr Glu Ile Ser Glu Glu Ser Gly Glu
 390 395

<210> 311
 <211> 466
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 311
 Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser
 -15 -10 -5
 Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn
 1 5 10 15
 Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala
 20 25 30
 Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu Leu Arg Ala Glu Lys
 35 40 45
 Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu
 50 55 60
 Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp Lys Ala Leu Leu Gly
 65 70 75 80
 Arg His Gln Ala Arg Leu Lys Ala Glu Leu Ala Arg Leu Lys Val His
 85 90 95
 Arg Gly Val Ser Arg Asn Glu Asp Leu Leu Glu Val Gly Ser Arg Pro
 100 105 110
 Gly Pro Ala Ser Gln Leu Pro Arg Phe Val Arg Val Asn Thr Leu Lys
 115 120 125
 Thr Cys Ser Asp Asp Val Val Asp Tyr Phe Lys Arg Gln Gly Phe Ser
 130 135 140
 Tyr Gln Gly Arg Ala Ser Ser Leu Asp Asp Leu Arg Ala Leu Lys Gly
 145 150 155 160
 Lys His Phe Leu Leu Asp Pro Leu Met Pro Glu Leu Leu Val Phe Pro
 165 170 175
 Ala Gln Thr Asp Leu His Glu His Pro Leu Tyr Arg Ala Gly His Leu
 180 185 190
 Ile Leu Gln Asp Arg Ala Ser Cys Leu Pro Ala Met Leu Leu Asp Pro
 195 200 205
 Pro Pro Gly Ser His Val Ile Asp Ala Cys Ala Ala Pro Gly Asn Lys
 210 215 220
 Thr Ser His Leu Ala Ala Leu Leu Lys Asn Gln Gly Lys Ile Phe Ala
 225 230 235 240
 Phe Asp Leu Asp Ala Lys Arg Leu Ala Ser Met Ala Thr Leu Leu Ala
 245 250 255
 Arg Ala Gly Val Ser Cys Cys Glu Leu Ala Glu Glu Asp Phe Leu Ala
 260 265 270
 Val Ser Pro Ser Asp Pro Arg Tyr His Glu Val His Tyr Ile Leu Leu
 275 280 285
 Asp Pro Ser Cys Ser Gly Ser Gly Met Pro Ser Arg Gln Leu Glu Glu

290	295	300
Pro Gly Ala Gly Thr	Pro Ser Pro Val Arg Leu	His Ala Leu Ala Gly
305	310	315
Phe Gln Gln Arg Ala Leu Cys His Ala Leu Thr Phe Pro Ser Leu Gln		320
	325	330
Arg Leu Val Tyr Ser Thr Cys Ser Leu Cys Gln Glu Glu Asn Glu Asp		335
	340	345
Val Val Arg Asp Ala Leu Gln Gln Asn Pro Gly Ala Phe Arg Leu Ala		350
	355	360
Pro Ala Leu Pro Ala Trp Pro His Arg Gly Leu Ser Thr Phe Pro Gly		365
	370	375
Ala Glu His Cys Leu Arg Ala Ser Pro Glu Thr Thr Leu Ser Ser Gly		380
385	390	395
Phe Phe Val Ala Val Ile Glu Arg Val Glu Val Pro Ser Ser Ala Ser		400
	405	410
Gln Ala Lys Ala Ser Ala Pro Glu Arg Thr Pro Ser Pro Ala Pro Lys		415
	420	425
Arg Lys Lys Arg Gln Gln Arg Ala Ala Ala Gly Ala Cys Thr Pro Pro		430
	435	440
Cys Thr		445
450		

<210> 312
 <211> 382
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16..-1

<400> 312

Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser	
-15	-10
Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn	
1	5
Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala	
	20
Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu Leu Arg Ala Glu Lys	
	35
Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu	
50	55
Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp Lys Ala Leu Leu Gly	
65	70
Arg His Gln Ala Arg Leu Lys Ala Glu Leu Ala Arg Leu Lys Val His	
	85
Arg Gly Val Ser Arg Asn Glu Asp Leu Leu Glu Val Gly Ser Arg Pro	
	100
Gly Pro Ala Ser Gln Leu Pro Arg Phe Val Arg Val Asn Thr Leu Lys	
	115
Thr Cys Ser Asp Asp Val Val Asp Tyr Phe Lys Arg Gln Gly Phe Ser	
130	135
Tyr Gln Gly Arg Ala Ser Ser Leu Asp Asp Leu Arg Ala Leu Lys Gly	
145	150
	155
	160

Lys His Phe Leu Leu Asp Pro Leu Met Pro Glu Leu Leu Val Phe Pro
 165 170 175
 Ala Gln Thr Asp Leu His Glu His Pro Leu Tyr Arg Ala Gly His Leu
 180 185 190
 Ile Leu Gln Asp Arg Ala Ser Cys Leu Pro Ala Met Leu Leu Asp Pro
 195 200 205
 Pro Pro Gly Ser His Val Ile Asp Ala Cys Ala Ala Pro Gly Asn Lys
 210 215 220
 Thr Ser His Leu Ala Ala Leu Leu Lys Asn Gln Gly Lys Ile Phe Ala
 225 230 235 240
 Phe Asp Leu Asp Ala Lys Arg Leu Ala Ser Met Ala Thr Leu Leu Ala
 245 250 255
 Arg Ala Gly Val Ser Cys Cys Glu Leu Ala Glu Glu Asp Phe Leu Ala
 260 265 270
 Val Ser Pro Ser Asp Pro Arg Tyr His Glu Val His Tyr Ile Leu Leu
 275 280 285
 Asp Pro Ser Cys Ser Gly Ser Gly Met Pro Ser Arg Gln Leu Glu Glu
 290 295 300
 Pro Gly Ala Gly Thr Pro Ser Pro Val Arg Leu His Ala Leu Ala Ala
 305 310 315 320
 Ser Ser Ser Glu Pro Cys Ala Thr Arg Ser Leu Ser Leu Pro Cys Ser
 325 330 335
 Gly Ser Ser Thr Pro Arg Ala Pro Ser Ala Arg Arg Arg Met Lys Thr
 340 345 350
 Trp Cys Glu Met Arg Cys Ser Arg Thr Arg Ala Pro Ser Gly
 355 360 365

<210> 313
 <211> 258
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 313
 Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Glu Leu Arg Leu Cys Phe
 -35 -30 -25
 Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala
 -20 -15 -10 -5
 Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
 1 5 10
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly
 15 20 25
 Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu Gly
 30 35 40
 Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser Gly
 45 50 55 60
 Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile Ile
 65 70 75
 Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly His
 80 85 90
 Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr Gly

	95					100				105					
Gly	Tyr	Ser	Glu	Gly	Asp	Ala	Val	Ser	Gln	Pro	Gln	Met	Ala	Leu	Glu
	110					115					120				
Glu	Val	Ser	Val	Ser	Asp	Pro	Leu	Ala	Ser	Asn	Gln	Gly	Gln	Ser	Leu
125					130					135					140
Pro	Gly	Ser	Ser	Arg	Glu	His	Met	Ala	Gln	Trp	Glu	Val	Arg	Ser	Gln
				145					150					155	
Thr	His	Val	Pro	Asn	Arg	Glu	Pro	Val	Gln	Ala	Leu	Pro	Ser	Ser	Ala
			160					165					170		
Ser	Arg	Lys	Arg	Leu	Asp	Lys	Lys	Arg	Ser	Val	Pro	Val	Ala	Thr	Val
	175					180						185			
Glu	Leu	Glu	Glu	Lys	Arg	Phe	Arg	Thr	Leu	Pro	Leu	Val	Pro	Pro	Pro
	190					195					200				
Thr	Arg	Pro	Asp	Gln	Ser	Gly	Phe	Thr	Arg	Gly	Arg	Arg	Leu	Gly	Ala
205					210					215					220
Arg	Arg														

<210> 314
 <211> 280
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 314															
Met	Lys	Ser	Cys	Gly	Ser	Met	Leu	Gly	Leu	Trp	Gly	Gln	Arg	Leu	Pro
			-30					-25				-20			
Ala	Ala	Trp	Val	Leu	Leu	Leu	Leu	Pro	Phe	Leu	Pro	Leu	Leu	Leu	Leu
		-15					-10					-5			
Ala	Ala	Pro	Ala	Pro	His	Arg	Ala	Ser	Tyr	Lys	Pro	Val	Ile	Val	Val
1					5					10					15
His	Gly	Leu	Phe	Asp	Ser	Ser	Tyr	Ser	Phe	Arg	His	Leu	Leu	Glu	Tyr
				20					25					30	
Ile	Asn	Glu	Thr	His	Pro	Gly	Thr	Val	Val	Thr	Val	Leu	Asp	Leu	Phe
		35					40					45			
Asp	Gly	Arg	Glu	Ser	Leu	Arg	Pro	Leu	Trp	Glu	Gln	Val	Gln	Gly	Phe
	50						55					60			
Arg	Glu	Ala	Val	Val	Pro	Ile	Met	Ala	Lys	Ala	Pro	Gln	Gly	Val	His
	65					70					75				
Leu	Ile	Cys	Tyr	Ser	Gln	Gly	Gly	Leu	Val	Cys	Arg	Ala	Leu	Leu	Ser
80					85					90					95
Val	Met	Asp	Asp	His	Asn	Val	Asp	Ser	Phe	Ile	Ser	Leu	Ser	Ser	Pro
				100					105					110	
Gln	Met	Gly	Gln	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Lys	Trp	Leu	Phe	Pro
			115					120					125		
Thr	Ser	Met	Arg	Ser	Asn	Leu	Tyr	Arg	Ile	Cys	Tyr	Ser	Pro	Leu	Ile
		130					135					140			
Asn	Gly	Glu	Arg	Asp	His	Pro	Asn	Ala	Thr	Val	Trp	Arg	Lys	Asn	Phe
	145					150					155				
Leu	Arg	Val	Gly	His	Leu	Val	Leu	Ile	Gly	Gly	Pro	Asp	Asp	Gly	Val
160					165					170					175
Ile	Thr	Pro	Trp	Gln	Ser	Ser	Phe	Phe	Gly	Phe	Tyr	Asp	Ala	Asn	Glu

				180					185					190			
Thr	Val	Leu	Glu	Met	Glu	Glu	Gln	Leu	Val	Tyr	Leu	Arg	Asp	Ser	Phe		
			195					200					205				
Gly	Leu	Lys	Thr	Leu	Leu	Ala	Arg	Gly	Ala	Ile	Val	Arg	Cys	Pro	Met		
		210					215					220					
Ala	Gly	Ile	Ser	His	Thr	Ala	Trp	His	Ser	Asn	Arg	Thr	Leu	Tyr	Glu		
	225					230					235						
Thr	Cys	Ile	Glu	Pro	Trp	Leu	Ser										
240					245												

<210> 315
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 315																	
Met	Lys	Ser	Cys	Gly	Ser	Met	Leu	Gly	Leu	Trp	Gly	Gln	Arg	Leu	Pro		
			-30					-25					-20				
Ala	Ala	Trp	Val	Leu	Leu	Leu	Leu	Pro	Phe	Leu	Pro	Leu	Leu	Leu	Leu		
		-15					-10					-5					
Ala	Ala	Pro	Ala	Pro	His	Arg	Ala	Ser	Tyr	Lys	Pro	Val	Ile	Val	Val		
1					5					10					15		
His	Gly	Leu	Phe	Asp	Ser	Ser	Tyr	Ser	Phe	Arg	His	Leu	Leu	Glu	Tyr		
			20						25					30			
Ile	Asn	Glu	Thr	His	Pro	Gly	Thr	Val	Val	Thr	Val	Leu	Asp	Leu	Phe		
			35					40					45				
Asp	Gly	Arg	Glu	Ser	Leu	Arg	Pro	Leu	Trp	Glu	Gln	Val	Gln	Gly	Phe		
		50					55					60					
Arg	Glu	Ala	Val	Val	Pro	Ile	Met	Ala	Lys	Ala	Pro	Gln	Gly	Val	His		
		65				70					75						
Leu	Ile	Cys	Tyr	Ser	Gln	Gly	Gly	Leu	Val	Cys	Arg	Ala	Leu	Leu	Ser		
80					85					90					95		
Val	Met	Asp	Asp	His	Asn	Val	Asp	Ser	Phe	Ile	Ser	Leu	Ser	Ser	Pro		
			100						105					110			
Gln	Met	Gly	Gln	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Lys	Trp	Leu	Phe	Pro		
			115					120					125				
Thr	Ser	Met	Arg	Ser	Asn	Leu	Tyr	Arg	Ile	Cys	Tyr	Ser	Pro				
		130					135						140				

<210> 316
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 316
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ser Leu Val Leu

	-15					-10					-5				
Cys	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala	Phe	Asp
1					5					10					15
Glu	Leu	Arg	Thr	Asp	Phe	Lys	Ser	Pro	Ile	Asp	Gln	Cys	Asn	Pro	Val
				20						25				30	
His	Ala	Arg	Glu	Arg	Leu	Arg	Asn	Ile	Glu	Arg	Ile	Cys	Phe	Leu	Leu
			35					40					45		
Arg	Lys	Leu	Val	Leu	Pro	Glu	Tyr	Ser	Ile	His	Ser	Leu	Phe	Cys	Ile
		50					55					60			
Met	Phe	Leu	Cys	Ala	Gln	Glu	Trp	Leu	Thr	Leu	Gly	Leu	Asn	Val	Pro
	65					70					75				
Leu	Leu	Phe	Tyr	His	Phe	Trp	Arg	Tyr	Phe	His	Cys	Pro	Ala	Asp	Ser
80					85					90					95
Ser	Glu	Leu	Ala	Tyr	Asp	Pro	Pro	Val	Val	Met	Asn	Pro	Asp	Thr	Leu
				100						105				110	
Ser	Tyr	Cys	Gln	Lys	Glu	Ala	Trp	Cys	Lys	Leu	Ala	Phe	Tyr	Leu	Leu
			115					120					125		
Ser	Phe	Phe	Tyr	Tyr	Leu	Tyr	Cys	Met	Ile	Tyr	Thr	Leu	Val	Ser	Ser
		130					135						140		

<210> 317
 <211> 426
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 317															
Met	Ser	Pro	Ala	Phe	Arg	Ala	Met	Asp	Val	Glu	Pro	Arg	Ala	Lys	Gly
			-25					-20					-15		
Val	Leu	Leu	Glu	Pro	Phe	Val	His	Gln	Val	Gly	Gly	His	Ser	Cys	Val
		-10					-5					1			
Leu	Arg	Phe	Asn	Glu	Thr	Thr	Leu	Cys	Lys	Pro	Leu	Val	Pro	Arg	Glu
5					10					15					20
His	Gln	Phe	Tyr	Glu	Thr	Leu	Pro	Ser	Glu	Met	Arg	Lys	Phe	Thr	Pro
			25						30					35	
Gln	Tyr	Lys	Gly	Val	Val	Ser	Val	Arg	Phe	Glu	Glu	Asp	Glu	Asp	Arg
			40					45					50		
Asn	Leu	Cys	Leu	Ile	Ala	Tyr	Pro	Leu	Lys	Gly	Asp	His	Gly	Ile	Val
		55					60					65			
Asp	Ile	Val	Asp	Asn	Ser	Asp	Cys	Glu	Pro	Lys	Ser	Lys	Leu	Leu	Arg
	70					75					80				
Trp	Thr	Thr	Asn	Lys	Lys	His	His	Val	Leu	Glu	Thr	Glu	Lys	Thr	Pro
85					90					95					100
Lys	Asp	Trp	Val	Arg	Gln	His	Arg	Lys	Glu	Glu	Lys	Met	Lys	Ser	His
				105					110					115	
Lys	Leu	Glu	Glu	Glu	Phe	Glu	Trp	Leu	Lys	Lys	Ser	Glu	Val	Leu	Tyr
			120					125					130		
Tyr	Thr	Val	Glu	Lys	Lys	Gly	Asn	Ile	Ser	Ser	Gln	Leu	Lys	His	Tyr
		135					140					145			
Asn	Pro	Trp	Ser	Met	Lys	Cys	His	Gln	Gln	Gln	Leu	Gln	Arg	Met	Lys
		150				155					160				

Glu	Asn	Ala	Lys	His	Arg	Asn	Gln	Tyr	Lys	Phe	Ile	Leu	Leu	Glu	Asn
165					170					175					180
Leu	Thr	Ser	Arg	Tyr	Glu	Val	Pro	Cys	Val	Leu	Asp	Leu	Lys	Met	Gly
				185					190						195
Thr	Arg	Gln	His	Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln
			200					205						210	
Ile	Arg	Lys	Cys	Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val
		215					220						225		
Cys	Gly	Met	Gln	Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met
	230					235					240				
Asn	Lys	Tyr	His	Gly	Arg	Lys	Leu	Ser	Val	Gln	Gly	Phe	Lys	Glu	Ala
245					250					255					260
Leu	Phe	Gln	Phe	Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu
				265					270						275
Gly	Pro	Val	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg
			280					285					290		
Gln	Glu	Ser	Tyr	Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp
		295					300					305			
Gly	Lys	Glu	Arg	Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu
	310					315					320				
Glu	Asp	Leu	Ser	Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala
325					330					335					340
Tyr	Lys	Pro	Ile	Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe
				345					350					355	
Ala	His	Thr	Thr	Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu
			360					365					370		
Gly	Gln	Asp	Ala	Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu	Ile	Asp	Ile
		375				380						385			
Val	Thr	Glu	Ile	Ser	Glu	Glu	Ser	Gly	Glu						
	390					395									

<210> 318
 <211> 301
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 318
 Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val
 -20 -15 -10 -5
 Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
 1 5 10
 Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
 15 20 25
 Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile
 30 35 40
 Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu
 45 50 55 60
 Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Leu Ser Phe Val Phe
 65 70 75
 Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met

<211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39..-1

<400> 320
 Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe Lys His
 -35 -30 -25
 Ala Phe Ala Asp Gly Ala Trp Asp Leu Ser Phe Leu Cys Ala Leu Cys
 -20 -15 -10
 Ser Phe Cys Pro Ile Ser Ala Ala Ser Gly Arg Pro Tyr Arg Tyr Leu
 -5 1 5
 Glu Phe Trp Arg Leu Tyr Leu Ser Pro Ser Ser Met Glu Asn Gly Val
 10 15 20 25
 Gln Lys Phe His Glu Thr Phe Phe Ile Val Phe Leu Leu Leu Phe Asp
 30 35 40
 Ile Glu Arg Lys Gly Lys Ser Ser Val Cys Pro Phe Cys Tyr Arg
 45 50 55

<210> 321
 <211> 191
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39..-1

<400> 321
 Met Met Thr Ile Thr Phe Leu Pro Tyr Thr Phe Ser Leu Met Val Thr
 -35 -30 -25
 Phe Pro Asp Val Pro Leu Gly Ile Phe Leu Phe Cys Val Cys Val Ile
 -20 -15 -10
 Ala Ile Gly Val Val Gln Ala Leu Ile Val Gly Tyr Ala Phe His Phe
 -5 1 5
 Pro His Leu Leu Ser Pro Gln Ile Gln Arg Ser Ala His Arg Ala Leu
 10 15 20 25
 Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln Gly Pro Ala Leu Cys
 30 35 40
 Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val Pro Leu Ser Tyr Leu
 45 50 55
 Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val Ser Lys Val Thr Gly
 60 65 70
 Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu Pro Ser Ala His Pro
 75 80 85
 Val Glu Val Phe Ser Phe Asp Leu His Glu Pro Leu Ser Lys Glu Arg
 90 95 100 105
 Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile Val Ala Thr Leu Leu
 110 115 120
 Ile Leu Asp Ile Cys Pro Ser Cys Ser Leu Trp Leu Ala Val Ala Ser
 125 130 135

Phe Gln Arg Leu Leu Leu Arg Gly Leu Ile Cys Leu Phe Val Cys
140 145 150

<210> 322
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41...-1

<400> 322
Met Pro Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp
-40 -35 -30
Asp Ser Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu
-25 -20 -15 -10
Ala Gln Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val
-5 1 5
Met Ser Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser
10 15 20
Gly Thr Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser
25 30 - 35
Ser Arg Leu Thr Phe Gln Arg Arg Phe
40 45

<210> 323
<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -38...-1

<400> 323
Met Ser Ser Pro Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu
-35 -30 -25
Thr Thr Ala Ile Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe
-20 -15 -10
Phe Thr Pro Leu Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys
-5 1 5 10
Val Thr Lys Asp Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys
15 20 25
Glu Ala Thr Trp Leu Pro
30

<210> 324
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -25...-1

<400> 324

```
Met Arg Gly Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu
-25          -20          -15          -10
Leu Val Val Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp
          -5          1          5
Glu Arg Leu Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu
10          15          20
Val Leu Ala Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met
25          30          35
Leu Ala Ala Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe
40          45          50          55
Leu Ile Ala Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala
60          65          70
Asp Leu Val Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala
75          80          85
Ala Pro Ala Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala
90          95          100
Thr Ala Met Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro
105          110          115
Gly Val Leu Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala
120          125          130          135
Cys Trp Ile Pro Ser Pro Pro Ala
          140
```

<210> 325

<211> 166

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -15...-1

<400> 325

```
Met Leu Pro Leu Leu Ile Ile Cys Leu Leu Pro Ala Ile Glu Gly Lys
-15          -10          -5          1
Asn Cys Leu Arg Cys Trp Pro Glu Leu Ser Ala Leu Ile Asp Tyr Asp
5          10          15
Leu Gln Ile Leu Trp Val Thr Pro Gly Pro Pro Thr Glu Leu Ser Gln
20          25          30
Asn Arg Asp His Leu Glu Glu Glu Thr Ala Lys Phe Phe Thr Gln Val
35          40          45
His Gln Ala Ile Lys Thr Leu Arg Asp Asp Lys Thr Val Leu Leu Glu
50          55          60          65
Glu Ile Tyr Thr His Lys Asn Leu Phe Thr Glu Arg Leu Asn Lys Ile
70          75          80
Ser Asp Gly Leu Lys Glu Lys Asp Ile Gln Ser Thr Leu Lys Val Thr
85          90          95
Ser Cys Ala Asp Cys Arg Thr His Phe Leu Ser Cys Asn Asp Pro Thr
100          105          110
Phe Cys Pro Ala Arg Asn Arg Arg Thr Ser Leu Trp Ala Val Ser Leu
115          120          125
```

Ser Ser Ala Leu Leu Leu Ala Ile Ala Gly Asp Val Ser Phe Thr Gly
 130 135 140 145
 Lys Gly Arg Arg Arg Gln
 150

<210> 326
 <211> 156
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 326
 Met Asn Ile Leu Met Leu Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg
 -15 -10 -5 1
 Val Thr Lys Gly Ser Phe Glu Pro Gln Lys Cys Trp Lys Asn Asn Val
 5 10 15
 Gly His Cys Arg Arg Arg Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu
 20 25 30
 Cys Arg Asn Lys Leu Ser Cys Cys Ile Ser Ile Ile Ser His Glu Tyr
 35 40 45
 Thr Arg Arg Pro Ala Phe Pro Val Ile His Leu Glu Asp Ile Thr Leu
 50 55 60 65
 Asp Tyr Ser Asp Val Asp Ser Phe Thr Gly Ser Pro Val Ser Met Leu
 70 75 80
 Asn Asp Leu Ile Thr Phe Asp Thr Thr Lys Phe Gly Glu Thr Met Thr
 85 90 95
 Pro Glu Thr Asn Thr Pro Glu Thr Thr Met Pro Pro Ser Glu Ala Thr
 100 105 110
 Thr Pro Glu Thr Thr Met Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr
 115 120 125
 Met Pro Pro Pro Ser Gln Thr Ala Leu Thr His Asn
 130 135 140

<210> 327
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 327
 Met Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu
 -30 -25 -20
 Ser Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys
 -15 -10 -5
 Leu Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp
 1 5 10 15
 Ala Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr
 20 25 30

Asn	Ser	Gln	Ala	Lys	Ala	Thr	Thr	Met	Glu	Ser	Cys	Pro	Ser	Leu	Gln
		35					40					45			
Cys	Cys	Glu	Gly	Cys	Arg	Met	His	Ala	Ser	Ser	Asp	Ser	Leu	Pro	Pro
	50					55					60				
Cys	Cys	Cys	Asp	Ile	Asn	Glu	Gly	Leu							
65					70										

<210> 328
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

Met	Ser	Asp	Glu	Asp	Glu	Ser	Ser	Asp	Tyr	Leu	Cys	Leu	Ser	Ile	Leu
		-25				-20					-15				
Gly	Leu	Phe	Cys	Cys	Leu	Pro	Leu	Ala	Ile	Pro	Ala	Val	Ile	Phe	Ser
	-10				-5					1				5	
Cys	Leu	Thr	Lys	Asn	Tyr	Asn	Lys	Ser	Ser	Asp	Tyr	Glu	Leu	Ala	Ala
			10					15					20		
Lys	Thr	Ser	Lys	Gln	Ala	Tyr	Tyr	Trp	Ala	Ile	Ala	Ser	Ile	Thr	Val
		25					30					35			
Gly	Ile	Leu	Gly	Thr	Ile	Leu	Tyr	Thr	Tyr	Leu	Ile	Tyr	Leu	Leu	Arg
	40					45					50				

Leu

<210> 329
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27..-1

Met	Thr	Asp	Gln	Asp	Arg	Ile	Ile	Asn	Leu	Val	Val	Gly	Ser	Leu	Thr
		-25				-20						-15			
Ser	Leu	Leu	Ile	Leu	Val	Thr	Leu	Ile	Ser	Ala	Phe	Val	Phe	Pro	Gln
	-10				-5					1				5	
Leu	Pro	Pro	Lys	Pro	Leu	Asn	Ile	Phe	Phe	Ala	Val	Cys	Ile	Ser	Leu
			10					15					20		
Ser	Ser	Ile	Thr	Ala	Cys	Ile	Ile	Tyr	Trp	Tyr	Arg	Gln	Gly	Asp	Leu
		25					30					35			
Glu	Pro	Lys	Phe	Arg	Lys	Leu	Ile	Tyr	Tyr	Ile	Ile	Phe	Ser	Ile	Ile
	40					45					50				
Met	Leu	Cys	Ile	Cys	Ala	Asn	Leu	Tyr	Phe	His	Asp	Val	Gly	Arg	
	55					60					65				

<210> 330
 <211> 84

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 330
 Met Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His
 -20 -15 -10 -5
 Gln Gly Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly
 1 5 10
 Val Leu His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys
 15 20 25
 Ser Arg Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser
 30 35 40
 Leu Cys Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn
 45 50 55 60
 Thr Val Arg Thr

<210> 331
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32..-1

<400> 331
 Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly Val Pro
 -30 -25 -20
 Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu Phe Ala
 -15 -10 -5
 Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys Lys Phe
 1 5 10 15
 Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys Asp Lys
 20 25 30
 Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly Cys Pro
 35 40 45
 Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn Gly Met
 50 55 60
 Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro Arg Asp
 65 70 75 80
 Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val
 85 90

<210> 332
 <211> 62
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -46...-1

<400> 332

```
Met Asp Gln Leu Val Phe Lys Glu Thr Ile Trp Asn Asp Ala Phe Trp
   -45               -40               -35
Gln Asn Pro Trp Asp Gln Gly Gly Leu Ala Val Ile Ile Leu Phe Ile
-30               -25               -20               -15
Thr Ala Val Leu Leu Ile Leu Phe Ala Ile Val Phe Gly Leu Leu
               -10               -5               1
Thr Ser Thr Glu Asn Thr Gln Cys Glu Ala Gly Glu Glu Glu
      5               10               15
```

<210> 333

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 333

```
Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
   -20               -15               -10
Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys
   -5               1               5
Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly Cys
10               15               20               25
Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe
               30               35               40
Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys
   45               50               55
Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu
   60               65               70
Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr
   75               80               85
Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro
90               95               100               105
Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu
               110               115               120
Glu Gly Ala Arg Arg Tyr
               125
```

<210> 334

<211> 198

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -13...-1

<400> 334

```
Met Leu Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp
```


<220>
 <221> SIGNAL
 <222> -45...-1

<400> 336
 Met Val Leu Met Trp Thr Ser Gly Asp Ala Phe Lys Thr Ala Tyr Phe
 -45 -40 -35 -30
 Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser Val Cys Gly Leu Leu Gln
 -25 -20 -15
 Val Leu Val Asp Leu Ala Ile Leu Gly Gln Ala Tyr Ala Phe Ala Pro
 -10 -5 1
 Pro Pro Glu Ala Gly Ala Pro Arg Arg Ala Pro His Trp His Gln Gly
 5 10 15
 Pro Leu Thr Val Gly Arg Thr Arg Met Trp Asp Arg Gln Pro Arg Ala
 20 25 30 35
 Leu Val Gly Pro Asp Leu Pro Ala Gly Arg Val Gly Ala Val Ala Pro
 40 45 50
 Ala Gly Val Ala Glu Met Gly His Gly His Trp Gly Leu His Gln Pro
 55 60 65
 Leu Trp Gly Val Ser Gly Trp Ala Val Gly Val Gly Leu Gly Arg Cys
 70 75 80
 Leu Cys Ser Ala Gly Thr Ala Arg Val Asp Leu Ala Pro Arg Val Leu
 85 90 95
 Asp Val Phe Arg Met Thr
 100 105

<210> 337
 <211> 142
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 337
 Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn Gly Gln
 -15 -10 -5
 Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr
 1 5 10
 Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu Glu Glu
 15 20 25
 Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln Ala Leu
 30 35 40 45
 Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn Pro Tyr
 50 55 60
 Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val Phe Gly
 65 70 75
 Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe Ser Pro
 80 85 90
 Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser Thr Ser
 95 100 105
 Lys Leu Gln Lys Phe Thr Arg Ser Ala Ser Cys Ser Thr His
 110 115 120

<210> 338
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<220>
 <221> UNSURE
 <222> 21
 <223> Xaa = Ala,Pro

<400> 338
 Thr Ser Glu Glu Arg Thr Ala Met Lys Arg Glu Gly Gly Ala Ala His
 -25 -20 -15
 Leu Cys Ser Asp Ser Leu Pro Glu Ser Gln Gln Gln Asp Gly Asn His
 -10 -5 1 5
 Ala Pro Asn Phe Ser Ser His Gly Ser Cys Arg Arg Arg Gln Arg Xaa
 10 15 20
 Asp Met Thr Arg Arg Cys Met Pro Ala Arg Pro Gly Phe Pro Ser Ser
 25 30 35
 Pro Ala Pro Gly Ser Ser Pro Pro Arg Cys His Leu Arg Pro Gly Ser
 40 45 50
 Thr Ala His Ala Ala Ala Gly Lys Arg Thr Glu Ser Pro Gly Asp Arg
 55 60 65
 Tyr Arg Ala Glu Gly Leu Arg Arg Gly Arg Val Ala Gly Ala Arg Val
 70 75 80 85

<210> 339
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 339
 Met Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro
 -30 -25 -20
 Ala Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly Phe Leu Thr Ala
 -15 -10 -5
 Gln Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp Arg Tyr Thr Leu
 1 5 10 15
 Val Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu
 20 25 30
 Val Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His
 35 40 45
 Gln Ser Ile Thr Val Ala Asp Thr Asn Lys
 50 55

<210> 340
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35..-1

<400> 340
 Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly
 -35 -30 -25 -20
 Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala
 -15 -10 -5
 Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro
 1 5 10
 Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala
 15 20 25
 Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
 30 35 40 45

<210> 341
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15..-1

<400> 341
 Met Ser Leu Leu Met Phe Thr Gln Leu Leu Leu Cys Gly Phe Leu Tyr
 -15 -10 -5 1
 Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe Pro Pro Arg
 5 10 15
 Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly Glu Pro Thr
 20 25 30
 Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr Ile Glu Trp
 35 40 45
 Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp Pro Arg Ser
 50 55 60 65
 His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu Arg Ile Val
 70 75 80
 His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val Cys Val Ala
 85 90 95
 Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser Leu Glu Val
 100 105 110
 Ala Cys Lys
 115

<210> 342
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 342
 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
 -5 1 5
 Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
 10 15 20 25
 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
 Leu Leu Leu
 60

<210> 343
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

<400> 343
 Met Cys Glu Thr Leu Leu Thr Ser Lys Trp Ala Ser Val Ser Pro Ile
 -40 -35 -30
 Pro Ala Leu Leu Gln Glu Gly Glu Asn Arg Asp Ser Arg Arg Leu Gly
 -25 -20 -15
 Asp Ala Leu Leu Phe Leu Arg Pro Ala Gly Ser Cys Ala Leu Gln Val
 -10 -5 1 5
 Ser Trp Pro Ala Ala Leu Ala Gly Pro Arg Ser His Thr Gly Gln Leu
 10 15 20
 Thr Gln His Phe Cys His Leu Lys Asn Asp Thr Cys Ile Pro Pro Ser
 25 30 35
 Leu Gly Pro Pro Arg Asn Ser Gly Ser Leu Glu Ser Leu Arg Ser Lys
 40 45 50
 Arg Tyr
 55

<210> 344
 <211> 217
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<220>
 <221> UNSURE
 <222> 185
 <223> Xaa = Phe,Val

<400> 344
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser Leu
 -15 -10 -5
 Cys Cys Ser Ser Tyr Val Pro Ser Val Ala Pro Thr Ala Ala His Ser
 1 5 10
 Val Arg Val Pro His Ser Ala Gly His Cys Gly Gln Arg Val Leu Ala
 15 20 25
 Cys Ser Leu Pro Gln Val Phe Leu Lys Pro Trp Ile Phe Val Glu His
 30 35 40 45
 Phe Ser Ser Trp Leu Ser Leu Glu Leu Phe Ser Phe Leu Arg Tyr Leu
 50 55 60
 Gly Thr Leu Leu Cys Ala Cys Gly His Arg Leu Arg Glu Gly Arg Leu
 65 70 75
 Leu Pro Cys Leu Leu Gly Val Gly Ser Trp Leu Leu Phe Asn Asn Trp
 80 85 90
 Thr Gly Gly Ser Trp Phe Ser Leu His Leu Gln Gln Val Ser Leu Ser
 95 100 105
 Gln Gly Ser His Val Ala Ala Phe Leu Pro Glu Ala Ile Gly Pro Gly
 110 115 120 125
 Val Pro Val Pro Val Ser Gly Glu Ser Thr Ser Ala Gln Gln Ser His
 130 135 140
 Ala Gly Trp Gln Leu Ser Ala Glu Ala Asp Ala Cys Pro Ser Val Leu
 145 150 155
 Tyr Ser Glu Val Leu Glu Trp Asn Lys Asn Ile Asn Thr Tyr Thr Ser
 160 165 170
 Phe His Asp Phe Cys Leu Ile Leu Gly Ile Phe Xaa Val Leu Phe Cys
 175 180 185
 Phe Gly Gly Asp Arg Leu Thr Leu His
 190 195

<210> 345
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 345
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 -20 -15 -10 -5
 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 1 5 10
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 15 20 25
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 30 35 40

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
 45 50 55 60
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 65 70 75
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 80 85 90
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 95 100 105
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
 110 115 120
 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 125 130 135 140
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
 145 150 155
 Asp Arg His Lys Met Leu Ser
 160

<210> 346
 <211> 247
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 346
 Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr
 -10 -5 1
 Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
 5 10 15
 Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys
 20 25 30 35
 Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala His Leu Arg Thr
 40 45 50
 Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Glu Phe Gly Gly Arg
 55 60 65
 Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg
 70 75 80
 Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln
 85 90 95
 Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys Gln Glu Ser Glu Ile
 100 105 110 115
 Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys Pro Pro Lys Glu Gly
 120 125 130
 Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro Gly Gly Pro Ala Leu
 135 140 145
 Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala His Val Asn Leu Gly
 150 155 160
 Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu Tyr Gly Ala Leu Asn
 165 170 175
 Arg Val His Val Leu Trp Trp Asn Glu Ser Ala Asp Ser Arg Ala Ala
 180 185 190 195
 Gly Arg His Lys Ser His Glu Asp Pro Arg Val Val Ala Ala Val Arg

				200						205				210
Glu	Ser	Val	Asn	Tyr	Leu	Val	Ser	Gln	Gln	Asn	Met	Leu	Leu	Ile
			215					220					225	
Thr	Ser	Phe	Ser	Pro	Leu	Lys								
			230											

<210> 347
 <211> 104
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47...-1

<400> 347

Met	Phe	Ser	Pro	Arg	Gln	Ala	Leu	Thr	Pro	Asp	Pro	Leu	His	Ser	Pro
		-45					-40					-35			
Ala	Tyr	Ser	Pro	Val	Leu	Gly	Gly	Trp	Ser	Arg	Phe	Arg	Ser	Val	Asp
	-30					-25					-20				
Phe	Arg	Phe	Leu	Tyr	Leu	Thr	Leu	Asn	Gln	Ser	Cys	Ile	Phe	Ala	Asn
-15					-10					-5					1
Tyr	Lys	Glu	Ala	His	Ala	Asn	Arg	Tyr	Cys	Thr	Glu	Gly	Arg	Tyr	Thr
			5					10					15		
Arg	Glu	Ile	Gln	Arg	Leu	Thr	Ser	Pro	Ala	Ala	Trp	Pro	Thr	Arg	Asp
		20					25					30			
Lys	Asn	Arg	Met	Ile	Ser	Asn	Gly	Met	Ala	Leu	Asn	Ser	Pro	Ala	Glu
	35					40					45				
Gly	Leu	Ala	Phe	Gln	Cys	Arg	Phe								
50						55									

<210> 348
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 348

Met	Ala	Lys	Tyr	Leu	Ala	Gln	Ile	Ile	Val	Met	Gly	Val	Gln	Val	Val
	-20					-15					-10				
Gly	Arg	Ala	Phe	Ala	Arg	Ala	Leu	Arg	Gln	Glu	Phe	Ala	Ala	Ser	Arg
-5					1				5					10	
Ala	Ala	Ala	Asp	Ala	Arg	Gly	Arg	Ala	Gly	His	Arg	Ser	Ala	Ala	Ala
			15					20					25		
Ser	Asn	Leu	Ser	Gly	Leu	Ser	Leu	Gln	Glu	Ala	Gln	Gln	Ile	Leu	Asn
		30					35					40			
Val	Ser	Lys	Leu	Ser	Pro	Glu	Glu	Val	Gln	Lys	Asn	Tyr	Glu	His	Leu
	45					50					55				
Phe	Lys	Val	Asn	Asp	Lys	Ser	Val	Gly	Gly	Ser	Phe	Tyr	Leu	Gln	Ser
60					65					70					75
Lys	Val	Val	Arg	Ala	Lys	Glu	Arg	Leu	Asp	Glu	Glu	Leu	Lys	Ile	Gln

				80						85				90
Ala	Gln	Glu	Asp	Arg	Glu	Lys	Gly	Gln	Met	Pro	His	Thr		
			95					100						

<210> 349
 <211> 302
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 349

Met	Ala	Pro	Asn	Ser	Ile	Thr	Leu	Leu	Gly	Leu	Ala	Val	Asn	Val	Val
			-15					-10					-5		
Thr	Thr	Leu	Val	Leu	Ile	Ser	Tyr	Cys	Pro	Thr	Ala	Thr	Glu	Glu	Ala
		1			5					10					
Pro	Tyr	Trp	Thr	Tyr	Leu	Leu	Cys	Ala	Leu	Gly	Leu	Phe	Ile	Tyr	Gln
15				20					25					30	
Ser	Leu	Asp	Ala	Ile	Asp	Gly	Lys	Gln	Ala	Arg	Arg	Thr	Asn	Ser	Cys
			35					40					45		
Ser	Pro	Leu	Gly	Glu	Leu	Phe	Asp	His	Gly	Cys	Asp	Ser	Leu	Ser	Thr
		50					55					60			
Val	Phe	Met	Ala	Val	Gly	Ala	Ser	Ile	Ala	Ala	Arg	Leu	Gly	Thr	Tyr
	65					70					75				
Pro	Asp	Trp	Phe	Phe	Phe	Cys	Ser	Phe	Ile	Gly	Met	Phe	Val	Phe	Tyr
	80					85			90						
Cys	Ala	His	Trp	Gln	Thr	Tyr	Val	Ser	Gly	Met	Leu	Arg	Phe	Gly	Lys
95				100					105					110	
Val	Asp	Val	Thr	Glu	Ile	Gln	Ile	Ala	Leu	Val	Ile	Val	Phe	Val	Leu
			115					120					125		
Ser	Ala	Phe	Gly	Gly	Ala	Thr	Met	Trp	Asp	Tyr	Thr	Gly	Thr	Ser	Val
		130				135					140				
Leu	Ser	Pro	Gly	Leu	His	Ile	Gly	Leu	Ile	Ile	Ile	Leu	Ala	Ile	Met
	145				150				155						
Ile	Tyr	Lys	Lys	Ser	Ala	Thr	Asp	Val	Phe	Glu	Lys	His	Pro	Cys	Leu
	160			165					170						
Tyr	Ile	Leu	Met	Phe	Gly	Cys	Val	Phe	Ala	Lys	Val	Ser	Gln	Lys	Leu
175				180					185					190	
Val	Val	Ala	His	Met	Thr	Lys	Ser	Glu	Leu	Tyr	Leu	Gln	Asp	Thr	Val
			195					200					205		
Phe	Leu	Gly	Pro	Gly	Leu	Leu	Phe	Leu	Asp	Gln	Tyr	Phe	Asn	Asn	Phe
		210				215						220			
Ile	Asp	Glu	Tyr	Val	Val	Leu	Trp	Met	Ala	Met	Val	Ile	Ser	Ser	Phe
	225					230					235				
Asp	Met	Val	Ile	Tyr	Phe	Ser	Ala	Leu	Cys	Leu	Gln	Ile	Ser	Arg	His
	240				245					250					
Leu	His	Leu	Asn	Ile	Phe	Lys	Thr	Ala	Cys	His	Gln	Ala	Pro	Glu	Gln
255				260					265					270	
Val	Gln	Val	Leu	Ser	Lys	Ser	His	Gln	Asn	Asn	Met	Asp			
			275					280							

<210> 350

<211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 350
 Met Ile Leu Val Thr Val Pro Gly Val Cys Pro Ala Gln Cys Cys Trp
 -10 -5 1
 Ala Glu Gln Arg Gly Arg Gly Ser Gly Met Tyr Phe Ile Asp Lys Trp
 5 10 15
 Ala Arg Pro Ser Trp Val Pro His Trp Leu Asn Asp Leu Phe Ile Val
 20 25 30
 Lys Ser Gly Tyr Leu Val Cys Ile Arg Thr Thr Val Ile Arg Gln Gly
 35 40 45 50
 Ile Val Arg Ile Gly Arg Asn Lys Ile Ser Glu Ser Gly Arg Ser Ala
 55 60 65
 Leu Tyr Thr Ile Ala Lys Asn Lys Met Val Ile Phe Lys Val Pro Asp
 70 75 80
 Cys Met His Leu Asn Ala Asp Tyr Phe Gly Val
 85 90

<210> 351
 <211> 229
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 351
 Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
 -30 -25 -20
 Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Ala
 -15 -10 -5
 Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
 1 5 10
 Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
 15 20 25 30
 Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
 35 40 45
 Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
 50 55 60
 Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
 65 70 75
 Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
 80 85 90
 Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
 95 100 105 110
 Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
 115 120 125

<221> SIGNAL
 <222> -44...-1

<400> 353
 Met Ala Ala Glu Gly Trp Ile Trp Arg Trp Gly Trp Gly Arg Arg Cys
 -40 -35 -30
 Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly Pro Thr Thr Pro
 -25 -20 -15
 Leu Phe Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp
 -10 -5 1
 Gly Asn Ile Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr
 5 10 15 20
 Gln Gly Val Gly Ser Ser Ser Pro Ser Gly Thr Ser Arg Ala Ala Leu
 25 30 35
 Cys Ser Arg Ala Ser Thr Tyr Val
 40

<210> 354
 <211> 151
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 354
 Met Asp Ser Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg
 -30 -25 -20
 His Arg Pro Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser
 -15 -10 -5
 Ala Val Arg Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu
 1 5 10 15
 Arg Arg Asp Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser
 20 25 30
 Asp Arg Tyr Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp
 35 40 45
 Pro Ser Ser Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala
 50 55 60
 Asp Pro Gln Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile
 65 70 75 80
 Asp Gly Lys Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr
 85 90 95
 Met Gly Leu Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp
 100 105 110
 Arg Leu Lys Gln Gly Lys Phe
 115

<210> 355
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
 <222> -16...-1

<400> 355
 Met Ala Glu Leu Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala
 -15 -10 -5
 Cys Lys Val Arg Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly
 1 5 10 15
 His Val Met Leu Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser
 20 25 30
 Arg Pro Arg Cys Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr
 35 40 45
 Leu

<210> 356
 <211> 189
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<220>
 <221> UNSURE
 <222> 41
 <223> Xaa = Ala,Gly

<400> 356
 Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
 -20 -15 -10
 Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
 -5 1 5
 Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
 10 15 20
 Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
 25 30 35 40
 Xaa Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
 45 50 55
 Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu
 60 65 70
 Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala
 75 80 85
 Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly
 90 95 100
 Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg
 105 110 115 120
 Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr
 125 130 135
 His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly
 140 145 150
 Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser Leu
 155 160 165

<210> 357
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

<400> 357
 Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro Phe Ala Phe Glu
 -45 -40 -35
 Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser Leu Ser Asp Pro
 -30 -25 -20
 Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met Ala Leu Cys Ala
 -15 -10 -5 1
 Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys Lys Leu Ile Leu
 5 10 15
 Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile Val Ala Leu Leu
 20 25 30
 Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser Lys Glu Gln Gln
 35 40 45
 Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu Cys Gly Gly Val
 50 55 60 65
 Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser Ser Asp Ser Ser
 70 75 80
 Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr Arg His His Ala
 85 90 95
 Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser Pro Tyr Trp Pro
 100 105 110
 Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu Pro Gln Pro Pro
 115 120 125
 Lys Val Leu Gly Leu Pro Ala
 130 135

<210> 358
 <211> 102
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14..-1

<400> 358
 Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
 -10 -5 1
 Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
 5 10 15
 Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
 20 25 30
 Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala
 35 40 45 50
 Val Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser

				55					60				65		
Lys	Phe	Pro	Pro	His	Arg	Phe	Ile	Ala	Asp	Gln	Leu	Asp	His	Leu	Asn
			70					75					80		
Val	Thr	Lys	Lys	Trp	Ser										
			85												

<210> 359
 <211> 244
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29..-1

Met	Glu	Leu	Thr	Ile	Phe	Ile	Leu	Arg	Leu	Ala	Ile	Tyr	Ile	Leu	Thr
				-25					-20					-15	
Phe	Pro	Leu	Tyr	Leu	Leu	Asn	Phe	Leu	Gly	Leu	Trp	Ser	Trp	Ile	Cys
			-10					-5					1		
Lys	Lys	Trp	Phe	Pro	Tyr	Phe	Leu	Val	Arg	Phe	Thr	Val	Ile	Tyr	Asn
	5					10					15				
Glu	Gln	Met	Ala	Ser	Lys	Lys	Arg	Glu	Leu	Phe	Ser	Asn	Leu	Gln	Glu
20					25					30				35	
Phe	Ala	Gly	Pro	Ser	Gly	Lys	Leu	Ser	Leu	Leu	Glu	Val	Gly	Cys	Gly
				40					45					50	
Thr	Gly	Ala	Asn	Phe	Lys	Phe	Tyr	Pro	Pro	Gly	Cys	Arg	Val	Thr	Cys
			55					60					65		
Ile	Asp	Pro	Asn	Pro	Asn	Phe	Glu	Lys	Phe	Leu	Ile	Lys	Ser	Ile	Ala
		70					75					80			
Glu	Asn	Arg	His	Leu	Gln	Phe	Glu	Arg	Phe	Val	Val	Ala	Ala	Gly	Glu
	85					90				95					
Asn	Met	His	Gln	Val	Ala	Asp	Gly	Ser	Val	Asp	Val	Val	Val	Cys	Thr
100					105				110					115	
Leu	Val	Leu	Cys	Ser	Val	Lys	Asn	Gln	Glu	Arg	Ile	Leu	Arg	Glu	Val
				120					125					130	
Cys	Arg	Val	Leu	Arg	Pro	Gly	Gly	Ala	Phe	Tyr	Phe	Met	Glu	His	Val
			135					140					145		
Ala	Ala	Glu	Cys	Ser	Thr	Trp	Asn	Tyr	Phe	Trp	Gln	Gln	Val	Leu	Asp
		150					155					160			
Pro	Ala	Trp	His	Leu	Leu	Phe	Asp	Gly	Cys	Asn	Leu	Thr	Arg	Glu	Ser
		165				170					175				
Trp	Lys	Ala	Leu	Glu	Arg	Ala	Ser	Phe	Ser	Lys	Leu	Lys	Leu	Gln	His
180					185					190				195	
Ile	Gln	Ala	Pro	Leu	Ser	Trp	Glu	Leu	Val	Arg	Pro	His	Ile	Tyr	Gly
				200					205					210	
Tyr	Ala	Val	Lys												
			215												

<210> 360
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 360
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
 -20 -15 -10
 Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys
 -5 1 5
 Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val Lys
 10 15 20 25
 Gly Ser Pro Ser His Cys Leu Pro Tyr Leu Leu Asp Lys Leu Cys Cys
 30 35 40
 Asp Phe Ala Asn Met Asp Ile Phe Gln Gly Cys Leu Tyr Leu Ile Tyr
 45 50 55
 Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe Val Leu Ser Val His
 60 65 70
 Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys Lys Leu Lys Lys Gln
 75 80 85
 Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu Ser Pro Leu Ile Asn
 90 95 100 105
 Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr Thr Ala Ser Val Ile
 110 115 120
 Tyr Lys Ile Trp Glu His Arg Ser His His Pro Ser Ser Lys Lys Ile
 125 130 135
 Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu Glu Gly Ala Arg Arg
 140 145 150
 Tyr

<210> 361
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 361
 Met Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala
 -20 -15 -10
 Pro Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln
 -5 1 5 10
 Met Met Asn Asn Gly Leu Leu Gln Gln Pro Ser Ala Leu Met Leu Leu
 15 20 25
 Pro Cys Arg Pro Val Leu Thr Ser Val Ala Leu Asn Ala Asn Phe Val
 30 35 40
 Ser Trp Lys Ser Arg Thr Lys Tyr Thr Ile Thr Pro Val Lys Met Arg
 45 50 55
 Lys Ser Gly Gly Arg Asp His Thr Gly Ala Gly Asn Val Arg Arg Thr
 60 65 70 75
 Val Gly Arg Val Ser Asn Val Asp His Asn Lys Arg Val Ile Gly Lys
 80 85 90
 Ala Gly Arg Asn Arg Trp Leu Gly Lys Arg Pro Asn Ser Gly Arg Trp

			95					100				105					
His	Arg	Lys	Gly	Gly	Trp	Ala	Gly	Arg	Lys	Ile	Arg	Pro	Leu	Pro	Pro		
		110					115					120					
Met	Lys	Ser	Tyr	Val	Lys	Leu	Pro	Ser	Ala	Ser	Ala	Gln	Ser				
	125					130					135						

<210> 362
 <211> 186
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400>	362																
Met	Ala	Thr	Ala	Ser	Pro	Ser	Val	Phe	Leu	Leu	Met	Val	Asn	Gly	Gln		
				-15				-10					-5				
Val	Glu	Ser	Ala	Gln	Phe	Pro	Glu	Tyr	Asp	Asp	Leu	Tyr	Cys	Lys	Tyr		
		1				5					10						
Cys	Phe	Val	Tyr	Gly	Gln	Asp	Trp	Ala	Pro	Thr	Ala	Gly	Leu	Glu	Glu		
	15				20				25								
Gly	Ile	Ser	Gln	Ile	Thr	Ser	Lys	Ser	Gln	Asp	Val	Arg	Gln	Ala	Leu		
30				35					40						45		
Val	Trp	Asn	Phe	Pro	Ile	Asp	Val	Thr	Phe	Lys	Ser	Thr	Asn	Pro	Tyr		
		50						55					60				
Gly	Trp	Pro	Gln	Ile	Val	Leu	Ser	Val	Tyr	Gly	Pro	Asp	Val	Phe	Gly		
		65				70						75					
Asn	Asp	Val	Val	Arg	Gly	Tyr	Gly	Ala	Val	His	Val	Pro	Phe	Ser	Pro		
	80					85					90						
Gly	Arg	His	Lys	Arg	Thr	Ile	Pro	Met	Phe	Val	Pro	Glu	Ser	Thr	Ser		
	95				100						105						
Lys	Leu	Gln	Lys	Phe	Thr	Ser	Trp	Phe	Met	Gly	Arg	Arg	Pro	Glu	Tyr		
110				115					120					125			
Thr	Asp	Pro	Lys	Val	Val	Ala	Gln	Gly	Glu	Gly	Arg	Glu	Ala	Ile	Thr		
			130			135							140				
Ala	Pro	Arg	Lys	Ala	Val	Phe	Ser	Val	His	Gly	Leu	Thr	Ser	Pro	Arg		
		145				150						155					
Ala	Leu	Ala	Leu	Val	His	Ile	Lys	Gly	Thr								
	160					165											

<210> 363
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -47..-1

<400>	363																
Met	Gly	Asp	Arg	Val	Lys	Gly	Ser	Lys	Ser	Arg	Ala	Phe	Val	Ser	Pro		
	-45					-40					-35						
Trp	Pro	His	Thr	Pro	Met	Ala	Ser	Gly	Leu	Arg	Asp	Pro	Trp	Leu	Gln		

-30 -25 -20
 Pro Thr Ala Leu Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val
 -15 -10 -5 1
 Gly Ser Ala Pro Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala
 5 10 15
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
 20 25 30
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
 35 40 45
 Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg
 50 55 60 65
 Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
 70 75 80
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
 85 90 95
 Pro Gly Ile His Leu Cys
 100

<210> 364
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -45...-1

<400> 364
 Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu Leu His Leu
 -45 -40 -35 -30
 Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser Val Ser Ala
 -25 -20 -15
 Phe Ile Leu Leu Leu Leu Leu Ser Gly Pro Ala Glu Met Ser Ala Ser
 -10 -5 1
 Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala Ser Leu Ile
 5 10 15
 Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser Thr Leu Leu
 20 25 30 35
 Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val Asn Leu
 40 45 50

<210> 365
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 365
 Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln Gly Phe Cys Gly
 -25 -20 -15
 Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe Phe Lys Lys Asn

-10				-5					1			5		
Ala	Cys	Leu	Leu	Arg	Glu	Ile	Leu	Gln	Ser	Lys	Leu	Gly	Gly	Met Gly
		10						15				20		
Pro	Val	Val	Phe	Ser	Tyr	Arg	Gly	Leu	Pro	Leu	Trp	Leu	Phe	Ala Trp
		25					30				35			
Leu	Phe	Pro	Arg	Cys	Thr	Val	Pro	Leu	Thr	Phe	Gly	Phe	Glu	Asn Met
	40					45				50				
Arg	Gly	Leu	Gly	Val	Val	Ala	Tyr	Ala	Cys	Asn	Pro	Ser	Thr	
55					60					65				

<210> 366
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40...-1

<400> 366														
Met	Thr	Ser	Met	Thr	Gln	Ser	Leu	Arg	Glu	Val	Ile	Lys	Ala	Met Thr
-40					-35				-30					-25
Lys	Ala	Arg	Asn	Phe	Glu	Arg	Val	Leu	Gly	Lys	Ile	Thr	Leu	Val Ser
			-20					-15						-10
Ala	Ala	Pro	Gly	Lys	Val	Ile	Cys	Glu	Met	Lys	Val	Glu	Glu	Glu His
		-5					1				5			
Thr	Asn	Ala	Ile	Gly	Thr	Leu	His	Gly	Gly	Leu	Thr	Ala	Thr	Leu Val
10					15					20				
Asp	Asn	Ile	Ser	Thr	Met	Ala	Leu	Leu	Cys	Thr	Glu	Arg	Gly	Ala Pro
25					30				35					40
Gly	Val	Ser	Val	Asp	Met	Asn	Ile	Thr	Tyr	Met	Ser	Pro	Ala	Lys Leu
			45					50					55	
Gly	Glu	Asp	Ile	Val	Ile	Thr	Ala	His	Val	Leu	Lys	Gln	Gly	Lys Thr
		60				65						70		
Leu	Ala	Phe	Thr	Ser	Val	Asp	Leu	Thr	Asn	Lys	Ala	Thr	Gly	Lys Leu
	75					80						85		
Ile	Ala	Gln	Gly	Arg	His	Thr	Lys	His	Leu	Gly	Asn			
90					95					100				

<210> 367
 <211> 39
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35...-1

<400> 367														
Met	Asp	Pro	Gly	Trp	Pro	His	Phe	Lys	Leu	Thr	His	Ser	Arg	Cys Met
-35					-30				-25					-20
Ala	Val	Leu	Phe	Leu	Gly	Thr	Leu	Pro	Leu	Cys	Pro	Val	Thr	Ser Pro
			-15					-10					-5	
Val	Trp	Gly	Trp	Ser	Pro	Gly								

1

<210> 368
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 368
Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr
-40 -35 -30
Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu
-25 -20 -15 -10
Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val
-5 1 5
Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val
10 15 20
Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly
25 30 35

<210> 369
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40..-1

<400> 369
Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
-40 -35 -30 -25
Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
-20 -15 -10
Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
-5 1 5
Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
10 15 20
Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
25 30 35 40
Lys Ser Lys

<210> 370
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 370

```
Met Ala Val Leu Ala Gly Ser Leu Leu Gly Pro Thr Ser Arg Ser Ala
-15          -10          -5          1
Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro Arg Ala Trp Leu Gly Phe
      5          10          15
Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln Gln Ala Arg Gly Lys Ala
      20          25          30
Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile Lys Arg Lys Asn Lys His
      35          40          45
Gly Trp Val Arg Arg Leu Ser Thr Pro Ala Gly Val Gln Val Ile Leu
50          55          60          65
Arg Arg Met Leu Lys Gly Arg Lys Ser Leu Ser His
      70          75
```

<210> 371

<211> 279

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42...-1

<400> 371

```
Met Ala Ala Pro Val Arg Arg Thr Leu Leu Gly Val Ala Gly Gly Trp
      -40          -35          -30
Arg Arg Phe Glu Arg Leu Trp Ala Gly Ser Leu Ser Ser Arg Ser Leu
      -25          -20          -15
Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp Arg Leu Leu
      -10          -5          1          5
Gly Ala Leu Cys Leu Gln Arg Pro Pro Val Val Ser Lys Pro Leu Thr
      10          15          20
Pro Leu Gln Glu Glu Met Ala Ser Leu Leu Gln Gln Ile Glu Ile Glu
      25          30          35
Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp Glu Asn Gln
      40          45          50
Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu Asp Glu Gln
55          60          65          70
Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu Gln Lys Phe
      75          80          85
Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp Glu Lys Asn
      90          95          100
Asp Arg Thr Ser Leu Asn Arg Asn Leu Asp Arg Asn Leu Val Leu Leu
      105          110          115
Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu Pro Gln Ala
      120          125          130
Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu Arg Thr Leu
135          140          145          150
Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu Gly Asn Ala
      155          160          165
Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met Arg Thr Glu
      170          175          180
Ser Asn Leu Gly Ala Lys Val Phe Phe Lys Ala Leu Leu Leu Thr
      185          190          195
```


Gly	Asp	Phe	Ser	Gln	Ala	Gly	Asn	Lys	Gly	His	His	Val	Trp	Val	Ile
200						205				210					
Lys	Asp	Glu	Leu	Gly	Asp	Tyr	Leu	Lys	Pro	Lys	Tyr	Leu	Ala	Gln	Val
215					220					225					230
Arg	Arg	Phe	Val	Ser	Asp	Leu									
				235											

<210> 372
 <211> 184
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31..-1

Met	Ala	Cys	Thr	Thr	Thr	Ala	Pro	Ala	Gln	Glu	His	Met	Leu	Leu	Thr
-30						-25					-20				
Pro	Leu	Thr	Ala	Leu	Met	Val	Gly	Ala	Ala	Ser	Leu	Leu	Glu	Gly	Arg
-15					-10					-5					1
Pro	Gln	Ile	Ser	Ala	Pro	Tyr	Ser	Arg	Ala	Ala	Cys	Cys	Ser	Pro	Gly
			5				10						15		
Ala	Leu	Gly	Cys	Pro	Ala	Ala	Arg	Val	Gly	Ile	Leu	Asp	Leu	Met	Tyr
		20					25					30			
Ser	Trp	Val	Ala	Arg	Lys	Val	Leu	Arg	Cys	Ser	Asn	Thr	Gly	Leu	Gln
35						40					45				
Gly	Leu	His	Cys	Ala	Pro	Ala	Tyr	Ala	Ala	Gln	Leu	Gly	Met	Asp	Pro
50					55					60					65
Gly	Arg	Gly	Gln	Arg	Ala	Gly	Gly	Pro	Val	Glu	Gln	Thr	Tyr	Phe	Ser
				70				75						80	
Pro	Met	Gly	Lys	Leu	Pro	Thr	Leu	Ser	Trp	Leu	Glu	Gly	Cys	Thr	Ala
			85				90						95		
Val	Met	Thr	Leu	Ala	Ser	Ala	Trp	Leu	Leu	Gly	Ser	Pro	Arg	Glu	Thr
		100					105					110			
Tyr	Asn	His	Glu	Lys	Val	Lys	Glu	Lys	Gln	Cys	Pro	Phe	Ser	Ser	Met
115						120					125				
Val	Leu	Gly	Glu	Tyr	Gly	Phe	Leu	Pro	Thr	Val	Asp	His	Leu	Ser	Thr
130					135					140					145
Leu	Gly	Cys	Asn	Met	Arg	Glu	Leu								
				150											

<210> 373
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -42..-1

Met	Ala	His	Val	Ala	Glu	Lys	Asp	Gly	Leu	Asp	Trp	Ala	Ser	Gly	Cys
-40							-35				-30				

Ile Pro Gly Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys
 -25 -20 -15
 Phe His Leu Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr
 -10 -5 1 5
 Ala Pro Val Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu
 10 15 20
 Asp Leu Val Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val
 25 30 35
 Ile Ile Val Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala
 40 45 50
 Cys Thr His Arg Asp
 55

<210> 374
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20..-1

<400> 374
 Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val Ala Ser
 -20 -15 -10 -5
 Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala His Leu
 1 5 10
 Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val Phe Gln
 15 20 25
 Gln Pro Cys Lys Ser Gly Gly Gly Gly Val Gly Glu Pro Asn Ala Gln
 30 35 40
 Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn Cys Ser
 45 50 55 60
 His Gly Gln Ala Phe
 65

<210> 375
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28..-1

<400> 375
 Met Ala Phe Pro Gly Gln Ser Asp Thr Lys Met Gln Trp Pro Glu Val
 -25 -20 -15
 Pro Ala Leu Pro Leu Leu Ser Ser Leu Cys Met Ala Met Val Arg Lys
 -10 -5 1
 Ser Ser Ala Leu Gly Lys Glu Val Gly Arg Arg Val Lys Glu Met Val
 5 10 15 20
 Met Leu Val Ala Pro Phe Arg Gln Ser Ser Ser Leu Ser Arg Thr Phe
 25 30 35

Ser Ser Arg Lys Val Val Lys Ala His Ala Ser Leu His Gly Ala Arg
40 45 50
Leu Ser Pro Leu Ser Arg Asn Ile Arg Gly
55 60

<210> 376
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<220>
<221> UNSURE
<222> 47
<223> Xaa = Ala,Pro,Ser,Thr

<400> 376
Met Ala Gln Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu
-30 -25 -20
Ala Pro Thr Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser
-15 -10 -5
Ser Ala Pro Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu
1 5 10 15
Leu Leu Leu Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala
20 25 30
Pro Ala Arg Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa
35 40 45
Gly Pro Leu Ile Pro Gly Gln Cys Pro
50 55

<210> 377
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 377
Met Asn Arg Val Leu Cys Ala Pro Ala Ala Gly Ala Val Arg Ala Leu
-15 -10 -5 1
Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu His Pro Leu Pro Gly Ser
5 10 15
Arg Asp Arg Ala His Pro Ala Ala Glu Glu Glu Asp Asp Pro Asp Arg
20 25 30
Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn Pro His Arg Trp Ser Val
35 40 45
Gly His Thr Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu
50 55 60 65
Pro Leu Ser Cys Phe Leu Val Ala Leu Ile Ile Trp Cys Tyr Leu Arg

				70						75					80			
Glu	Glu	Ser	Glu	Ala	Asp	Gln	Trp	Leu	Arg	Gln	Val	Trp	Gly	Glu	Val			
			85					90					95					
Pro	Glu	Pro	Ser	Asp	Arg	Ser	Glu	Glu	Pro	Glu	Thr	Pro	Ala	Ala	Tyr			
		100					105					110						
Arg	Ala	Arg	Thr															
		115																

<210> 378
 <211> 102
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<220>
 <221> UNSURE
 <222> 50
 <223> Xaa = Ala,Gly

<220>
 <221> UNSURE
 <222> 51
 <223> Xaa = Leu,Met,Val

<400> 378																		
Met	Phe	Leu	Thr	Ala	Leu	Leu	Trp	Arg	Gly	Arg	Ile	Pro	Gly	Arg	Gln			
				-10					-5					1				
Trp	Ile	Gly	Lys	His	Arg	Arg	Pro	Arg	Phe	Val	Ser	Leu	Arg	Ala	Lys			
		5					10					15						
Gln	Asn	Met	Ile	Arg	Arg	Leu	Glu	Ile	Asp	Ala	Glu	Asn	His	Tyr	Trp			
		20				25					30							
Leu	Ser	Met	Pro	Tyr	Met	Thr	Arg	Glu	Gln	Glu	Arg	Gly	His	Ala	Xaa			
35					40					45					50			
Xaa	Arg	Arg	Arg	Glu	Ala	Phe	Glu	Ala	Ile	Lys	Ala	Ala	Ala	Thr	Ser			
			55						60					65				
Lys	Phe	Pro	Pro	His	Arg	Phe	Ile	Ala	Asp	Gln	Leu	Asp	His	Leu	Asn			
			70					75					80					
Val	Thr	Lys	Lys	Trp	Ser													
		85																

<210> 379
 <211> 504
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 379
 Met Gly Ile Lys Thr Ala Leu Pro Ala Ala Glu Leu Gly Leu Tyr Ser

				-20				-15				-10			
Leu	Val	Leu	Ser	Gly	Ala	Leu	Ala	Tyr	Ala	Gly	Arg	Gly	Leu	Leu	Glu
			-5					1				5			
Ala	Ser	Gln	Asp	Gly	Ala	His	Arg	Lys	Ala	Phe	Arg	Glu	Ser	Val	Arg
	10					15					20				
Pro	Gly	Trp	Glu	Tyr	Ile	Gly	Arg	Lys	Met	Asp	Val	Ala	Asp	Phe	Glu
25					30					35					40
Trp	Val	Met	Trp	Phe	Thr	Ser	Phe	Arg	Asn	Val	Ile	Ile	Phe	Ala	Leu
				45					50					55	
Ser	Gly	His	Val	Leu	Phe	Ala	Lys	Leu	Cys	Thr	Met	Val	Ala	Pro	Lys
			60					65					70		
Leu	Arg	Ser	Trp	Met	Tyr	Ala	Val	Tyr	Gly	Ala	Leu	Ala	Val	Met	Gly
		75					80					85			
Thr	Met	Gly	Pro	Trp	Tyr	Leu	Leu	Leu	Leu	Leu	Gly	His	Cys	Val	Gly
	90					95					100				
Leu	Tyr	Val	Ala	Ser	Leu	Leu	Gly	Gln	Pro	Trp	Leu	Cys	Leu	Gly	Leu
105					110					115					120
Gly	Leu	Ala	Ser	Leu	Ala	Ser	Phe	Lys	Met	Asp	Pro	Leu	Ile	Ser	Trp
				125					130					135	
Gln	Ser	Gly	Phe	Val	Thr	Gly	Thr	Phe	Asp	Leu	Gln	Glu	Val	Leu	Phe
			140					145					150		
His	Gly	Gly	Ser	Ser	Phe	Thr	Val	Leu	Arg	Cys	Thr	Ser	Phe	Ala	Leu
		155					160					165			
Glu	Ser	Cys	Ala	His	Pro	Asp	Arg	His	Tyr	Ser	Leu	Ala	Asp	Leu	Leu
	170					175					180				
Lys	Tyr	Ser	Phe	Tyr	Leu	Pro	Phe	Phe	Phe	Phe	Gly	Pro	Ile	Met	Thr
185					190					195					200
Phe	Asp	Arg	Phe	His	Ala	Gln	Val	Ser	Gln	Val	Glu	Pro	Val	Arg	Arg
				205					210					215	
Glu	Gly	Glu	Leu	Trp	His	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Ser	Val	Val
			220					225					230		
Ala	Ile	Met	Ala	Val	Asp	Ile	Phe	Phe	His	Phe	Phe	Tyr	Ile	Leu	Thr
		235					240					245			
Ile	Pro	Ser	Asp	Leu	Lys	Phe	Ala	Asn	Arg	Leu	Pro	Asp	Ile	Ala	Leu
	250					255					260				
Ala	Gly	Leu	Ala	Tyr	Ser	Asn	Leu	Val	Tyr	Asp	Trp	Val	Lys	Ala	Ala
265					270					275					280
Val	Leu	Phe	Gly	Val	Val	Asn	Thr	Val	Ala	Cys	Leu	Asp	His	Leu	Asp
				285					290					295	
Pro	Pro	Gln	Pro	Pro	Lys	Cys	Ile	Thr	Ala	Leu	Tyr	Val	Phe	Ala	Glu
			300					305					310		
Thr	His	Phe	Asp	Arg	Gly	Ile	Asn	Asp	Trp	Leu	Cys	Lys	Tyr	Val	Tyr
		315					320					325			
Asn	His	Ile	Gly	Gly	Glu	His	Ser	Ala	Val	Ile	Pro	Glu	Leu	Ala	Ala
	330					335					340				
Thr	Val	Ala	Thr	Phe	Ala	Ile	Thr	Thr	Leu	Trp	Leu	Gly	Pro	Cys	Asp
345					350					355					360
Ile	Val	Tyr	Leu	Trp	Ser	Phe	Leu	Asn	Cys	Phe	Gly	Leu	Asn	Phe	Glu
				365					370					375	
Leu	Trp	Met	Gln	Lys	Leu	Ala	Glu	Trp	Gly	Pro	Leu	Ala	Arg	Ile	Glu
			380					385					390		
Ala	Ser	Leu	Ser	Val	Gln	Met	Ser	Arg	Arg	Val	Arg	Ala	Leu	Phe	Gly
	395						400					405			
Ala	Met	Asn	Phe	Trp	Ala	Ile	Ile	Met	Tyr	Asn	Leu	Val	Ser	Leu	Asn

410		415		420
Ser Leu Lys Phe Thr Glu Leu Val Ala Arg Arg Leu Leu Leu Thr Gly				
425		430		440
Phe Pro Gln Thr Thr Leu Ser Ile Leu Phe Val Thr Tyr Cys Gly Val				
	445		450	455
Gln Leu Val Lys Glu Arg Glu Arg Thr Leu Ala Leu Glu Glu Glu Gln				
	460		465	470
Lys Gln Asp Lys Glu Lys Pro Glu				
	475		480	

<210> 380
 <211> 152
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 380
Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe Leu Phe Cys Val
-25 -20 -15
Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile Val Gly Tyr Ala
-10 -5 1 5
Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln Arg Ser Ala His
10 15 20
Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln Gly Pro
25 30 35
Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val Pro Leu
40 45 50
Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val Ser Lys
55 60 65 70
Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu Pro Ser
75 80 85
Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro Leu Ser
90 95 100
Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile Val Ala
105 110 115
Thr Leu Leu Ile Leu Asp Ile Trp
120 125

<210> 381
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -26...-1

<400> 381
Met Glu Met Leu Phe Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe
-25 -20 -15
Lys Phe Ser Leu Cys Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe

-10 -5 1 5
 Gly Ser Val Ala Cys Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly
 10 15 20
 Ser Arg Leu
 25

<210> 382
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 382
 Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu
 -20 -15 -10
 Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
 -5 1 5
 Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
 10 15 20 25
 Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
 30 35 40
 Val Tyr Lys Pro Ile Arg Arg Arg
 45

<210> 383
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48...-1

<400> 383
 Met Ala Ser Ser His Trp Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr
 -45 -40 -35
 Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro Phe His Asp Asn Trp Asn
 -30 -25 -20
 Thr Ala Cys Phe Val Ile Leu Leu Leu Phe Ile Phe Thr Val Val Ser
 -15 -10 -5
 Leu Val Val Leu Ala Phe Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys
 1 5 10 15
 Val Lys Asn Lys Thr Val Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu
 20 25 30
 Arg Ser Met Met Asp Asn Ile Arg Lys Arg Glu Thr Glu Val Val
 35 40 45

<210> 384
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL

<222> -20..-1

<400> 384

Met	Ala	Arg	His	Gly	Leu	Pro	Leu	Leu	Pro	Leu	Leu	Ser	Leu	Leu	Val
-20					-15					-10					-5
Gly	Ala	Trp	Leu	Lys	Leu	Gly	Asn	Gly	Gln	Ala	Thr	Ser	Met	Val	Gln
			1				5					10			
Leu	Gln	Gly	Gly	Arg	Phe	Leu	Met	Gly	Thr	Asn	Ser	Pro	Asp	Ser	Arg
	15					20						25			
Asp	Gly	Glu	Gly	Pro	Val	Arg	Glu	Ala	Thr	Val	Lys	Pro	Phe	Ala	Ile
30						35					40				
Asp	Ile	Phe	Pro	Val	Thr	Asn	Lys	Asp	Phe	Arg	Asp	Phe	Val	Arg	Glu
45					50					55					60
Lys	Lys	Tyr	Arg	Thr	Glu	Ala	Glu	Met	Phe	Gly	Trp	Ser	Phe	Val	Phe
				65					70					75	
Glu	Asp	Phe	Val	Ser	Asp	Glu	Leu	Arg	Asn	Lys	Ala	Thr	Gln	Pro	Met
		80					85						90		
Lys	Val	Lys	Phe	Thr	His	Gly	Gly	Thr	Gly	Ser	Ser	Gln	Thr	Ala	Pro
	95					100						105			
Thr	Cys	Gly	Arg	Glu	Ser	Ser	Pro	Arg	Glu	Thr	Lys	Leu	Arg	Met	Ala
110						115					120				
Ser	Met	Glu	Ser	Pro	Gln										
125					130										

<210> 385

<211> 354

<212> PRT

<213> Homo sapiens

<400> 385

Met	Ser	Ala	Gly	Gly	Gly	Arg	Ala	Phe	Ala	Trp	Gln	Val	Phe	Pro	Pro
1			5					10						15	
Met	Pro	Thr	Cys	Arg	Val	Tyr	Gly	Thr	Val	Ala	His	Gln	Asp	Gly	His
		20					25						30		
Leu	Leu	Val	Leu	Gly	Gly	Cys	Gly	Arg	Ala	Gly	Leu	Pro	Leu	Asp	Thr
	35					40						45			
Ala	Glu	Thr	Leu	Asp	Met	Ala	Ser	His	Thr	Trp	Leu	Ala	Leu	Ala	Pro
50						55					60				
Leu	Pro	Thr	Ala	Arg	Ala	Gly	Ala	Ala	Ala	Val	Val	Leu	Gly	Lys	Gln
65				70						75					80
Val	Leu	Val	Val	Cys	Gly	Val	Asp	Glu	Val	Gln	Ser	Pro	Val	Ala	Ala
			85					90						95	
Val	Glu	Ala	Phe	Leu	Met	Asp	Glu	Gly	Arg	Trp	Glu	Arg	Arg	Ala	Thr
		100					105						110		
Leu	Pro	Gln	Ala	Ala	Met	Gly	Val	Ala	Thr	Val	Glu	Arg	Asp	Gly	Met
	115					120						125			
Val	Tyr	Ala	Leu	Gly	Gly	Met	Gly	Pro	Asp	Thr	Ala	Pro	Gln	Ala	Gln
130					135						140				
Val	Arg	Val	Tyr	Asp	Pro	Arg	Arg	Asp	Cys	Trp	Leu	Ser	Leu	Pro	Ser
145					150					155					160
Met	Pro	Thr	Pro	Cys	Tyr	Gly	Ala	Ser	Thr	Phe	Leu	His	Gly	Asn	Lys

				165				170					175			
Ile	Tyr	Val	Leu	Gly	Gly	Arg	Gln	Gly	Lys	Leu	Pro	Val	Thr	Ala	Phe	
			180					185					190			
Glu	Ala	Phe	Asp	Leu	Glu	Ala	Arg	Thr	Trp	Thr	Arg	His	Pro	Ser	Leu	
		195					200					205				
Pro	Ser	Arg	Arg	Ala	Phe	Ala	Gly	Cys	Ala	Met	Ala	Glu	Gly	Ser	Val	
	210					215					220					
Phe	Ser	Leu	Gly	Gly	Leu	Gln	Gln	Pro	Gly	Pro	His	Asn	Phe	Tyr	Ser	
225					230					235					240	
Arg	Pro	His	Phe	Val	Asn	Thr	Val	Glu	Met	Phe	Asp	Leu	Glu	His	Gly	
			245					250						255		
Ser	Trp	Thr	Lys	Leu	Pro	Arg	Ser	Leu	Arg	Met	Arg	Asp	Lys	Arg	Ala	
			260					265					270			
Asp	Phe	Val	Val	Gly	Ser	Leu	Gly	Gly	His	Ile	Val	Ala	Ile	Gly	Gly	
	275						280					285				
Leu	Gly	Asn	Gln	Pro	Cys	Pro	Leu	Gly	Ser	Val	Glu	Ser	Phe	Ser	Leu	
	290					295					300					
Ala	Arg	Arg	Arg	Trp	Glu	Ala	Leu	Pro	Ala	Met	Pro	Thr	Ala	Arg	Cys	
305					310					315					320	
Ser	Cys	Ser	Ser	Leu	Gln	Ala	Gly	Pro	Arg	Leu	Phe	Val	Ile	Gly	Gly	
			325					330						335		
Val	Ala	Gln	Gly	Pro	Ser	Gln	Ala	Val	Glu	Ala	Leu	Cys	Leu	Arg	Asp	
			340					345					350			
Gly	Val															

<210> 386

<211> 207

<212> PRT

<213> Homo sapiens

<400> 386

Met	Ala	Leu	Leu	Phe	Ala	Arg	Ser	Leu	Arg	Leu	Cys	Arg	Trp	Gly	Ala	
1				5				10					15			
Lys	Arg	Leu	Gly	Val	Ala	Ser	Thr	Glu	Ala	Gln	Arg	Gly	Val	Ser	Phe	
		20						25					30			
Lys	Leu	Glu	Glu	Lys	Thr	Ala	His	Ser	Ser	Leu	Ala	Leu	Phe	Arg	Asp	
	35					40					45					
Asp	Thr	Gly	Val	Lys	Tyr	Gly	Leu	Val	Gly	Leu	Glu	Pro	Thr	Lys	Val	
	50				55					60						
Ala	Leu	Asn	Val	Glu	Arg	Phe	Arg	Glu	Trp	Ala	Val	Val	Leu	Ala	Asp	
65				70				75							80	
Thr	Ala	Val	Thr	Ser	Gly	Arg	His	Tyr	Trp	Glu	Val	Thr	Val	Lys	Arg	
			85					90					95			
Ser	Gln	Gln	Phe	Arg	Ile	Gly	Val	Ala	Asp	Val	Asp	Met	Ser	Arg	Asp	
		100						105					110			
Ser	Cys	Ile	Gly	Val	Asp	Asp	Arg	Ser	Trp	Val	Phe	Thr	Tyr	Ala	Gln	
	115					120						125				
Arg	Lys	Trp	Tyr	Thr	Met	Leu	Ala	Asn	Glu	Lys	Ala	Pro	Val	Glu	Gly	
	130				135						140					
Ile	Gly	Gln	Pro	Glu	Lys	Val	Gly	Leu	Leu	Leu	Glu	Tyr	Glu	Ala	Gln	
145				150					155						160	
Lys	Leu	Ser	Leu	Val	Asp	Val	Ser	Gln	Val	Ser	Val	Val	His	Thr	Leu	
			165					170					175			
Gln	Thr	Asp	Phe	Arg	Gly	Pro	Val	Val	Pro	Ala	Phe	Ala	Leu	Trp	Asp	

	180		185		190
Gly	Glu	Leu	Leu	Thr	His
	195		200		205

<210> 387
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 387
 Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly
 1 5 10 15
 Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg
 20 25 30
 Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp
 35 40 45
 Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala
 50 55 60
 Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala
 65 70 75 80
 Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val
 85 90 95
 Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu
 100 105 110
 Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu
 115 120 125
 Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala
 130 135 140
 Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp
 145 150 155 160
 Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro
 165 170 175
 Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu
 180 185 190
 Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly
 195 200 205
 Leu Gln
 210

<210> 388
 <211> 375
 <212> PRT
 <213> Homo sapiens

<400> 388
 Met Ala Val Thr Glu Ala Ser Leu Leu Arg Gln Cys Pro Leu Leu Leu
 1 5 10 15
 Pro Gln Asn Arg Ser Lys Thr Val Tyr Glu Gly Phe Ile Ser Ala Gln
 20 25 30
 Gly Arg Asp Phe His Leu Arg Ile Val Leu Pro Glu Asp Leu Gln Leu
 35 40 45
 Lys Asn Ala Arg Leu Leu Cys Ile Trp Gln Leu Arg Thr Ile Leu Ser
 50 55 60
 Gly Tyr His Arg Ile Val Gln Gln Arg Met Gln His Ser Pro Asp Leu

65					70					75					80
Met	Ser	Phe	Met	Met	Glu	Leu	Lys	Met	Leu	Leu	Glu	Val	Ala	Leu	Lys
				85					90					95	
Asn	Arg	Gln	Glu	Leu	Tyr	Ala	Leu	Pro	Pro	Pro	Pro	Gln	Phe	Tyr	Ser
			100					105					110		
Ser	Leu	Ile	Glu	Glu	Ile	Gly	Thr	Leu	Gly	Trp	Asp	Lys	Leu	Val	Tyr
		115					120					125			
Ala	Asp	Thr	Cys	Phe	Ser	Thr	Ile	Lys	Leu	Lys	Ala	Glu	Asp	Ala	Ser
	130					135					140				
Gly	Arg	Glu	His	Leu	Ile	Thr	Leu	Lys	Leu	Lys	Ala	Lys	Tyr	Pro	Ala
145					150					155					160
Glu	Ser	Pro	Asp	Tyr	Phe	Val	Asp	Phe	Pro	Val	Pro	Phe	Cys	Ala	Ser
			165						170					175	
Trp	Thr	Pro	Gln	Ser	Ser	Leu	Ile	Ser	Ile	Tyr	Ser	Gln	Phe	Leu	Ala
		180						185					190		
Ala	Ile	Glu	Ser	Leu	Lys	Ala	Phe	Trp	Asp	Val	Met	Asp	Glu	Ile	Asp
	195					200						205			
Glu	Lys	Thr	Trp	Val	Leu	Glu	Pro	Glu	Lys	Pro	Pro	Arg	Ser	Ala	Thr
	210					215					220				
Ala	Arg	Arg	Ile	Ala	Leu	Gly	Asn	Asn	Val	Ser	Ile	Asn	Ile	Glu	Val
225					230					235					240
Asp	Pro	Arg	His	Pro	Thr	Met	Leu	Pro	Glu	Cys	Phe	Phe	Leu	Gly	Ala
			245						250					255	
Asp	His	Val	Val	Lys	Pro	Leu	Gly	Ile	Lys	Leu	Ser	Arg	Asn	Ile	His
		260						265					270		
Leu	Trp	Asp	Pro	Glu	Asn	Ser	Val	Leu	Gln	Asn	Leu	Lys	Asp	Val	Leu
	275					280						285			
Glu	Ile	Asp	Phe	Pro	Ala	Arg	Ala	Ile	Leu	Glu	Lys	Ser	Asp	Phe	Thr
	290					295					300				
Met	Asp	Cys	Gly	Ile	Cys	Tyr	Ala	Tyr	Gln	Leu	Asp	Gly	Thr	Ile	Pro
305					310					315					320
Asp	Gln	Val	Cys	Asp	Asn	Ser	Gln	Cys	Gly	Gln	Pro	Phe	His	Gln	Ile
			325						330					335	
Cys	Leu	Tyr	Glu	Trp	Leu	Arg	Gly	Leu	Leu	Thr	Ser	Arg	Gln	Ser	Phe
		340					345					350			
Asn	Ile	Ile	Phe	Gly	Glu	Cys	Pro	Tyr	Cys	Ser	Lys	Pro	Ile	Thr	Leu
	355					360						365			
Lys	Met	Ser	Gly	Arg	Lys	His									
	370				375										

<210> 389
 <211> 509
 <212> PRT
 <213> Homo sapiens

<400> 389
 Met Ala Ala Ile Gly Val His Leu Gly Cys Thr Ser Ala Cys Val Ala
 1 5 10 15
 Val Tyr Lys Asp Gly Arg Ala Gly Val Val Ala Asn Asp Ala Gly Asp
 20 25 30
 Arg Val Thr Pro Ala Val Val Ala Tyr Ser Glu Asn Glu Ile Val
 35 40 45
 Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn Thr Val
 50 55 60

Met	Lys	Val	Lys	Gln	Ile	Leu	Gly	Arg	Ser	Ser	Ser	Asp	Pro	Gln	Ala	65	70	75	80
Gln	Lys	Tyr	Ile	Ala	Glu	Ser	Lys	Cys	Leu	Val	Ile	Glu	Lys	Asn	Gly	85	90	95	
Lys	Leu	Arg	Tyr	Glu	Ile	Asp	Thr	Gly	Glu	Glu	Thr	Lys	Phe	Val	Asn	100	105	110	
Pro	Glu	Asp	Val	Ala	Arg	Leu	Ile	Phe	Ser	Lys	Met	Lys	Glu	Thr	Ala	115	120	125	
His	Ser	Val	Leu	Gly	Ser	Asp	Ala	Asn	Asp	Val	Val	Ile	Thr	Val	Pro	130	135	140	
Phe	Asp	Phe	Gly	Glu	Lys	Gln	Lys	Asn	Ala	Leu	Gly	Glu	Ala	Ala	Arg	145	150	155	160
Ala	Ala	Gly	Phe	Asn	Val	Leu	Arg	Leu	Ile	His	Glu	Pro	Ser	Ala	Ala	165	170	175	
Leu	Leu	Ala	Tyr	Gly	Ile	Gly	Gln	Asp	Ser	Pro	Thr	Gly	Lys	Ser	Asn	180	185	190	
Ile	Leu	Val	Phe	Lys	Leu	Gly	Gly	Thr	Ser	Leu	Ser	Leu	Ser	Val	Met	195	200	205	
Glu	Val	Asn	Ser	Gly	Ile	Tyr	Arg	Val	Leu	Ser	Thr	Asn	Thr	Asp	Asp	210	215	220	
Asn	Ile	Gly	Gly	Ala	His	Phe	Thr	Glu	Thr	Leu	Ala	Gln	Tyr	Leu	Ala	225	230	235	240
Ser	Glu	Phe	Gln	Arg	Ser	Phe	Lys	His	Asp	Val	Arg	Gly	Asn	Ala	Arg	245	250	255	
Ala	Met	Met	Lys	Leu	Thr	Asn	Ser	Ala	Glu	Val	Ala	Lys	His	Ser	Leu	260	265	270	
Ser	Thr	Leu	Gly	Ser	Ala	Asn	Cys	Phe	Leu	Asp	Ser	Leu	Tyr	Glu	Gly	275	280	285	
Gln	Asp	Phe	Asp	Cys	Asn	Val	Ser	Arg	Ala	Arg	Phe	Glu	Leu	Leu	Cys	290	295	300	
Ser	Pro	Leu	Phe	Asn	Lys	Cys	Ile	Glu	Ala	Ile	Arg	Gly	Leu	Leu	Asp	305	310	315	320
Gln	Asn	Gly	Phe	Thr	Thr	Asp	Asp	Ile	Asn	Lys	Val	Val	Leu	Cys	Gly	325	330	335	
Gly	Ser	Ser	Arg	Ile	Pro	Lys	Leu	Gln	Gln	Leu	Ile	Lys	Asp	Leu	Phe	340	345	350	
Pro	Ala	Val	Glu	Leu	Leu	Asn	Ser	Ile	Pro	Pro	Asp	Glu	Val	Ile	Pro	355	360	365	
Ile	Gly	Ala	Ala	Ile	Glu	Ala	Gly	Ile	Leu	Ile	Gly	Lys	Glu	Asn	Leu	370	375	380	
Leu	Val	Glu	Asp	Ser	Leu	Met	Ile	Glu	Cys	Ser	Ala	Arg	Asp	Ile	Leu	385	390	395	400
Val	Lys	Gly	Val	Asp	Glu	Ser	Gly	Ala	Ser	Arg	Phe	Thr	Val	Leu	Phe	405	410	415	
Pro	Ser	Gly	Thr	Pro	Leu	Pro	Ala	Arg	Arg	Gln	His	Thr	Leu	Gln	Ala	420	425	430	
Pro	Gly	Ser	Ile	Ser	Ser	Val	Cys	Leu	Glu	Leu	Tyr	Glu	Ser	Asp	Gly	435	440	445	
Lys	Asn	Ser	Ala	Lys	Glu	Glu	Thr	Lys	Phe	Ala	Gln	Val	Val	Leu	Gln	450	455	460	
Asp	Leu	Asp	Lys	Lys	Glu	Asn	Gly	Leu	Arg	Asp	Ile	Leu	Ala	Val	Leu	465	470	475	480
Thr	Met	Lys	Arg	Asp	Gly	Ser	Leu	His	Val	Thr	Cys	Thr	Asp	Gln	Glu	485	490	495	

Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser
500 505

<210> 390
<211> 78
<212> PRT
<213> Homo sapiens

<400> 390
Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys Glu His
1 5 10 15
Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg Leu Glu
20 25 30
Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser Glu His
35 40 45
Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg Asp Leu
50 55 60
Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr
65 70 75

<210> 391
<211> 162
<212> PRT
<213> Homo sapiens

<400> 391
Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
1 5 10 15
Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val
20 25 30
Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
35 40 45
Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
50 55 60
Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
65 70 75 80
Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
85 90 95
Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
100 105 110
Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
115 120 125
Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
130 135 140
Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
145 150 155 160
Leu Gly

<210> 392
<211> 146
<212> PRT
<213> Homo sapiens

<400> 392

Met Asn Ser Leu Leu His Phe Gly Ile Leu Leu Glu Leu Ser Leu Leu
 1 5 10 15
 Lys Gln Phe Lys Ser Val Tyr Val Pro Gly Asn His Thr His Gln Ala
 20 25 30
 Ser Tyr Lys Pro Leu Leu Lys Gln Val Val Glu Glu Ile Phe His Pro
 35 40 45
 Glu Arg Pro Asp Ser Val Asp Ile Glu His Met Ser Ser Gly Leu Thr
 50 55 60
 Asp Leu Leu Lys Thr Gly Phe Ser Met Phe Met Lys Val Ser Arg Pro
 65 70 75 80
 His Pro Ser Asp Tyr Pro Leu Leu Ile Leu Phe Val Val Gly Gly Val
 85 90 95
 Thr Val Ser Glu Val Lys Met Val Lys Asp Leu Val Ala Ser Leu Lys
 100 105 110
 Pro Gly Thr Gln Val Ile Val Leu Ser Thr Arg Leu Leu Lys Pro Leu
 115 120 125
 Asn Ile Pro Glu Leu Leu Phe Ala Thr Asp Arg Leu His Pro Asp Leu
 130 135 140
 Gly Phe
 145

<210> 393

<211> 225

<212> PRT

<213> Homo sapiens

<400> 393

Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Ala Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
 165 170 175
 Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
 180 185 190
 Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
 195 200 205
 Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr

210 215 220

Val
225

<210> 394
<211> 114
<212> PRT
<213> Homo sapiens

<400> 394

Met	Arg	Leu	Gln	Asp	Arg	Ile	Ala	Thr	Phe	Phe	Phe	Pro	Lys	Gly	Met
1			5						10					15	
Met	Leu	Thr	Thr	Ala	Ala	Leu	Met	Leu	Phe	Phe	Leu	His	Leu	Gly	Ile
			20					25					30		
Phe	Ile	Arg	Asp	Val	His	Asn	Phe	Cys	Ile	Thr	Tyr	His	Tyr	Asp	His
		35					40					45			
Met	Ser	Phe	His	Tyr	Thr	Val	Val	Leu	Met	Phe	Ser	Gln	Val	Ile	Ser
	50					55					60				
Ile	Cys	Trp	Ala	Ala	Met	Gly	Ser	Leu	Tyr	Ala	Glu	Met	Thr	Glu	Asn
65					70					75				80	
Asn	Ala	Gln	Arg	Ser	His	Val	Leu	Gln	Pro	Pro	Val	Leu	Gly	Val	Ser
			85						90					95	
Gly	His	Arg	Val	Pro	Gly	Gly	Ala	Pro	Leu	Arg	Pro	Gly	Glu	Ser	Glu
			100					105					110		

Gln Gly

<210> 395
<211> 367
<212> PRT
<213> Homo sapiens

<400> 395

Met	Ala	Thr	Pro	Asn	Asn	Leu	Thr	Pro	Thr	Asn	Cys	Ser	Trp	Trp	Pro
1				5					10					15	
Ile	Ser	Ala	Leu	Glu	Ser	Asp	Ala	Ala	Lys	Pro	Ala	Glu	Ala	Pro	Asp
			20					25					30		
Ala	Pro	Glu	Ala	Ala	Ser	Pro	Ala	His	Trp	Pro	Arg	Glu	Ser	Leu	Val
		35					40					45			
Leu	Tyr	His	Trp	Thr	Gln	Ser	Phe	Ser	Ser	Gln	Lys	Val	Arg	Leu	Val
	50					55					60				
Ile	Ala	Glu	Lys	Gly	Leu	Val	Cys	Glu	Glu	Arg	Asp	Val	Ser	Leu	Pro
65					70					75				80	
Gln	Ser	Glu	His	Lys	Glu	Pro	Trp	Phe	Met	Arg	Leu	Asn	Leu	Gly	Glu
			85						90					95	
Glu	Val	Pro	Val	Ile	Ile	His	Arg	Asp	Asn	Ile	Ile	Ser	Asp	Tyr	Asp
			100					105					110		
Gln	Ile	Ile	Asp	Tyr	Val	Glu	Arg	Thr	Phe	Thr	Gly	Glu	His	Val	Val
		115					120					125			
Ala	Leu	Met	Pro	Glu	Val	Gly	Ser	Leu	Gln	His	Ala	Arg	Val	Leu	Gln
		130				135					140				
Tyr	Arg	Glu	Leu	Leu	Asp	Ala	Leu	Pro	Met	Asp	Ala	Tyr	Thr	His	Gly
145					150					155				160	
Cys	Ile	Leu	His	Pro	Glu	Leu	Thr	Thr	Asp	Ser	Met	Ile	Pro	Lys	Tyr
				165					170					175	

Ala	Thr	Ala	Glu	Ile	Arg	Arg	His	Leu	Ala	Asn	Ala	Thr	Thr	Asp	Leu
			180					185					190		
Met	Lys	Leu	Asp	His	Glu	Glu	Glu	Pro	Gln	Leu	Ser	Glu	Pro	Tyr	Leu
		195					200					205			
Ser	Lys	Gln	Lys	Lys	Leu	Met	Val	Lys	Ile	Leu	Glu	His	Asp	Asp	Val
	210				215					220					
Ser	Tyr	Leu	Lys	Lys	Ile	Leu	Gly	Glu	Leu	Ala	Met	Val	Leu	Asp	Gln
225					230					235					240
Ile	Glu	Ala	Glu	Leu	Glu	Lys	Arg	Lys	Leu	Glu	Asn	Glu	Gly	Gln	Lys
				245					250					255	
Cys	Glu	Leu	Trp	Leu	Cys	Gly	Cys	Ala	Phe	Thr	Leu	Ala	Asp	Val	Leu
		260						265					270		
Leu	Gly	Ala	Thr	Leu	His	Arg	Leu	Lys	Phe	Leu	Gly	Leu	Ser	Lys	Lys
	275						280					285			
Tyr	Trp	Glu	Asp	Gly	Ser	Arg	Pro	Asn	Leu	Gln	Ser	Phe	Phe	Glu	Arg
	290					295					300				
Val	Gln	Arg	Arg	Phe	Ala	Phe	Arg	Lys	Val	Leu	Gly	Asp	Ile	His	Thr
305					310					315					320
Thr	Leu	Leu	Ser	Ala	Val	Ile	Pro	Asn	Ala	Phe	Arg	Leu	Val	Lys	Arg
				325					330					335	
Lys	Pro	Pro	Ser	Phe	Phe	Gly	Ala	Ser	Phe	Leu	Met	Gly	Ser	Leu	Gly
		340					345					350			
Gly	Met	Gly	Tyr	Phe	Ala	Tyr	Trp	Tyr	Leu	Lys	Lys	Lys	Tyr	Ile	
		355					360					365			

<210> 396

<211> 279

<212> PRT

<213> Homo sapiens

<400> 396

Met	Pro	Val	Cys	Ala	Pro	Val	Leu	Trp	Arg	Ala	Arg	Arg	Leu	Cys	Gly
1				5					10					15	
Met	Pro	Val	Cys	Ala	Pro	Val	Pro	Trp	Arg	Ala	Arg	Arg	Leu	Cys	Thr
			20					25					30		
Arg	Ala	Val	Val	Cys	Pro	Ser	Ser	Val	Pro	Phe	Ile	Ala	Gly	Gln	Gly
	35					40						45			
Cys	Thr	His	Met	Cys	Lys	Pro	Ala	Thr	Asp	Pro	Arg	Phe	Thr	Arg	Ser
	50				55					60					
Pro	Leu	Ala	Gly	Gly	Val	Ile	Leu	Gly	Val	Ala	Leu	Trp	Leu	Arg	His
	65				70				75						80
Asp	Pro	Gln	Thr	Thr	Asn	Leu	Leu	Tyr	Leu	Glu	Leu	Gly	Asp	Lys	Pro
				85					90					95	
Ala	Pro	Asn	Thr	Phe	Tyr	Val	Gly	Ile	Tyr	Ile	Leu	Ile	Ala	Val	Gly
		100					105						110		
Ala	Val	Met	Met	Phe	Val	Gly	Phe	Leu	Gly	Cys	Tyr	Gly	Ala	Ile	Gln
	115					120						125			
Glu	Ser	Gln	Cys	Leu	Leu	Gly	Thr	Phe	Phe	Thr	Cys	Leu	Val	Ile	Leu
	130					135					140				
Phe	Ala	Cys	Glu	Val	Ala	Ala	Gly	Ile	Trp	Gly	Phe	Val	Asn	Lys	Asp
145					150				155						160
Gln	Ile	Ala	Lys	Asp	Val	Lys	Gln	Phe	Tyr	Asp	Gln	Ala	Leu	Gln	Gln
			165						170					175	
Ala	Val	Val	Asp	Asp	Asp	Ala	Asn	Asn	Ala	Lys	Ala	Val	Val	Lys	Thr

			180					185				190					
Phe	His	Glu	Thr	Leu	Asp	Cys	Cys	Gly	Ser	Ser	Thr	Leu	Thr	Ala	Leu		
		195					200					205					
Thr	Thr	Ser	Val	Leu	Lys	Asn	Asn	Leu	Cys	Pro	Ser	Gly	Ser	Asn	Ile		
	210					215					220						
Ile	Ser	Asn	Leu	Phe	Lys	Glu	Asp	Cys	His	Gln	Lys	Ile	Asp	Asp	Leu		
225					230					235					240		
Phe	Ser	Gly	Lys	Leu	Tyr	Leu	Ile	Gly	Ile	Ala	Ala	Ile	Val	Val	Ala		
			245						250					255			
Val	Ile	Met	Ile	Phe	Glu	Met	Ile	Leu	Ser	Met	Val	Leu	Cys	Cys	Gly		
		260						265					270				
Ile	Arg	Asn	Ser	Ser	Val	Tyr											
		275															

<210> 397
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 397																	
Met	Cys	Leu	Leu	Leu	Gly	Ala	Thr	Gly	Val	Gly	Lys	Thr	Leu	Leu	Val		
1			5					10					15				
Lys	Arg	Leu	Gln	Glu	Val	Ser	Ser	Arg	Asp	Gly	Lys	Gly	Asp	Leu	Gly		
		20						25				30					
Glu	Pro	Pro	Pro	Thr	Arg	Pro	Thr	Val	Gly	Thr	Asn	Leu	Thr	Asp	Ile		
	35					40					45						
Val	Ala	Gln	Arg	Lys	Ile	Thr	Ile	Arg	Glu	Leu	Gly	Gly	Cys	Met	Gly		
	50				55					60							
Pro	Ile	Trp	Ser	Ser	Tyr	Tyr	Gly	Asn	Cys	Arg	Ser	Leu	Leu	Phe	Val		
65				70				75						80			
Met	Asp	Ala	Ser	Asp	Pro	Thr	Gln	Leu	Ser	Ala	Ser	Cys	Val	Gln	Leu		
			85					90					95				
Leu	Gly	Leu	Leu	Ser	Ala	Glu	Gln	Leu	Ala	Glu	Ala	Ser	Val	Leu	Ile		
		100						105					110				
Leu	Phe	Asn	Lys	Ile	Asp	Leu	Pro	Cys	Tyr	Met	Ser	Thr	Glu	Glu	Met		
	115					120					125						
Lys	Ser	Leu	Ile	Arg	Leu	Pro	Asp	Ile	Ile	Ala	Cys	Ala	Lys	Gln	Asn		
	130				135					140							
Ile	Thr	Thr	Ala	Glu	Ile	Ser	Ala	Arg	Glu	Gly	Thr	Gly	Leu	Ala	Gly		
145				150					155					160			
Val	Leu	Ala	Trp	Leu	Gln	Ala	Thr	His	Arg	Ala	Asn	Asp					
			165					170									

<210> 398
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 398																	
Met	Ala	Ala	Ala	Arg	Pro	Ser	Leu	Gly	Arg	Val	Leu	Pro	Gly	Ser	Ser		
1			5					10					15				
Val	Leu	Phe	Leu	Cys	Asp	Met	Gln	Glu	Lys	Phe	Arg	His	Asn	Ile	Ala		
		20					25					30					
Tyr	Phe	Pro	Gln	Ile	Val	Ser	Val	Ala	Ala	Arg	Met	Leu	Lys	Val	Ala		

<211> 150
 <212> PRT
 <213> Homo sapiens

<400> 400
 Met Cys Thr Ala Leu Leu Leu Tyr Leu Arg Trp Cys Phe Asn Leu
 1 5 10 15
 Lys Leu Val Asn Val Lys Tyr Glu Pro Lys Asp Ser Leu Gly Pro Glu
 20 25 30
 Met Thr Phe Val Ala Asp Ala Ala Arg Gly Pro Leu Leu Ser Ser Leu
 35 40 45
 Asp Ser Pro Ala Asn Leu Met Ser Thr Ala Ser Val Cys Ile Ser Leu
 50 55 60
 Pro Glu Gly Cys Ser Gly Gly Arg Ser Pro Cys Tyr Ser Gln Lys Trp
 65 70 75 80
 Pro Pro Glu Val Pro Glu Lys Leu Thr Ser Leu Gly Gln Gln Ser Ser
 85 90 95
 Thr Ser Ser Leu Thr Asp Thr Asp Val Gln Val Ser Pro Met Leu Val
 100 105 110
 Ala Gly Val Asn His Ser Ser Ser Leu Leu Asp Asn Ile Pro Phe Thr
 115 120 125
 Gly Cys Leu Pro Phe His Leu Ser Ser Ser Leu Pro Tyr Leu Cys Leu
 130 135 140
 Leu Gly Ser Pro Phe Lys
 145 150

<210> 401
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 401
 Met Glu Asp Pro Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro
 1 5 10 15
 Lys Glu Arg Ser Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly
 20 25 30
 Ala Pro Lys Cys Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe
 35 40 45
 Gln Glu Arg His Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln
 50 55 60
 Lys Leu Gln Gly Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe
 65 70 75 80
 Pro Ser Ser Lys Ala Leu Ile Thr His Gln Arg Ser His Gly Pro Ala
 85 90 95
 Ala Lys Pro Thr Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe
 100 105 110
 Pro Cys Pro Asp Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg
 115 120 125
 Arg His Arg Gln Met His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala
 130 135 140
 Cys Thr Glu Cys Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln
 145 150 155 160
 His Tyr Ile Arg His Ala Arg Gly Glu Leu
 165 170

<210> 402
 <211> 169
 <212> PRT
 <213> Homo sapiens

<400> 402
 Met Glu Asp Pro Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro
 1 5 10 15
 Lys Glu Arg Ser Pro Gln Pro Arg Arg Gln His Leu Pro Pro Gly Gly
 20 25 30
 Pro Glu Val His Pro Leu Pro His His Leu Arg Arg Phe Gln Val Pro
 35 40 45
 Gly Ala Ser His Glu Ala Gly Ala Pro Ser Gly Leu Arg Gly Pro Glu
 50 55 60
 Ala Ala Gly Gly Pro Leu His Leu Leu His Leu Arg Pro Leu Leu Pro
 65 70 75 80
 Leu Leu Gln Ser Pro Asn His Pro Pro Ala Gln His Gly Pro Ala Ala
 85 90 95
 Lys Pro Thr Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro
 100 105 110
 Cys Pro Asp Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg
 115 120 125
 His Arg Gln Met His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys
 130 135 140
 Thr Glu Cys Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His
 145 150 155 160
 Tyr Ile Arg His Ala Arg Gly Glu Leu
 165

<210> 403
 <211> 367
 <212> PRT
 <213> Homo sapiens

<400> 403
 Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
 1 5 10 15
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
 20 25 30
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
 35 40 45
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val
 50 55 60
 Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro
 65 70 75 80
 Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu
 85 90 95
 Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp
 100 105 110
 Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val
 115 120 125
 Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln
 130 135 140

Tyr	Arg	Glu	Leu	Leu	Asp	Ala	Leu	Pro	Met	Asp	Ala	Tyr	Thr	His	Gly
145					150					155					160
Cys	Ile	Leu	His	Leu	Glu	Leu	Thr	Thr	Asp	Ser	Met	Ile	Pro	Lys	Tyr
				165					170						175
Ala	Thr	Ala	Glu	Ile	Arg	Arg	His	Leu	Ala	Asn	Ala	Thr	Thr	Asp	Leu
			180					185						190	
Met	Lys	Leu	Asp	His	Glu	Glu	Glu	Pro	Gln	Leu	Ser	Glu	Pro	Tyr	Leu
		195						200				205			
Ser	Lys	Gln	Lys	Lys	Leu	Met	Ala	Lys	Ile	Leu	Glu	His	Asp	Asp	Val
	210					215					220				
Ser	Tyr	Leu	Lys	Lys	Ile	Leu	Gly	Glu	Leu	Ala	Met	Val	Leu	Asp	Gln
225					230					235					240
Ile	Glu	Ala	Glu	Leu	Glu	Lys	Arg	Lys	Leu	Glu	Asn	Glu	Gly	Gln	Lys
				245					250					255	
Cys	Glu	Leu	Trp	Leu	Cys	Gly	Cys	Ala	Phe	Thr	Leu	Ala	Asp	Val	Leu
			260					265					270		
Leu	Gly	Ala	Thr	Leu	His	Arg	Leu	Lys	Phe	Leu	Gly	Leu	Ser	Lys	Lys
			275				280					285			
Tyr	Trp	Glu	Asp	Gly	Ser	Arg	Pro	Asn	Leu	Gln	Ser	Phe	Phe	Glu	Arg
	290					295					300				
Val	Gln	Arg	Arg	Phe	Ala	Phe	Arg	Lys	Val	Leu	Gly	Asp	Ile	His	Thr
305					310					315					320
Thr	Leu	Leu	Ser	Ala	Val	Ile	Pro	Asn	Ala	Phe	Arg	Leu	Val	Lys	Arg
				325					330					335	
Lys	Pro	Pro	Ser	Phe	Phe	Gly	Ala	Ser	Phe	Leu	Met	Gly	Ser	Leu	Gly
			340					345					350		
Gly	Met	Gly	Tyr	Phe	Ala	Tyr	Trp	Tyr	Leu	Lys	Lys	Lys	Tyr	Ile	
		355					360					365			

<210> 404
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 404
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser
 1 5 10 15
 Pro Val Pro Val
 20

<210> 405
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 405
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60

Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	Asp	Leu	Gln	Ala	Ala
65					70					75					80
Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	Ser	Phe	Leu	Ala	Phe	Met
				85					90					95	
Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	Arg	Cys	Thr	Gly	Asp	Asn	Glu
			100					105					110		
Lys	Val	Lys	Ala	His	Ile	Leu	Leu	Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile
		115					120						125		
Thr	Gly	Met	Val	Val	Leu	Ile	Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile
	130					135					140				
Ile	Arg	Asp	Phe	Tyr	Asn	Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu
145					150				155						160
Leu	Gly	Glu	Ala	Leu	Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile
				165				170						175	
Val	Gly	Gly	Ala	Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser
			180					185					190		
Ser	Ser	Tyr	Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser
		195					200					205			
Tyr	His	Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr
	210					215						220			
Val															
225															

<210> 406

<211> 378

<212> PRT

<213> Homo sapiens

<400> 406

Met	Asp	Pro	Gly	Asp	Asp	Trp	Leu	Val	Glu	Ser	Leu	Arg	Leu	Tyr	Gln
1				5					10					15	
Asp	Phe	Tyr	Ala	Phe	Asp	Leu	Ser	Gly	Ala	Thr	Arg	Val	Leu	Glu	Trp
			20					25					30		
Ile	Asp	Asp	Lys	Gly	Val	Phe	Val	Ala	Gly	Tyr	Glu	Ser	Leu	Lys	Lys
			35				40					45			
Asn	Glu	Ile	Leu	His	Leu	Lys	Leu	Pro	Leu	Arg	Leu	Ser	Val	Lys	Glu
	50				55						60				
Asn	Lys	Gly	Leu	Phe	Pro	Glu	Arg	Asp	Phe	Lys	Val	Arg	His	Gly	Gly
65				70					75					80	
Phe	Ser	Asp	Arg	Ser	Ile	Phe	Asp	Leu	Lys	His	Val	Pro	His	Thr	Arg
				85				90					95		
Leu	Leu	Val	Thr	Ser	Gly	Leu	Pro	Gly	Cys	Tyr	Leu	Gln	Val	Trp	Gln
			100					105					110		
Val	Ala	Glu	Asp	Ser	Asp	Val	Ile	Lys	Ala	Val	Ser	Thr	Ile	Ala	Val
			115				120					125			
His	Glu	Lys	Glu	Glu	Ser	Leu	Trp	Pro	Arg	Val	Ala	Val	Phe	Ser	Thr
	130					135					140				
Leu	Ala	Pro	Gly	Val	Leu	His	Gly	Ala	Arg	Leu	Arg	Ser	Leu	Gln	Val
145					150				155					160	
Val	Asp	Leu	Glu	Ser	Arg	Lys	Thr	Thr	Tyr	Thr	Ser	Asp	Val	Ser	Asp
				165				170					175		
Ser	Glu	Glu	Leu	Ser	Ser	Leu	Gln	Val	Leu	Asp	Ala	Asp	Thr	Phe	Ala
			180				185					190			
Phe	Cys	Cys	Ala	Ser	Gly	Arg	Leu	Gly	Leu	Val	Asp	Thr	Arg	Gln	Lys

	195		200		205										
Trp	Ala	Pro	Leu	Glu	Asn	Arg	Ser	Pro	Gly	Pro	Gly	Ser	Gly	Gly	Glu
	210					215					220				
Arg	Trp	Cys	Ala	Glu	Val	Gly	Ser	Trp	Gly	Gln	Gly	Pro	Gly	Pro	Ser
225						230					235				240
Ile	Ala	Ser	Leu	Ser	Ser	Asp	Gly	Arg	Leu	Cys	Leu	Leu	Asp	Pro	Arg
				245					250					255	
Asp	Leu	Cys	His	Pro	Val	Ser	Ser	Val	Gln	Cys	Pro	Val	Ser	Val	Pro
			260					265					270		
Ser	Pro	Asp	Pro	Glu	Leu	Leu	Arg	Val	Thr	Trp	Ala	Pro	Gly	Leu	Lys
	275						280					285			
Asn	Cys	Leu	Ala	Ile	Ser	Gly	Phe	Asp	Gly	Thr	Val	Gln	Val	Tyr	Asp
	290					295					300				
Ala	Thr	Ser	Trp	Asp	Gly	Thr	Arg	Ser	Gln	Asp	Gly	Thr	Arg	Ser	Gln
305					310					315					320
Val	Glu	Pro	Leu	Phe	Thr	His	Arg	Gly	His	Ile	Phe	Leu	Asp	Gly	Asn
				325				330						335	
Gly	Met	Asp	Pro	Ala	Pro	Leu	Val	Thr	Thr	His	Thr	Trp	His	Pro	Cys
			340					345					350		
Arg	Pro	Arg	Thr	Leu	Leu	Ser	Ala	Thr	Asn	Asp	Ala	Ser	Leu	His	Val
	355					360						365			
Trp	Asp	Trp	Val	Asp	Leu	Cys	Ala	Pro	Arg						
	370					375									

<210> 407

<211> 43

<212> PRT

<213> Homo sapiens

<400> 407

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	Val
1				5				10					15		
Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	Arg	Val
		20					25					30			
Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe					
	35						40								

<210> 408

<211> 345

<212> PRT

<213> Homo sapiens

<400> 408

Met	Ala	Trp	Arg	Gly	Trp	Ala	Gln	Arg	Gly	Trp	Gly	Cys	Gly	Gln	Ala
1				5				10					15		
Trp	Gly	Ala	Ser	Val	Gly	Gly	Arg	Ser	Cys	Glu	Glu	Leu	Thr	Ala	Val
		20					25					30			
Leu	Thr	Pro	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn	Phe	Phe	Ile	Gln
		35					40				45				
Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val	Glu	Pro	Arg	Arg
	50					55				60					
Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg	Ser	Ala	Leu	Ile
65					70					75				80	
Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro	Tyr	Pro	Ile	Arg

Leu	Ser	Gln	Pro	Arg	Met	Glu	Ser	Leu	Asp	Thr	Pro	Ala	Ala	Tyr	Ser
		115					120					125			
Leu	Val	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Val	Val	Leu	Val	Leu	Ser	Ser
		130				135					140				
Phe	Phe	Ala	Leu	Gly	Phe	Ala	Gly	Thr	Phe	Leu	Gly	Asp	Tyr	Phe	Gly
145				150					155						160
Ile	Leu	Lys	Glu	Ala	Arg	Val	Thr	Val	Phe	Pro	Phe	Asn	Ile	Leu	Asp
			165						170					175	
Asn	Pro	Met	Tyr	Trp	Gly	Ser	Thr	Ala	Asn	Tyr	Leu	Gly	Trp	Ala	Ile
		180					185						190		
Met	His	Ala	Ser	Pro	Thr	Gly	Leu	Leu	Leu	Thr	Val	Leu	Val	Ala	Leu
		195					200					205			
Thr	Tyr	Ile	Val	Ala	Leu	Leu	Tyr	Glu	Glu	Pro	Phe	Thr	Ala	Glu	Ile
	210					215					220				
Tyr	Arg	Gln	Lys	Ala	Ser	Gly	Ser	His	Lys	Arg	Ser				
225					230					235					

<210> 410
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 410															
Met	Asn	Thr	Glu	Ala	Glu	Gln	Gln	Leu	Leu	His	His	Ala	Arg	Asn	Gly
1				5					10					15	
Asn	Ala	Glu	Glu	Val	Arg	Gln	Leu	Leu	Glu	Thr	Met	Ala	Ser	Asn	Glu
		20					25					30			
Val	Ile	Ala	Asp	Ile	Asn	Cys	Lys	Gly	Arg	Ser	Lys	Ser	Asn	Leu	Gly
	35					40					45				
Trp	Thr	Pro	Leu	His	Leu	Ala	Cys	Tyr	Phe	Gly	His	Arg	Gln	Val	Val
	50				55				60						
Gln	Asp	Leu	Leu	Lys	Ala	Gly	Ala	Glu	Val	Asn	Val	Leu	Asn	Asp	Met
65				70					75						80
Gly	Asp	Thr	Pro	Leu	His	Arg	Ala	Ala	Phe	Thr	Gly	Arg	Lys	Val	Lys
			85					90					95		
Ile	Ile	Leu	Cys	Ser	Met	Phe	Val	Ser	Glu	Val	Phe	Gly	Gly	Val	Val
		100					105						110		
Thr	Ile	Val	Phe	Ser	Val	Ile	Thr	Ile							
	115					120									

<210> 411
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 411															
Met	Arg	Leu	Gln	Gly	Ala	Ile	Phe	Val	Leu	Leu	Pro	His	Leu	Gly	Pro
1				5					10					15	
Ile	Leu	Val	Trp	Leu	Phe	Thr	Arg	Asp	His	Met	Ser	Gly	Trp	Cys	Glu
		20					25					30			
Gly	Pro	Arg	Met	Leu	Ser	Trp	Cys	Pro	Phe	Tyr	Lys	Val	Leu	Leu	Leu
	35					40					45				
Val	Gln	Thr	Ala	Ile	Tyr	Ser	Val	Val	Gly	Tyr	Ala	Ser	Tyr	Leu	Val
	50					55				60					

Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
 65 70 75 80
 Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
 85 90 95
 Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
 100 105 110
 Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
 115 120 125
 Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
 130 135 140
 Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
 145 150 155 160
 His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 165 170

<210> 412

<211> 236

<212> PRT

<213> Homo sapiens

<400> 412

Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys
 1 5 10 15
 Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala
 20 25 30
 Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu
 35 40 45
 Ser Val Leu Lys Leu His His Ser Leu Gln Gln Ser Glu Pro Asp Leu
 50 55 60
 Arg His Leu Val Leu Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser
 65 70 75 80
 Met Ala Pro Ala Ala Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala
 85 90 95
 Pro Ser Val Ala Asp Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser
 100 105 110
 Ala Ser Met Ala Ser Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu
 115 120 125
 Ser Gln Ala Pro Gln Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser
 130 135 140
 Ile Gly Gly Ala Ala Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro
 145 150 155 160
 Ala Thr Gly Cys Leu Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp
 165 170 175
 Ile Asp Thr Ser Met Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu
 180 185 190
 Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro
 195 200 205
 Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly
 210 215 220
 Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg
 225 230 235

<210> 413

<211> 191

<212> PRT
 <213> Homo sapiens

<400> 413

Met	Lys	Gly	Leu	Tyr	Phe	Gln	Gln	Ser	Ser	Thr	Asp	Glu	Glu	Ile	Thr
1			5					10						15	
Phe	Val	Phe	Gln	Glu	Lys	Glu	Asp	Leu	Pro	Val	Thr	Glu	Asp	Asn	Phe
		20					25					30			
Val	Lys	Leu	Gln	Val	Lys	Ala	Cys	Ala	Leu	Ser	Gln	Ile	Asn	Thr	Lys
	35					40					45				
Leu	Leu	Ala	Glu	Met	Lys	Met	Lys	Lys	Asp	Leu	Phe	Pro	Val	Gly	Arg
	50				55					60					
Glu	Ile	Ala	Gly	Ile	Val	Leu	Asp	Val	Gly	Ser	Lys	Val	Ser	Phe	Phe
65				70					75					80	
Gln	Pro	Asp	Asp	Glu	Val	Val	Gly	Ile	Leu	Pro	Leu	Asp	Ser	Glu	Asp
		85					90					95			
Pro	Gly	Leu	Cys	Glu	Val	Val	Arg	Val	His	Glu	His	Tyr	Leu	Val	His
		100					105					110			
Lys	Pro	Glu	Lys	Val	Thr	Trp	Thr	Glu	Ala	Ala	Gly	Ser	Ile	Arg	Asp
	115					120					125				
Gly	Val	Arg	Ala	Tyr	Thr	Ala	Leu	His	Tyr	Leu	Ser	His	Leu	Ser	Pro
	130					135				140					
Gly	Lys	Ser	Val	Leu	Ile	Met	Asp	Gly	Ala	Ser	Ala	Phe	Gly	Thr	Ile
145				150					155					160	
Ala	Ile	Gln	Leu	Ala	His	His	Arg	Gly	Ala	Lys	Val	Phe	Gln	Gln	His
		165					170					175			
Ala	Ala	Leu	Lys	Ile	Ser	Ser	Ala	Leu	Lys	Asp	Ser	Asp	Leu	Pro	
		180					185					190			

<210> 414
 <211> 389
 <212> PRT
 <213> Homo sapiens

<400> 414

Met	Ala	Glu	Pro	Asp	Pro	Ser	His	Pro	Leu	Glu	Thr	Gln	Ala	Gly	Lys
1			5					10						15	
Val	Gln	Glu	Ala	Gln	Asp	Ser	Asp	Ser	Asp	Ser	Glu	Gly	Gly	Ala	Ala
		20					25					30			
Gly	Gly	Glu	Ala	Asp	Met	Asp	Phe	Leu	Arg	Asn	Leu	Phe	Ser	Gln	Thr
	35					40				45					
Leu	Ser	Leu	Gly	Ser	Gln	Lys	Glu	Arg	Leu	Leu	Asp	Glu	Leu	Thr	Leu
	50				55				60						
Glu	Gly	Val	Ala	Arg	Tyr	Met	Gln	Ser	Glu	Arg	Cys	Arg	Arg	Val	Ile
65				70					75					80	
Cys	Leu	Val	Gly	Ala	Gly	Ile	Ser	Thr	Ser	Ala	Gly	Ile	Pro	Asp	Phe
		85					90					95			
Arg	Ser	Pro	Ser	Thr	Gly	Leu	Tyr	Asp	Asn	Leu	Glu	Lys	Tyr	His	Leu
		100					105					110			
Pro	Tyr	Pro	Glu	Ala	Ile	Phe	Glu	Ile	Ser	Tyr	Phe	Lys	Lys	His	Pro
	115					120					125				
Glu	Pro	Phe	Phe	Ala	Leu	Ala	Lys	Glu	Leu	Tyr	Pro	Gly	Gln	Phe	Lys
	130					135				140					
Pro	Thr	Ile	Cys	His	Tyr	Phe	Met	Arg	Leu	Leu	Lys	Asp	Lys	Gly	Leu

145					150				155					160
Leu	Leu	Arg	Cys	Tyr	Thr	Gln	Asn	Ile	Asp	Thr	Leu	Glu	Arg	Ile
				165					170					175
Gly	Leu	Glu	Gln	Glu	Asp	Leu	Val	Glu	Ala	His	Gly	Thr	Phe	Tyr
			180					185					190	
Ser	His	Cys	Val	Ser	Ala	Ser	Cys	Arg	His	Glu	Tyr	Pro	Leu	Ser
		195					200					205		Trp
Met	Lys	Glu	Lys	Ile	Phe	Ser	Glu	Val	Thr	Pro	Lys	Cys	Glu	Asp
	210					215					220			Cys
Gln	Ser	Leu	Val	Lys	Pro	Asp	Ile	Val	Phe	Phe	Gly	Glu	Ser	Leu
225					230					235				240
Ala	Arg	Phe	Phe	Ser	Cys	Met	Gln	Ser	Asp	Phe	Leu	Lys	Val	Asp
				245					250					255
Leu	Leu	Val	Met	Gly	Thr	Ser	Leu	Gln	Val	Gln	Pro	Phe	Ala	Ser
			260					265					270	Leu
Ile	Ser	Lys	Ala	Pro	Leu	Ser	Thr	Pro	Arg	Leu	Leu	Ile	Asn	Lys
		275					280					285		Glu
Lys	Ala	Gly	Gln	Ser	Asp	Pro	Phe	Leu	Gly	Met	Ile	Met	Gly	Leu
	290					295				300				Gly
Gly	Gly	Met	Asp	Phe	Asp	Ser	Lys	Lys	Ala	Tyr	Arg	Asp	Val	Ala
305					310					315				Trp
Leu	Gly	Glu	Cys	Asp	Gln	Gly	Cys	Leu	Ala	Leu	Ala	Glu	Leu	Leu
			325						330					Gly
Trp	Lys	Lys	Glu	Leu	Glu	Asp	Leu	Val	Arg	Arg	Glu	His	Ala	Ser
			340					345					350	Ile
Asp	Ala	Gln	Ser	Gly	Ala	Gly	Val	Pro	Asn	Pro	Ser	Thr	Ser	Ala
		355					360					365		Ser
Pro	Lys	Lys	Ser	Pro	Pro	Pro	Ala	Lys	Asp	Glu	Ala	Arg	Thr	Thr
	370					375					380			Glu
Arg	Glu	Lys	Pro	Gln										
385														

<210> 415
 <211> 481
 <212> PRT
 <213> Homo sapiens

<400> 415

Met	Ser	Leu	Asn	Leu	Pro	Glu	Ala	Ser	Leu	Leu	Ser	Arg	Ala	Ser	Trp
1				5					10					15	
Pro	Glu	Gln	Ala	Lys	Glu	Pro	Arg	Arg	Glu	Gly	His	Thr	Asp	Lys	Gln
			20					25					30		
Gln	Thr	Glu	Asp	Val	Leu	Ala	Ala	Gly	Leu	Arg	Cys	Leu	Pro	His	Leu
		35					40					45			
Pro	Ala	Ile	Cys	Ala	Arg	Arg	Met	Ser	Pro	Ala	Phe	Arg	Ala	Met	Asp
	50					55					60				
Val	Glu	Pro	Arg	Ala	Lys	Gly	Val	Leu	Leu	Glu	Pro	Phe	Val	His	Gln
65					70				75					80	
Val	Gly	Gly	His	Ser	Cys	Val	Leu	Arg	Phe	Asn	Glu	Thr	Thr	Leu	Cys
			85					90						95	
Lys	Pro	Leu	Val	Pro	Arg	Glu	His	Gln	Phe	Tyr	Glu	Thr	Leu	Pro	Ala
		100					105						110		
Glu	Met	Arg	Lys	Phe	Thr	Pro	Gln	Tyr	Lys	Gly	Val	Val	Ser	Val	Arg
		115					120					125			

Phe Glu Glu Asp Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu
130 135 140
Lys Gly Asp His Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu
145 150 155 160
Pro Lys Ser Lys Leu Leu Arg Trp Thr Thr Asn Lys Lys His His Val
165 170 175
Leu Glu Thr Glu Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys
180 185 190
Glu Glu Lys Met Lys Ser His Lys Leu Glu Glu Glu Phe Glu Trp Leu
195 200 205
Lys Lys Ser Glu Val Leu Tyr Tyr Thr Val Glu Lys Lys Gly Asn Ile
210 215 220
Ser Ser Gln Leu Lys His Tyr Asn Pro Trp Ser Met Lys Cys His Gln
225 230 235 240
Gln Gln Leu Gln Arg Met Lys Glu Asn Ala Lys His Arg Asn Gln Tyr
245 250 255
Lys Phe Ile Leu Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys
260 265 270
Val Leu Asp Leu Lys Met Gly Thr Arg Gln His Gly Asp Asp Ala Ser
275 280 285
Glu Glu Lys Ala Ala Asn Gln Ile Arg Lys Cys Gln Gln Ser Thr Ser
290 295 300
Ala Val Ile Gly Val Arg Val Cys Gly Met Gln Val Tyr Gln Ala Gly
305 310 315 320
Ser Gly Gln Leu Met Phe Met Asn Lys Tyr His Gly Arg Lys Leu Ser
325 330 335
Val Gln Gly Phe Lys Glu Ala Leu Phe Gln Phe Phe His Asn Gly Arg
340 345 350
Tyr Leu Arg Arg Glu Leu Leu Gly Pro Val Leu Lys Lys Leu Thr Glu
355 360 365
Leu Lys Ala Val Leu Glu Arg Gln Glu Ser Tyr Arg Phe Tyr Ser Ser
370 375 380
Ser Leu Leu Val Ile Tyr Asp Gly Lys Glu Arg Pro Glu Val Val Leu
385 390 395 400
Asp Ser Asp Ala Glu Asp Leu Glu Asp Leu Ser Glu Glu Ser Ala Asp
405 410 415
Glu Ser Ala Gly Ala Tyr Ala Tyr Lys Pro Ile Gly Ala Ser Ser Val
420 425 430
Asp Val Arg Met Ile Asp Phe Ala His Thr Thr Cys Arg Leu Tyr Gly
435 440 445
Glu Asp Thr Val Val His Glu Gly Gln Asp Ala Gly Tyr Ile Phe Gly
450 455 460
Leu Gln Ser Leu Ile Asp Ile Val Thr Glu Ile Ser Glu Glu Ser Gly
465 470 475 480
Glu

<210> 416
<211> 354
<212> PRT
<213> Homo sapiens

<400> 416
Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro
1 5 10 15

Met	Pro	Thr	Cys	Arg	Val	Tyr	Gly	Thr	Val	Ala	His	Gln	Asp	Gly	His
			20					25					30		
Leu	Leu	Val	Leu	Gly	Gly	Cys	Gly	Arg	Ala	Gly	Leu	Pro	Leu	Asp	Thr
		35					40					45			
Ala	Glu	Thr	Leu	Asp	Met	Ala	Ser	His	Thr	Trp	Leu	Ala	Leu	Ala	Pro
	50					55					60				
Leu	Pro	Thr	Ala	Arg	Ala	Gly	Ala	Ala	Ala	Val	Val	Leu	Gly	Lys	Gln
65					70					75					80
Val	Leu	Val	Val	Gly	Gly	Val	Asp	Glu	Val	Gln	Ser	Pro	Val	Ala	Ala
				85					90					95	
Val	Glu	Ala	Phe	Leu	Met	Asp	Glu	Gly	Arg	Trp	Glu	Arg	Arg	Ala	Thr
			100					105					110		
Leu	Pro	Gln	Ala	Ala	Met	Gly	Val	Ala	Thr	Val	Glu	Arg	Asp	Gly	Met
		115					120					125			
Val	Tyr	Ala	Leu	Gly	Gly	Met	Gly	Pro	Asp	Thr	Ala	Pro	Gln	Ala	Gln
	130					135					140				
Val	Arg	Val	Tyr	Glu	Pro	Arg	Arg	Asp	Cys	Trp	Leu	Ser	Leu	Pro	Ser
145					150					155					160
Met	Pro	Thr	Pro	Cys	Tyr	Gly	Ala	Ser	Thr	Phe	Leu	His	Gly	Asn	Lys
				165					170					175	
Ile	Tyr	Val	Leu	Gly	Gly	Arg	Gln	Gly	Lys	Leu	Pro	Val	Thr	Ala	Phe
			180					185					190		
Glu	Ala	Phe	Asp	Leu	Glu	Ala	Arg	Thr	Trp	Thr	Arg	His	Pro	Ser	Leu
		195					200					205			
Pro	Ser	Arg	Arg	Ala	Phe	Ala	Gly	Cys	Ala	Met	Ala	Glu	Gly	Ser	Val
	210					215					220				
Phe	Ser	Leu	Gly	Gly	Leu	Gln	Gln	Pro	Gly	Pro	His	Asn	Phe	Tyr	Ser
225					230					235					240
Arg	Pro	His	Phe	Val	Asn	Thr	Val	Glu	Met	Phe	Asp	Leu	Glu	His	Gly
				245					250					255	
Ser	Trp	Thr	Lys	Leu	Pro	Arg	Ser	Leu	Arg	Met	Arg	Asp	Lys	Arg	Ala
			260					265					270		
Asp	Phe	Val	Val	Gly	Ser	Leu	Gly	Gly	His	Ile	Val	Ala	Ile	Gly	Gly
		275					280					285			
Leu	Gly	Asn	Gln	Pro	Cys	Pro	Leu	Gly	Ser	Val	Glu	Ser	Phe	Ser	Leu
	290					295					300				
Ala	Arg	Arg	Arg	Trp	Glu	Ala	Leu	Pro	Ala	Met	Pro	Thr	Ala	Arg	Cys
305					310					315					320
Ser	Cys	Ser	Ser	Leu	Gln	Ala	Gly	Pro	Arg	Leu	Phe	Val	Ile	Gly	Gly
				325					330					335	
Val	Ala	Gln	Gly	Pro	Ser	Gln	Ala	Val	Glu	Ala	Leu	Cys	Leu	Arg	Asp
			340					345					350		

Gly Val

<210> 417
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 417
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15
 Phe Val Phe Gln
 20

<210> 418
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 418
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15
 Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn Phe
 20 25 30
 Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn Thr Lys
 35 40 45
 Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val Gly Arg
 50 55 60
 Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser Phe Phe
 65 70 75 80
 Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser Glu Asp
 85 90 95
 Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu Val His
 100 105 110
 Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile Arg Asp
 115 120 125
 Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu Ser Pro
 130 135 140
 Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly Thr Ile
 145 150 155 160
 Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Ile Ser Thr Ala
 165 170 175
 Cys Ser Leu Glu Asp Lys Gln Cys Leu Glu Arg Phe Arg Pro Pro Ile
 180 185 190
 Ala Arg Val Ile Asp Val Ser Asn Gly Lys Val His Val Ala Glu Ser
 195 200 205
 Cys Leu Glu Glu Thr Gly Gly Leu Gly Val Asp Ile Val Leu Asp Ala
 210 215 220
 Gly Val Arg Leu Tyr Ser Lys Asp Asp Glu Pro Ala Val Lys Leu Gln
 225 230 235 240
 Leu Leu Pro His Lys His Asp Ile Ile Thr Leu Leu Gly Val Gly Gly
 245 250 255
 His Trp Val Thr Thr Glu Glu Asn Leu Gln Leu Asp Pro Pro Asp Ser
 260 265 270
 His Cys Leu Phe Leu Lys Gly Ala Thr Leu Ala Phe Leu Asn Asp Glu
 275 280 285
 Val Trp Asn Leu Ser Asn Val Gln Gln Gly Lys Tyr Leu Tyr Leu Lys
 290 295 300
 Gly Cys Asp Gly Glu Val Ile Asn Trp Cys Phe Gln Thr Ser Val Gly
 305 310 315 320

<210> 419
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 419

Met	Glu	Lys	Leu	Arg	Arg	Val	Leu	Ser	Gly	Gln	Asp	Asp	Glu	Glu	Gln
1				5					10					15	
Gly	Leu	Thr	Ala	Gln	Val	Leu	Asp	Ala	Ser	Ser	Leu	Ser	Phe	Asn	Thr
			20					25					30		
Arg	Leu	Lys	Trp	Phe	Ala	Ile	Cys	Phe	Val	Cys	Gly	Val	Phe	Phe	Ser
		35					40					45			
Ile	Leu	Gly	Thr	Gly	Leu	Leu	Trp	Leu	Pro	Gly	Gly	Ile	Lys	Leu	Phe
	50					55					60				
Ala	Val	Phe	Tyr	Thr	Leu	Gly	Asn	Leu	Ala	Ala	Leu	Ala	Ser	Thr	Cys
65					70					75					80
Phe	Leu	Met	Gly	Pro	Val	Lys	Gln	Leu	Lys	Lys	Met	Phe	Glu	Ala	Thr
				85					90					95	
Arg	Leu	Leu	Ala	Thr	Ile	Val	Met	Leu	Leu	Cys	Phe	Ile	Phe	Thr	Leu
			100					105					110		
Cys	Ala	Ala	Leu	Trp	Trp	His	Lys	Lys	Gly	Leu	Ala	Val	Leu	Phe	Cys
		115					120					125			
Ile	Leu	Gln	Phe	Leu	Ser	Met	Thr	Trp	Tyr	Ser	Leu	Ser	Tyr	Ile	Pro
	130					135					140				
Tyr	Ala	Arg	Asp	Ala	Val	Ile	Lys	Cys	Cys	Ser	Ser	Leu	Leu	Ser	
145					150					155					

<210> 420
 <211> 183
 <212> PRT
 <213> Homo sapiens

Met	Glu	Gln	Arg	Leu	Ala	Glu	Phe	Arg	Ala	Ala	Arg	Lys	Arg	Ala	Gly
1				5					10					15	
Leu	Ala	Ala	Gln	Pro	Pro	Ala	Ala	Ser	Gln	Gly	Ala	Gln	Thr	Pro	Gly
			20					25					30		
Glu	Lys	Ala	Glu	Ala	Ala	Ala	Thr	Leu	Lys	Ala	Ala	Pro	Gly	Trp	Leu
		35					40					45			
Lys	Arg	Phe	Leu	Val	Trp	Lys	Pro	Arg	Pro	Ala	Ser	Ala	Arg	Ala	Gln
	50					55					60				
Pro	Gly	Leu	Val	Gln	Glu	Ala	Ala	Gln	Pro	Gln	Gly	Ser	Thr	Ser	Glu
65				70					75					80	
Thr	Pro	Trp	Asn	Thr	Ala	Ile	Pro	Leu	Pro	Ser	Cys	Trp	Asp	Gln	Ser
			85					90					95		
Phe	Leu	Thr	Asn	Ile	Thr	Phe	Leu	Lys	Val	Leu	Leu	Trp	Leu	Val	Leu
			100					105					110		
Leu	Gly	Leu	Phe	Val	Glu	Leu	Glu	Phe	Gly	Leu	Ala	Tyr	Phe	Val	Leu
		115					120					125			
Ser	Leu	Phe	Tyr	Trp	Met	Tyr	Val	Gly	Thr	Arg	Gly	Pro	Glu	Glu	Lys
	130					135					140				
Lys	Glu	Gly	Glu	Lys	Ser	Ala	Tyr	Ser	Val	Phe	Asn	Pro	Gly	Cys	Glu
145				150						155				160	
Ala	Ile	Gln	Gly	Thr	Leu	Thr	Ala	Glu	Gln	Leu	Glu	Arg	Glu	Leu	Gln
				165					170					175	
Leu	Arg	Pro	Leu	Ala	Gly	Arg									
			180												

<210> 421
 <211> 143

<212> PRT
 <213> Homo sapiens

<400> 421
 Met Ala Ala Pro Arg Arg Gly Arg Gly Ser Ser Thr Val Leu Ser Ser
 1 5 10 15
 Val Pro Leu Gln Met Leu Phe Tyr Leu Ser Gly Thr Tyr Tyr Ala Leu
 20 25 30
 Tyr Phe Leu Ala Thr Leu Leu Met Ile Thr Tyr Lys Ser Gln Val Phe
 35 40 45
 Ser Tyr Pro His Arg Tyr Leu Val Leu Asp Leu Ala Leu Leu Phe Leu
 50 55 60
 Met Gly Ile Leu Glu Ala Val Arg Leu Tyr Leu Gly Thr Arg Gly Asn
 65 70 75 80
 Leu Thr Glu Ala Glu Arg Pro Leu Ala Ala Ser Leu Ala Leu Thr Ala
 85 90 95
 Gly Thr Ala Leu Leu Ser Ala His Phe Leu Leu Trp Gln Ala Leu Val
 100 105 110
 Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr Leu Leu Ala Leu His Gly
 115 120 125
 Leu Glu Ala Val Leu Gln Val Val Ala Ile Ala Ala Phe Thr Arg
 130 135 140

<210> 422
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 422
 Met Ser Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu
 1 5 10 15
 Pro Val Val Ser Ser Ser Arg Arg Leu Pro Arg Phe Val His Met Val
 20 25 30
 Ala Gly Val Ser Ser Lys Gln Glu Arg Ala Arg Ser Asn Thr Glu Ala
 35 40 45
 Leu Phe Lys Leu Cys Phe His His Ile Cys Gln Cys Leu Thr Asp Glu
 50 55 60
 His Lys Phe His Gly Gln Val Gln Phe
 65 70

<210> 423
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 423
 Met Pro Pro Phe Gly Gly His Pro Leu Ser Gln Glu Glu Asp Gly Ser
 1 5 10 15
 Gln Arg Cys Cys Cys Leu Ser Ser Leu Arg Ser Val Asp Asp Ser Asn
 20 25 30
 Gly Glu Thr Val Val Ile Met Ala Leu Phe Leu Ala Val Ser Tyr His
 35 40 45
 His Lys Thr Gln Ser Lys Arg Trp Pro Gly Leu Thr Pro Pro His Ser
 50 55 60

Ser	Leu	Leu	Cys	Arg	Pro	Leu	Gln	Leu	Ser	Phe	Leu	Val	Ile	Gln	Ser
65					70					75					80
Val	Arg	Met	Arg	Ala	Cys	Gly	Cys	Asp	Ser	Gly	His	Cys	Arg	Ile	Leu
				85					90					95	
Gly	Arg	Tyr	Ser	Leu	Leu	Gly	Trp	Ser	Gln	Gly	His	Arg	Ala	Arg	Gly
			100					105					110		
Arg	Gly	Gly	Val	Ser	Leu	Arg	Asp	Asn	Thr	Phe	Phe	Gln	Glu	Ala	Ser
		115					120					125			
Glu	Gly	Gln	Gly	Gln	Trp	Leu	Met	Pro	Val	Ile	Pro	Ala	Phe		
	130					135					140				

<210> 424
 <211> 149
 <212> PRT
 <213> Homo sapiens

Met	Leu	Ser	Ile	Leu	Lys	Pro	Arg	Arg	Ser	Gln	Glu	Trp	Arg	Thr	Ala
1				5					10					15	
Leu	Arg	Arg	Tyr	Cys	Cys	Pro	Thr	Asp	Leu	Gln	Ala	Pro	Arg	Ser	Pro
			20					25					30		
Val	Pro	Pro	Ile	Arg	Lys	Val	Gly	Ile	Ser	Asp	Val	Ile	Val	His	Ala
		35					40					45			
Asn	Leu	Ala	Thr	Ser	Leu	Lys	Lys	Asn	Thr	Cys	Asn	Cys	Gln	Ala	Asp
	50					55					60				
Leu	Leu	Ser	Trp	Arg	Ser	Trp	Val	Asn	Gly	Ile	Ser	Cys	His	Cys	Pro
65					70					75					80
Asn	Leu	Arg	Pro	Leu	Ser	Lys	Ser	Ile	Phe	Arg	Asp	Ser	Thr	Ser	Leu
				85					90					95	
Cys	Ser	Leu	Ser	Gln	Gln	Arg	Leu	Cys	Pro	Leu	His	Ser	Lys	Pro	Glu
			100					105					110		
Ala	Cys	Trp	Gly	Leu	Phe	Val	Ser	Val	His	Ala	His	Phe	Arg	Val	Gln
		115					120					125			
Ala	Gly	Gly	Arg	Gly	Asn	Arg	Val	Gly	Lys	Lys	Thr	Arg	Val	Ser	Arg
	130					135					140				
Asn	Asp	Glu	Thr	Leu											
145															

<210> 425
 <211> 75
 <212> PRT
 <213> Homo sapiens

Met	Tyr	Leu	Pro	Pro	Asn	Arg	Ser	Glu	Leu	Cys	Asn	Phe	Ala	Leu	Ser
1				5					10					15	
Leu	Asn	Leu	Tyr	Gly	Lys	Gly	Phe	Phe	Ser	Leu	Val	Glu	Lys	His	Asn
			20					25					30		
Ser	Arg	Asp	Leu	Glu	Asp	Arg	Ala	Ser	Ser	Gly	Pro	Ser	Leu	Ser	Ser
		35					40					45			
Pro	Ser	His	Pro	Asp	Trp	Gly	Tyr	Ile	Val	Leu	Ile	Leu	Val	Ala	Thr
	50					55					60				
Leu	Gly	Glu	Leu	Asp	Thr	Gln	Val	Gly	Gly	His					
65					70					75					

<210> 426
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 426
 Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys Pro Asn
 1 5 10 15
 Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Ile Gln Gln Ser
 20 25 30
 Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp Thr Gln
 35 40 45
 Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr Ser Ser
 50 55 60
 Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr Glu Trp
 65 70 75 80
 Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr Pro Glu
 85 90 95
 Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His Cys Leu
 100 105 110
 Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His Leu Phe
 115 120 125
 Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr Ile Leu
 130 135 140
 Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Phe Ile
 145 150 155 160
 Ile Val Phe Ile Leu Ile Phe Phe
 165

<210> 427
 <211> 160
 <212> PRT
 <213> Homo sapiens

<400> 427
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Val Ala His Asn Pro Arg Pro Arg Ile Ala Gln Arg Gly Arg
 20 25 30
 Asn Thr Ser Arg Met Ala Glu Asp Thr Ser Pro Asn Met Asn Asp Asn
 35 40 45
 Ile Leu Leu Pro Val Arg Asn Asn Asp Gln Ala Leu Gly Leu Thr Gln
 50 55 60
 Cys Met Leu Gly Cys Val Ser Trp Phe Thr Cys Phe Ala Cys Ser Leu
 65 70 75 80
 Arg Thr Gln Ala Gln Gln Val Leu Phe Asn Thr Cys Arg Asp Arg Val
 85 90 95
 Ser Pro Cys Cys Pro Gly Trp Ser Gln Thr Pro Val Ile Leu Pro Pro
 100 105 110
 Gln Pro Ser Glu Val Leu Gly Leu Gln Met Gln Ala Ala Val Pro Glu
 115 120 125
 Ala His Gly Glu Asp Arg His Ser Ala Pro Leu Cys Phe Arg Cys Val
 130 135 140

Pro Gly Pro Cys Pro Val Pro Gly Gly Gly Ile Pro Gly Pro Trp His
 145 150 155 160

<210> 428
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 428
 Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe
 1 5 10 15
 Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser
 20 25 30
 Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg
 35 40 45
 Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro
 50 55 60
 Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg
 65 70 75 80
 Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser
 85 90

<210> 429
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 429
 Met Lys Ala Ser Gly Pro Asp Leu Ser Asp Gly Leu His Cys Pro Ser
 1 5 10 15
 Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala Pro
 20 25 30
 Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu Cys
 35 40 45
 Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser His
 50 55 60
 Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr Asp
 65 70 75 80
 Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp
 85 90 95

<210> 430
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 430
 Met Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu
 1 5 10 15
 Pro Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His
 20 25 30
 Cys Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu
 35 40 45
 Leu Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val

50		55		60
Val Phe Leu Ser Phe	Leu Ile Phe Ser Thr	Ser Phe Tyr Ile Ser Asn		
65	70	75	80	
Ala Glu Gln Pro Phe	Phe Lys Glu Pro Pro	Thr Glu Ala Ala Lys Glu		
	85	90	95	
Leu Ser Leu				

<210> 431
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 431
 Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe Leu
 1 5 10 15
 Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp Gln
 20 25 30
 Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys Ala
 35 40 45
 Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val Cys
 50 55 60
 Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys Ile
 65 70 75 80
 Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val Met
 85 90 95
 Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys Glu
 100 105 110
 Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys
 115 120

<210> 432
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 432
 Met Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser
 1 5 10 15
 Leu Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys
 20 25 30
 Ser Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr
 35 40 45
 Gln Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln
 50 55 60
 Glu Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp
 65 70 75 80
 Arg Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile
 85 90 95
 Gly Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln
 100 105 110
 Glu Arg Thr Ser Ser Leu
 115

<210> 433

<211> 49
 <212> PRT
 <213> Homo sapiens

<400> 433
 Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro
 1 5 10 15
 Val Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe
 20 25 30
 Thr Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln
 35 40 45
 His

<210> 434
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 434
 Met Leu Ala Leu Phe His Phe His Leu Pro Pro Trp Asp Asp Ala Val
 1 5 10 15
 Arg Arg Pro Ser Val Asp Ala Ser Pro Ser Thr Leu Asn Phe Pro Asp
 20 25 30
 Ala Glu Leu Tyr Ala Ser Ile Phe Leu Cys Cys Met Ala Pro Gly Glu
 35 40 45
 Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala Asn Gly
 50 55 60
 Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Ala Cys Val Trp His
 65 70 75 80
 Glu Asn Ser Gln Glu Glu Arg Lys Tyr
 85

<210> 435
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 435
 Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys Ser
 1 5 10 15
 Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val Phe
 20 25 30
 Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val Glu
 35 40 45
 Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu Val
 50 55 60
 Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly Asp
 65 70 75 80
 Leu Leu Pro Val Asn Arg Ile
 85

<210> 436
 <211> 45
 <212> PRT

<213> Homo sapiens

<400> 436

```
Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
1          5          10          15
Asp Gly Pro Gln Ser Gln Thr Pro Glu Asp Cys Pro Ala Arg Pro Glu
          20          25          30
His Gln Gln Asp Gly Arg Gly His Leu Pro Lys His Glu
          35          40          45
```

<210> 437

<211> 65

<212> PRT

<213> Homo sapiens

<400> 437

```
Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile His Ser His
1          5          10          15
Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln Trp Leu Pro
          20          25          30
Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys Ser Cys Arg
          35          40          45
Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser Phe Leu Ile
          50          55          60
Ser
65
```

<210> 438

<211> 112

<212> PRT

<213> Homo sapiens

<400> 438

```
Met Arg Lys Lys Cys Lys Cys Phe Thr Ile Lys Lys Thr Asn Thr Tyr
1          5          10          15
Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln Lys Glu Ala Ile Ser Ile
          20          25          30
Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro Leu Trp Val Thr Arg Leu
          35          40          45
Ser Asp Leu Val Phe Ser Lys Glu Lys Ala His Gly Met Ile Pro Leu
          50          55          60
Leu Gly Ser His Arg Glu Lys Lys Thr Ser Lys Glu Met Lys Thr Ser
65          70          75          80
Ser Arg Asn Leu Arg Tyr Phe Ile Val Cys Arg Asp Ala Ser Ser Tyr
          85          90          95
Thr Pro Gln Ser Leu Ile Ser Gly Tyr Ile Gly Pro Cys Gln His Gln
          100          105          110
```

<210> 439

<211> 110

<212> PRT

<213> Homo sapiens

<400> 439

Met	Val	Phe	Gly	Ala	Met	Val	Leu	Leu	Val	Gly	Leu	Glu	Glu	Leu	Thr
1				5					10					15	
Asn	Ile	Arg	Asn	Val	Glu	Arg	Leu	Lys	Lys	Asp	Leu	Arg	Ala	Ser	Tyr
			20					25					30		
Cys	Leu	Ile	Asp	Ser	Phe	Leu	Gly	Asp	Ser	Glu	Leu	Ile	Gly	Asp	Leu
	35						40					45			
Thr	Gln	Cys	Val	Asp	Cys	Val	Ile	Pro	Pro	Glu	Gly	Ser	Leu	Leu	Gln
	50					55					60				
Ile	Ser	Ser	Tyr	Leu	Tyr	Leu	Asn	Thr	Ala	Leu	Val	Asp	Leu	Pro	Gly
65					70					75					80
Val	Ala	Ala	Ser	Gln	Ala	Cys	Asp	Ser	Gln	Gln	Val	Thr	Trp	Leu	Leu
				85					90					95	
Tyr	Val	Ala	Asn	Gly	Ala	Tyr	Ser	Ala	Cys	Asn	Arg	Pro	Gly		
			100					105					110		

<210> 440
 <211> 121
 <212> PRT
 <213> Homo sapiens

Thr	Ser	Ser	Ser	Gly	Ala	Glu	Val	Thr	Met	Ala	Ala	Ala	Leu	Ala	Arg
1				5					10					15	
Leu	Gly	Leu	Arg	Pro	Val	Lys	Gln	Val	Arg	Val	Gln	Phe	Cys	Pro	Phe
			20				25					30			
Glu	Lys	Asn	Val	Glu	Ser	Thr	Arg	Thr	Phe	Leu	Gln	Thr	Val	Ser	Ser
	35					40					45				
Glu	Lys	Val	Arg	Ser	Thr	Asn	Leu	Asn	Cys	Ser	Val	Ile	Ala	Asp	Val
	50				55					60					
Arg	His	Asp	Gly	Ser	Glu	Pro	Cys	Val	Asp	Val	Leu	Phe	Gly	Asp	Gly
65					70				75						80
His	Arg	Leu	Ile	Met	Arg	Gly	Ala	His	Leu	Thr	Ala	Leu	Glu	Met	Leu
			85					90						95	
Thr	Ala	Phe	Ala	Ser	His	Ile	Arg	Ala	Arg	Asp	Ala	Ala	Gly	Ser	Gly
			100				105						110		
Asp	Lys	Pro	Gly	Ala	Asp	Thr	Gly	Arg							
		115					120								

<210> 441
 <211> 99
 <212> PRT
 <213> Homo sapiens

Met	Leu	Ala	Arg	Ala	Thr	Phe	Arg	Ala	Ala	Ser	Ala	Pro	Thr	Leu	Val
1				5					10					15	
Ala	Arg	Arg	Gly	Phe	Gln	Ser	Thr	Arg	Ala	Gln	Met	Ala	Ser	Pro	Tyr
			20					25				30			
His	Tyr	Pro	Glu	Gly	Pro	Arg	Ser	Asn	Leu	Pro	Phe	Asp	Pro	Leu	Lys
	35					40					45				
Lys	Gly	Phe	Ala	Phe	Lys	Tyr	Trp	Gly	Phe	Met	Gly	Thr	Gly	Phe	Ala
	50				55					60					
Leu	Pro	Phe	Leu	Leu	Ala	Val	Trp	Gln	Thr	Glu	Gln	Ala	Val	Asn	Ala
65					70				75						80

Leu Arg His Gly Val Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala
85 90 95
Phe Val Asp

<210> 442
<211> 183
<212> PRT
<213> Homo sapiens

<400> 442
Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
1 5 10 15
Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
20 25 30
Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
35 40 45
Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
50 55 60
His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
65 70 75 80
Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu
85 90 95
Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu
100 105 110
Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val
115 120 125
Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp
130 135 140
Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser
145 150 155 160
Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu
165 170 175
Leu Pro Lys Lys Lys Lys Lys
180

<210> 443
<211> 94
<212> PRT
<213> Homo sapiens

<400> 443
Met Ser Asp Glu Ala Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr
1 5 10 15
Pro Glu Glu Pro Phe Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr
20 25 30
Cys Pro Ser Glu Glu Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys
35 40 45
Gln Leu Ser Ser Cys His Arg Thr Asp Pro Leu His Arg Phe His Thr
50 55 60
Asn Arg Trp Asn Leu Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu
65 70 75 80
Gly Ser Glu Glu Leu Phe Ser Ser Val Cys Trp Arg Ser Arg
85 90

<210> 444
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 444
 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu
 1 5 10 15
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly
 20 25 30
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly
 35 40 45
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly
 50 55 60
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
 65 70 75 80
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
 85 90 95
 Met Ala Ile Gly Met Gly Ile Arg Cys
 100 105

<210> 445
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 445
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Val Ala His Asn Pro Arg Pro Arg Arg Ile Ala Gln Arg Gly Arg
 20 25 30
 Asn Thr Ser Arg Met Ala Glu Asp Thr Ser Pro Asn Met Asn Asp Asn
 35 40 45
 Ile Leu Leu Pro Val Arg Asn Asn Asp Gln Ala Leu Gly Leu Thr Gln
 50 55 60
 Cys Met Leu Gly Cys Val Ser Trp Phe Thr Cys Phe Ala Cys Ser Leu
 65 70 75 80
 Arg Thr Gln Ala Gln Gln Val Leu Phe Asn Thr Cys Arg Cys Lys Leu
 85 90 95
 Leu Cys Gln Lys Leu Met Glu Lys Thr Gly Ile Leu Leu Leu Cys Ala
 100 105 110
 Phe Gly Val Ser Gln Gly Pro Ala Gln Ser Gln Val Glu Val Ser Leu
 115 120 125
 Gly Pro Gly Thr Asp Tyr Arg Thr Leu Gly Lys Thr Leu His Cys His
 130 135 140
 Val Thr Gln Phe Pro His Leu Pro Asp Gly Cys Cys Cys Glu Asn Tyr
 145 150 155 160
 Glu Met Lys

<210> 446
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 446

```
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro
1          5          10          15
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg
          20          25          30
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser
          35          40          45
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro
          50          55          60
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu
65          70          75          80
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
          85          90          95
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
          100          105          110
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
          115          120          125
```

<210> 447

<211> 96

<212> PRT

<213> Homo sapiens

<400> 447

```
Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val Lys Ala Cys Arg
1          5          10          15
Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro Gln Arg Gln Lys
          20          25          30
Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser Gln Gln Asn Met
          35          40          45
Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly Leu Phe Cys Ala
          50          55          60
Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe Trp Cys Arg Pro
65          70          75          80
Lys Thr Thr Ile Ile Ile Ile Asp Tyr Ser Ser Pro Arg Gln Cys Leu
          85          90          95
```

<210> 448

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 114

<223> Xaa = Glu,Val

<220>

<221> UNSURE

<222> 113

<223> Xaa = His,Gln

<220>

<221> UNSURE

<222> 115

<223> Xaa = Ile,Val

<400> 448

Met	Gly	Lys	Ile	Ala	Leu	Gln	Leu	Lys	Ala	Thr	Leu	Glu	Asn	Ile	Thr
1				5					10					15	
Asn	Leu	Arg	Pro	Val	Gly	Glu	Asp	Phe	Arg	Trp	Tyr	Leu	Lys	Met	Lys
			20					25					30		
Cys	Gly	Asn	Cys	Gly	Glu	Ile	Ser	Asp	Lys	Trp	Gln	Tyr	Ile	Arg	Leu
		35					40					45			
Met	Asp	Ser	Val	Ala	Leu	Lys	Gly	Gly	Arg	Gly	Ser	Ala	Ser	Met	Val
	50					55					60				
Gln	Lys	Cys	Lys	Leu	Cys	Ala	Arg	Glu	Asn	Ser	Ile	Glu	Ile	Leu	Ser
65					70					75					80
Ser	Thr	Ile	Lys	Pro	Tyr	Asn	Ala	Glu	Asp	Asn	Glu	Asn	Phe	Lys	Thr
				85					90					95	
Ile	Val	Glu	Phe	Glu	Cys	Arg	Gly	Leu	Glu	Pro	Val	Asp	Phe	Gln	Pro
			100					105					110		
Xaa	Xaa	Xaa	Leu	Leu	Leu	Lys	Val	Trp	Ser	Gln	Gly	Gln	Pro	Ser	Val
	115						120					125			
Thr	Leu	Ile	Cys	Arg	Arg	Arg	Thr	Gly	Thr	Asp	Tyr	Asp	Glu	Lys	Ala
	130					135					140				
Gln	Glu	Ser	Val	Gly	Ile	Tyr	Glu	Val	Thr	His	Gln	Phe	Val	Lys	Cys
145					150					155					160

<210> 449

<211> 117

<212> PRT

<213> Homo sapiens

<400> 449

Met	Asp	Ser	Leu	Ala	Ala	Gly	Glu	Leu	Asn	Ala	Ser	His	Gln	Pro	Trp
1				5					10					15	
Val	Pro	Glu	Phe	Val	Ala	Tyr	Trp	Arg	Lys	Thr	His	Gln	Asp	His	Leu
			20					25					30		
Cys	Ser	Leu	His	Ser	Arg	Ala	Phe	Gly	Leu	Leu	Asp	Ala	Arg	Val	Thr
		35					40					45			
Trp	Ala	Leu	Arg	Arg	Ala	Pro	Glu	Pro	Val	Pro	Gly	Lys	Asp	Arg	Leu
	50					55					60				
Leu	Leu	Ala	Ala	Phe	Pro	Ala	Glu	Ala	Ser	Pro	Val	Asp	Thr	Ala	Ser
65					70					75					80
Val	Ser	Val	Tyr	Gly	Arg	Ala	Pro	Arg	Tyr	Met	His	Lys	Gly	Val	Lys
				85					90					95	
Lys	Cys	Val	Cys	Thr	Pro	Val	Ser	Lys	Asn	Ser	Thr	Ala	Trp	Leu	Leu
			100					105					110		
Leu	Gly	Gly	Ile	Ser											
		115													

<210> 450

<211> 335

<212> PRT

<213> Homo sapiens

<400> 450

Met	Cys	Cys	Gln	Val	Cys	Glu	Ala	Val	Arg	Ser	Gly	Asn	Glu	Glu	Val
1				5					10				15		
Leu	Ala	Asp	Val	Arg	Thr	Ile	Val	Asn	Gln	Ile	Ser	Tyr	Thr	Pro	Gln
		20						25					30		
Asp	Pro	Arg	Asp	Leu	Cys	Gly	Arg	Ile	Leu	Thr	Thr	Cys	Tyr	Met	Ala
		35					40					45			
Ser	Lys	Asn	Ser	Ser	Gln	Glu	Thr	Cys	Thr	Arg	Ala	Arg	Glu	Leu	Ala
	50					55					60				
Gln	Gln	Ile	Gly	Ser	His	His	Ile	Ser	Leu	Asn	Ile	Asp	Pro	Ala	Val
65					70					75					80
Lys	Ala	Val	Met	Gly	Ile	Phe	Ser	Leu	Val	Thr	Gly	Lys	Ser	Pro	Leu
			85						90					95	
Phe	Ala	Ala	His	Gly	Gly	Ser	Ser	Arg	Glu	Asn	Leu	Ala	Leu	Gln	Asn
			100					105					110		
Val	Gln	Ala	Arg	Ile	Arg	Met	Val	Leu	Ala	Tyr	Leu	Phe	Ala	Gln	Leu
		115					120					125			
Ser	Leu	Trp	Ser	Arg	Gly	Val	His	Gly	Gly	Leu	Leu	Val	Leu	Gly	Ser
	130					135						140			
Ala	Asn	Val	Asp	Glu	Ser	Leu	Leu	Gly	Tyr	Leu	Thr	Lys	Tyr	Asp	Cys
145					150				155					160	
Ser	Ser	Ala	Asp	Ile	Asn	Pro	Ile	Gly	Gly	Ile	Ser	Lys	Thr	Asp	Leu
			165					170						175	
Arg	Ala	Phe	Val	Gln	Phe	Cys	Ile	Gln	Arg	Phe	Gln	Leu	Pro	Ala	Leu
		180						185					190		
Gln	Ser	Ile	Leu	Leu	Ala	Pro	Ala	Thr	Ala	Glu	Leu	Glu	Pro	Leu	Ala
	195						200					205			
Asp	Gly	Gln	Val	Ser	Gln	Thr	Asp	Glu	Glu	Asp	Met	Gly	Met	Thr	Tyr
	210					215					220				
Ala	Glu	Leu	Ser	Val	Tyr	Gly	Lys	Leu	Arg	Lys	Val	Ala	Lys	Met	Gly
225					230				235					240	
Pro	Tyr	Ser	Met	Phe	Cys	Lys	Leu	Leu	Gly	Met	Trp	Arg	His	Ile	Cys
			245						250					255	
Thr	Pro	Arg	Gln	Val	Ala	Asp	Lys	Val	Lys	Arg	Phe	Phe	Ser	Lys	Tyr
		260						265					270		
Ser	Met	Asn	Arg	His	Lys	Met	Thr	Thr	Leu	Thr	Pro	Ala	Tyr	His	Ala
		275					280					285			
Glu	Asn	Tyr	Ser	Pro	Glu	Asp	Asn	Arg	Phe	Asp	Leu	Arg	Pro	Phe	Leu
	290					295					300				
Tyr	Asn	Thr	Ser	Trp	Pro	Trp	Gln	Phe	Arg	Cys	Ile	Glu	Asn	Gln	Val
305					310					315					320
Leu	Gln	Leu	Glu	Arg	Ala	Glu	Pro	Gln	Ser	Leu	Asp	Gly	Val	Asp	
			325						330					335	

<210> 451

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 76

<223> Xaa = Lys,Asn

<400> 451